

<220>

<221> CDS

<222> 154..366

<400> 3205

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awaaaaggca aaagakttgt gttttttata caccatatgc agtakttcct gcccttttca      60
tcaaggctac ctgaacgtgt ctggtgaacc agggctggaa ggraccgctg ktgccgcctg      120
aagtgaaya ctctgtatatt ccacaaggat cac atg gac ctg cga acc cat gtg      174
                               Met Asp Leu Arg Thr His Val
                               1           5
aac gcc atc gcc ctg caa ggc tgt gag gtg gcc ccg ggc ttt ggg ccc      222
Asn Ala Ile Ala Leu Gln Gly Cys Glu Val Ala Pro Gly Phe Gly Pro
      10           15           20
cga cac cca ttt gcc ttc agg atc ctg cgc aac cgg cag gag gtg gcc      270
Arg His Pro Phe Ala Phe Arg Ile Leu Arg Asn Arg Gln Glu Val Ala
      25           30           35
atc ttg gag gca agc tgt tca gag gwc atg ggt cgc tgg ctc ggg ctg      318
Ile Leu Glu Ala Ser Cys Ser Glu Xaa Met Gly Arg Trp Leu Gly Leu
      40           45           50           55
ctg ctg gtg gag atg ggc tcc aga gtc act ccg gag gcg ctg cac tat      366
Leu Leu Val Glu Met Gly Ser Arg Val Thr Pro Glu Ala Leu His Tyr
      60           65           70
ga
ga

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<210> 3206

<211> 385

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 189..383

<400> 3206

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aggtctgcca gcctggactg gaagcgtgca acactccaga gtcgtaggag tgaacactgc      60
acaggaatct ctgcccattc caggagaaac caaacttggg gaaaatgttt gcggtccact      120
tgatggcatt ttacttcagc aagctgaagt aggaccagat caagaaggat gacaggttcc      180
tgtatcac atg cgd ctc tcc gat gac acc ctt ttg gac atc atg agg cgg      230
      Met Arg Leu Ser Asp Asp Thr Leu Leu Asp Ile Met Arg Arg
      1           5           10
ttc cgg gct gag atg gag aag ggc ctg gca aag gac acc aac ccc acg      278
Phe Arg Ala Glu Met Glu Lys Gly Leu Ala Lys Asp Thr Asn Pro Thr
      15           20           25           30
gct gca gtg aag atg ttg ccc acc ttc gtc arg gcc att ccc gat kgt      326
Ala Ala Val Lys Met Leu Pro Thr Phe Val Xaa Ala Ile Pro Asp Xaa
      35           40           45
tcc gaa aat ggg gag ttc ctt tcc ctg gat ctc gga ggg tcc aag ttc      374
Ser Glu Asn Gly Glu Phe Leu Ser Leu Asp Leu Gly Gly Ser Lys Phe
      50           55           60
cga gtg ctg aa
Arg Val Leu
      65

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<210> 3207
 <211> 331
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 19..330

<400> 3207
 caaacagaga gccaaatc atg agt gaa ctc cca ttc aca att gct tca aag 51
 Met Ser Glu Leu Pro Phe Thr Ile Ala Ser Lys
 1 5 10
 aga ata aaa tac cta gga atc caa ctt aca agg gat gtg aag gac ctc 99
 Arg Ile Lys Tyr Leu Gly Ile Gln Leu Thr Arg Asp Val Lys Asp Leu
 15 20 25
 ttc aag gag aac tac aaa cca ctg ctc aag gaa ata aaa gag gac aca 147
 Phe Lys Glu Asn Tyr Lys Pro Leu Leu Lys Glu Ile Lys Glu Asp Thr
 30 35 40
 aac aaa tgg aag aac att cca tgc tcg tgg gta gga aga atc aat atc 195
 Asn Lys Trp Lys Asn Ile Pro Cys Ser Trp Val Gly Arg Ile Asn Ile
 45 50 55
 gtg aaa atg gcc ata ctg ccc aag gta att tac aga ttc aat gcc atc 243
 Val Lys Met Ala Ile Leu Pro Lys Val Ile Tyr Arg Phe Asn Ala Ile
 60 65 70 75
 ccc atc aag cta cca atg act ttc ttc aca gaa ttg gaa aaa aac tac 291
 Pro Ile Lys Leu Pro Met Thr Phe Phe Thr Glu Leu Glu Lys Asn Tyr
 80 85 90
 ttt aaa gtt cat atg gaa tca aaa aag agc cca cat cgc c 331
 Phe Lys Val His Met Glu Ser Lys Lys Ser Pro His Arg
 95 100

<210> 3208
 <211> 213
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 2..211

<400> 3208
 c atg tgc cct agt ctg gaa gag gct ccc agt gtc aag ggg act ctg ccc 49
 Met Cys Pro Ser Leu Glu Glu Ala Pro Ser Val Lys Gly Thr Leu Pro
 1 5 10 15
 tgc tca gga caa cag cag cct ttc ccg ttt gga gcc tca aac atc cca 97
 Cys Ser Gly Gln Gln Gln Pro Phe Pro Phe Gly Ala Ser Asn Ile Pro
 20 25 30
 cta ctc ctg ggc agg agc aga aag gtg gct cga ggt gca ccg gtc ctg 145
 Leu Leu Leu Gly Arg Ser Arg Lys Val Ala Arg Gly Ala Pro Val Leu
 35 40 45

tgg cca ttt ctc act tgg ata aac cct gca ctg tcc atc tgt gac ccc 193
 Trp Pro Phe Leu Thr Trp Ile Asn Pro Ala Leu Ser Ile Cys Asp Pro
 50 55 60
 tta gga tcc tgc gga tgg ca 213
 Leu Gly Ser Cys Gly Trp
 65 70

<210> 3209
 <211> 301
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 144..299

<400> 3209
 cttttcattt agtagatatt cataagtcac atgtcagaat tgaaattata gtatatttta 60
 ccttgtagag ttctttttaa cagaatccta aaaataagaa ttatttagta tgtcaagagt 120
 taaaaaaaat cactactcat tta atg tct aat cta aaa tac aac agg cta aca 173
 Met Ser Asn Leu Lys Tyr Asn Arg Leu Thr
 1 5 10
 tct agc tca ggg atc agc aaa cct ttt ttg tgg ctt tgt ggg cca cgt 221
 Ser Ser Ser Gly Ile Ser Lys Pro Phe Leu Trp Leu Cys Gly Pro Arg
 15 20 25
 aca gtc tct gtc tca ttc ttt tgt ttt tgc atg tgt att tat gtt tat 269
 Thr Val Ser Val Ser Phe Phe Cys Phe Cys Met Cys Ile Tyr Val Tyr
 30 35 40
 aaa ctc ttt aaa aat gta aga aac agc cag at 301
 Lys Leu Phe Lys Asn Val Arg Asn Ser Gln
 45 50

<210> 3210
 <211> 345
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 168..344

<400> 3210
 caacaacaaa aaaaactggt accgctccac aacccttctt gaatatcggc aggcaagtat 60
 ttatcctaca actgcattgg gttggagcag tggagagtgg gctggagaag ctgaccaga 120
 gctcctaatt caagagactt catgtggcag aggtttgggt atagcgg atg ctg aaa 176
 Met Leu Lys
 1
 aca agg aga ata act gaa agt cta gaa cat ttc ctg tat cca gat gag 224
 Thr Arg Arg Ile Thr Glu Ser Leu Glu His Phe Leu Tyr Pro Asp Glu
 5 10 15
 cca agt aca agc cat ctg gca tcc act tcc cat cca ggt gat cag agg 272
 Pro Ser Thr Ser His Leu Ala Ser Thr Ser His Pro Gly Asp Gln Arg

20	25	30	35	
ata cgt ctc tgc aga aac cac caa ggt ctc aga aaa aaa agc ctg cac				320
Ile Arg Leu Cys Arg Asn His Gln Gly Leu Arg Lys Lys Ser Leu His				
	40	45	50	
aat ctg rca ttt agg agt ccc cag c				345
Asn Leu Xaa Phe Arg Ser Pro Gln				
	55			

<210> 3211
 <211> 198
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 38..196

<400> 3211		
aagtaattta acaacagatt tgctaattaa aaaaaaa atg aaa aaa aaa atc tta		55
	Met Lys Lys Lys Ile Leu	
	1 5	
cca gca gtt tgt aaa ggt ctg gaa tca cag ttg gca tcc ttt att crg		103
Pro Ala Val Cys Lys Gly Leu Glu Ser Gln Leu Ala Ser Phe Ile Xaa		
	10 15 20	
gtc tct tct ctc caa cgt aca ctt aaa att ggt gcc gag cag gga tat		151
Val Ser Ser Leu Gln Arg Thr Leu Lys Ile Gly Ala Glu Gln Gly Tyr		
	25 30 35	
aac ctg cag tta agt gaa aag aaa atc cag cct ccc cct cca aaa aa		198
Asn Leu Gln Leu Ser Glu Lys Lys Ile Gln Pro Pro Pro Pro Lys		
	40 45 50	

<210> 3212
 <211> 405
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 199..405

<400> 3212		
tgtttgctaa atgaatgaat gaatgacaaa caaataagta aacatctttt taataaayag		60
aattaaaagg aagtcaaata atttccaacg agatagatgc ttagaaatta aagtatttta		120
cattgatata tgtcctgctt ttgtaactaa ttgttaaggg gcctttgtgt atttcagcag		180
ggagttcaat accttgaa atg tat ctt gac cat gga tac ctt gat ttg aga		231
	Met Tyr Leu Asp His Gly Tyr Leu Asp Leu Arg	
	1 5 10	
aag tcc tct agt ttg agt gga agt gat tat tgc cat tat agt tta tca		279
Lys Ser Ser Ser Leu Ser Gly Ser Asp Tyr Cys His Tyr Ser Leu Ser		
	15 20 25	
cac cta gat ttc aaa gta ggt cag gtg aaa aga tgt aag ggc agt gtg		327
His Leu Asp Phe Lys Val Gly Gln Val Lys Arg Cys Lys Gly Ser Val		

30	35	40	
act gta act ggg aga gca gag tct aaa atc tca cct ttt act ttc kcc			375
Thr Val Thr Gly Arg Ala Glu Ser Lys Ile Ser Pro Phe Thr Phe Xaa			
45	50	55	
tta atg cag tgt ctc aga aat gaa cac ttt			405
Leu Met Gln Cys Leu Arg Asn Glu His Phe			
60	65		

<210> 3213
 <211> 385
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 88..384

<400> 3213			
tcaaagcaat ttcttaatca gtttctggag caggaaactc atctcttcag cgccattaac	60		
agccatttgc tgactgcgsa accttgg atg grc gat ctt gga acc atg att agc	114		
Met Xaa Asp Leu Gly Thr Met Ile Ser			
1	5		
cag att gaa gag atc gaa cgt cat ctt gct tac ctt aaa tgg att tca	162		
Gln Ile Glu Glu Ile Glu Arg His Leu Ala Tyr Leu Lys Trp Ile Ser			
10	15	20	25
caa att gaa gaa cta agt gat aac att cag caa tat ctg atg acc aat	210		
Gln Ile Glu Glu Leu Ser Asp Asn Ile Gln Gln Tyr Leu Met Thr Asn			
30	35	40	
aat gta ccg gag gca gcc tcc act cta gtg tct atg gca gaa ctt gac	258		
Asn Val Pro Glu Ala Ala Ser Thr Leu Val Ser Met Ala Glu Leu Asp			
45	50	55	
att aaa ctt cag gaa tca tct tgt act cat ctt ctt ggt ttc atg aga	306		
Ile Lys Leu Gln Glu Ser Ser Cys Thr His Leu Leu Gly Phe Met Arg			
60	65	70	
gcc aca gtt aaa ttc tgg cat aaa att ctc aag gac aag ctt aca agt	354		
Ala Thr Val Lys Phe Trp His Lys Ile Leu Lys Asp Lys Leu Thr Ser			
75	80	85	
gat ttt gag gaa att tta gca cag ctt cat t	385		
Asp Phe Glu Glu Ile Leu Ala Gln Leu His			
90	95		

<210> 3214
 <211> 410
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 64..408

<400> 3214	
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gtc atg gcg gca gct gga ata gca gcc att ggc cct gcc aaa gaa ctc	108
Met Ala Ala Ala Gly Ile Ala Ala Ile Gly Pro Ala Lys Glu Leu	
1 5 10 15	
gaa gct gag agg tcc ctt atg tca tct cct gag gat cta acc aag gac	156
Glu Ala Glu Arg Ser Leu Met Ser Ser Pro Glu Asp Leu Thr Lys Asp	
20 25 30	
ttt gaa gag tta aag gct gaa gag gtc gat gta aca aag gac atc aag	204
Phe Glu Glu Leu Lys Ala Glu Glu Val Asp Val Thr Lys Asp Ile Lys	
35 40 45	
cct cag ctg gag cta atc gaa gac gaa gag aaa ctg aag gaa act gag	252
Pro Gln Leu Glu Leu Ile Glu Asp Glu Glu Lys Leu Lys Glu Thr Glu	
50 55 60	
cca gtc gaa gcc tac gtc atc cag aag gag aga gaa gtc acc aaa ggt	300
Pro Val Glu Ala Tyr Val Ile Gln Lys Glu Arg Glu Val Thr Lys Gly	
65 70 75	
cct gcc gag tcc cct gat gag gga atc act acc act gaa ggg gag ggc	348
Pro Ala Glu Ser Pro Asp Glu Gly Ile Thr Thr Thr Glu Gly Glu Gly	
80 85 90 95	
gaa tgt gaa cag aca cct gag gag ctg gag ccc gtc gag aag cag gga	396
Glu Cys Glu Gln Thr Pro Glu Glu Leu Glu Pro Val Glu Lys Gln Gly	
100 105 110	
gta gac gac att ga	410
Val Asp Asp Ile	
115	

<210> 3215
 <211> 268
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 66..266

<400> 3215	
catgacaaaa aacgttacat aaggtacctg tctgaccttc atgcgtctgg tgacctgct	60
tgga atg cat tgg agc cca aca caa gtg gat ctt cag ctc atg cac agt	110
Met His Trp Ser Pro Thr Gln Val Asp Leu Gln Leu Met His Ser	
1 5 10 15	
tgc aaa gag ggc tac gtg aaa gat ctg aaa ggt aac cca ggc ctg cac	158
Cys Lys Glu Gly Tyr Val Lys Asp Leu Lys Gly Asn Pro Gly Leu His	
20 25 30	
agt ccc atg ttg gat ctt gat aat gat aca cgt ccc tca gtg ttg ggc	206
Ser Pro Met Leu Asp Leu Asp Asn Asp Thr Arg Pro Ser Val Leu Gly	
35 40 45	
cat ctc agt cag aca gcg tcc ctg aag agg ggc agc agc ttt cag tct	254
His Leu Ser Gln Thr Ala Ser Leu Lys Arg Gly Ser Ser Phe Gln Ser	
50 55 60	
ggt cga gac gac ag	268
Gly Arg Asp Asp	
65	

<210> 3216

<211> 202
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 41..202

<400> 3216
aatagttctt tgtaacctgt ttcataaaat atgcaaatgc atg aga cat tct ata 55
Met Arg His Ser Ile
1 5
tgt tgc tct gac tat ata ttt tta ccg ttt ata gat ttc atg atc ctt 103
Cys Cys Ser Asp Tyr Ile Phe Leu Pro Phe Ile Asp Phe Met Ile Leu
10 15 20
tgg ctg cat gga gaa aat ggg aca ggg cct gct aag ttc aac ata cct 151
Trp Leu His Gly Glu Asn Gly Thr Gly Pro Ala Lys Phe Asn Ile Pro
25 30 35
cac agt gtt aca ctt gat tca gct ggt cgg gtg tgg gtt gct gac cga 199
His Ser Val Thr Leu Asp Ser Ala Gly Arg Val Trp Val Ala Asp Arg
40 45 50
gat 202
Asp

<210> 3217
<211> 255
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 7..255

<400> 3217
agcatc atg gat ggc aaa caa ggg ggc atg gat ggg agc aag ccc gcg 48
Met Asp Gly Lys Gln Gly Gly Met Asp Gly Ser Lys Pro Ala
1 5 10
ggg cca agg gac ttt cct ggc atc agg ctt ctt tca aac cca ttg atg 96
Gly Pro Arg Asp Phe Pro Gly Ile Arg Leu Leu Ser Asn Pro Leu Met
15 20 25 30
ggc gat gct gtg tct gat tgg tct cct atg cat gaa gct gca atc cac 144
Gly Asp Ala Val Ser Asp Trp Ser Pro Met His Glu Ala Ala Ile His
35 40 45
gga cat cag ctg tct ctg agg aac ctc atc agc cag ggg tgg gct gtg 192
Gly His Gln Leu Ser Leu Arg Asn Leu Ile Ser Gln Gly Trp Ala Val
50 55 60
aac atc atc acg gca gat cat gtt tcc cca ctc cat gaa gcc tgt ctt 240
Asn Ile Ile Thr Ala Asp His Val Ser Pro Leu His Glu Ala Cys Leu
65 70 75
gga ggt cat ctc tct 255
Gly Gly His Leu Ser
80

<210> 3218
 <211> 422
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 258..422

<400> 3218
 ttttcttgta ggcaaaaaat cagtgagtct tgcawtttta cccattgagc caccatcatgt 60
 cttttgatta gagagtttag tccatttaca ttcagtgtta ttattgataa ataagcactt 120
 actccttcca ctttggttatt tattttctgg ttgttttgtg gtcttctttt ctttctttct 180
 ttccttctcg tcttcttttt ttgttaaagg tgcttttctc tgatgatata gtttcttggtg 240
 gccaggtgtg gtggctc atg gcc ata atc cca gca ttt tgg gag gcc gag 290
 Met Ala Ile Ile Pro Ala Phe Trp Glu Ala Glu
 1 5 10
 gca ggc gga tca cct gag gtc agg agt tgc gga ctg gcc tgg cca aca 338
 Ala Gly Gly Ser Pro Glu Val Arg Ser Ser Gly Leu Ala Trp Pro Thr
 15 20 25
 tgg aga aac mhg tkg tct ctg ctg gaa atg caa aaa ttg gct gga cgt 386
 Trp Arg Asn Xaa Xaa Ser Leu Leu Glu Met Gln Lys Leu Ala Gly Arg
 30 35 40
 ggt ggt ggg cac ctg tgg ycc agc tac ttg gga ggc 422
 Gly Gly Gly His Leu Trp Xaa Ser Tyr Leu Gly Gly
 45 50 55

<210> 3219
 <211> 365
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 137..364

<400> 3219
 tacagtaaaa agtggtttgt tatttgctgt tgatgggttc aatacagcct gctttctgaa 60
 gtgtaattta atttttcttt taccgcccc tmetgccatc tgcttttctc ctcatacctc 120
 acccagagtt tgttcc atg ggc aca ggt ttc ttt gag acg gac cgt gtt aaa 172
 Met Gly Thr Gly Phe Phe Glu Thr Asp Arg Val Lys
 1 5 10
 gcc tgt atc cag tca gga tgt gtg gca gtt cag atg ggt att ttc cat 220
 Ala Cys Ile Gln Ser Gly Cys Val Ala Val Gln Met Gly Ile Phe His
 15 20 25
 tca ccc gcc cct gcc gcc agc cct cac cct gag ctg agc ccc tcc tgc 268
 Ser Pro Ala Pro Ala Ala Ser Pro His Pro Glu Leu Ser Pro Ser Cys
 30 35 40
 cca ctg ctg aga cag ctt cct tca cca cac cca ggg ccc tgg ggc acg 316
 Pro Leu Leu Arg Gln Leu Pro Ser Pro His Pro Gly Pro Trp Gly Thr
 45 50 55 60

004220"66E99"0051399"0051400

gag cag agm btc aca act gac tca ctt gct gcc ttc tca cca aac gca c 365
 Glu Gln Xaa Xaa Thr Thr Asp Ser Leu Ala Ala Phe Ser Pro Asn Ala
 65 70 75

<210> 3220
 <211> 369
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 36..368

<400> 3220
 ataccggaag tagagtcacg gagaggtatt aagaa atg gag aga aaa ata agc 53
 Met Glu Arg Lys Ile Ser
 1 5
 aga atc cac ctt gtt tct gaa ccc agt ata act cat ttt cta caa gta 101
 Arg Ile His Leu Val Ser Glu Pro Ser Ile Thr His Phe Leu Gln Val
 10 15 20
 tct tgg gag aaa aca ctg gaa tct ggt ttt gtt att aca ctt act gat 149
 Ser Trp Glu Lys Thr Leu Glu Ser Gly Phe Val Ile Thr Leu Thr Asp
 25 30 35
 ggt cat tca gca tgg act ggg aca gtt tct gaa tca gag att tcc caa 197
 Gly His Ser Ala Trp Thr Gly Thr Val Ser Glu Ser Glu Ile Ser Gln
 40 45 50
 gaa gct gat gac atg gca atg gaa aaa ggg aaa tat gtt ggt gaa ctg 245
 Glu Ala Asp Asp Met Ala Met Glu Lys Gly Lys Tyr Val Gly Glu Leu
 55 60 65 70
 aga aaa gca ttg ttg tca gga gca gga cca gct gat gta tac acg ttt 293
 Arg Lys Ala Leu Leu Ser Gly Ala Gly Pro Ala Asp Val Tyr Thr Phe
 75 80 85
 aat ttt tct aaa gag tct tgt tat ttc ttc ttt gag ara mac ctg aaa 341
 Asn Phe Ser Lys Glu Ser Cys Tyr Phe Xaa Phe Glu Xaa Xaa Leu Lys
 90 95 100
 gat gtc tca ttc aga ctt ggt tcc ttc a 369
 Asp Val Ser Phe Arg Leu Gly Ser Phe
 105 110

<210> 3221
 <211> 281
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 24..281

<400> 3221
 gtttagcccg aggctggtct tag atg cag cga ctg ttt cag agt gac tca gaa 53
 Met Gln Arg Leu Phe Gln Ser Asp Ser Glu
 1 5 10

gaa aaa gaa gct gag gaa gct gtt ggg ggg ctg agg atg gga ttc tcg	101
Glu Lys Glu Ala Glu Glu Ala Val Gly Gly Leu Arg Met Gly Phe Ser	
15 20 25	
ctt ctt cat ttc agg tta ctc gtt cct cag caa gtt ggc aaa aca gat	149
Leu Leu His Phe Arg Leu Leu Val Pro Gln Gln Val Gly Lys Thr Asp	
30 35 40	
atc atg ctg gca att gaa aag ctg cag gcc ggt gct ctt gca act gac	197
Ile Met Leu Ala Ile Glu Lys Leu Gln Ala Gly Ala Leu Ala Thr Asp	
45 50 55	
gca gtc act gca gca ctg gtg gaa ctt gag gtg tac aca cac agt tat	245
Ala Val Thr Ala Ala Leu Val Glu Leu Glu Val Tyr Thr His Ser Tyr	
60 65 70	
gct tca tgg agt tgc atc caa cca agt atc cat gtt	281
Ala Ser Trp Ser Cys Ile Gln Pro Ser Ile His Val	
75 80 85	

<210> 3222
 <211> 370
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 81..368

<400> 3222	
acgggacgtg cggeccagcg agttggtcgg tcccggggtc acccgctacg ggaagcaggc	60
ctcgccacag actaagaaaa atg gct ttg tca gcc caa cag ata ccc aga tgg	113
Met Ala Leu Ser Ala Gln Gln Ile Pro Arg Trp	
1 5 10	
ttt aac tca gtt aag ttg agg agc ctc att aat gct gca caa ctc aca	161
Phe Asn Ser Val Lys Leu Arg Ser Leu Ile Asn Ala Ala Gln Leu Thr	
15 20 25	
aaa cgt ttt act aga cca gca aga aca ctg tta cat ggc ttt tct gct	209
Lys Arg Phe Thr Arg Pro Ala Arg Thr Leu Leu His Gly Phe Ser Ala	
30 35 40	
cag cct cag ata tcc tct gac aat tgc ttt ctc cag tgg gga ttt aag	257
Gln Pro Gln Ile Ser Ser Asp Asn Cys Phe Leu Gln Trp Gly Phe Lys	
45 50 55	
act tac agg act tcc tcc tta tgg aat agt tcc cag tct act agc tca	305
Thr Tyr Arg Thr Ser Ser Leu Trp Asn Ser Ser Gln Ser Thr Ser Ser	
60 65 70 75	
agt agt cag gag aat aat tct gcc caa agc agt ctg ctt cct tcc atg	353
Ser Ser Gln Glu Asn Ser Ala Gln Ser Ser Leu Leu Pro Ser Met	
80 85 90	
aat gaa cag cca cag ac	370
Asn Glu Gln Pro Gln	
95	

<210> 3223
 <211> 346
 <212> DNA
 <213> Homo sapiens

0957659

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<210> 3224
<211> 255
<212> DNA
<213> Homo sapiens
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<400>	3224	
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atg att gac gac ggc tgg tgg cgc ggg gtg ttg caa ggg ccg gta cgg		106
Met Ile Asp Asp Gly Trp Trp Arg Gly Val Leu Gln Gly Pro Val Arg		
1	5 10 15	
gct ctt ccc agc caa cta tgt gga gct gcg gca gta ggg ccc cca gcc		154
Ala Leu Pro Ser Gln Leu Cys Gly Ala Ala Ala Val Gly Pro Pro Ala		
	20 25 30	
ccc ccc cgg agc tgc gcc ctg kaw mct cay act aca gat cag gcc ttc		202
Pro Pro Arg Ser Cys Ala Leu Xaa Xaa His Thr Thr Asp Gln Ala Phe		
	35 40 45	
ttt ggt tct tgg gtg gtt ttg ggt ttt ttc tgt ttt ttt ttt ttt		250
Phe Gly Ser Trp Val Val Leu Gly Phe Phe Cys Phe Phe Phe Phe Phe		
	50 55 60	

ttt tt
Phe
65

255

<210> 3225
<211> 322
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 75..320

<400> 3225
tatggatgca gaatatgcca actactatac tagagaagtg atgttaatcc ttattcgaga 60
attccagtct cctg atg agg aaa tgr aaa aaa att gtg ctg aag gtg gta 110
Met Arg Lys Xaa Lys Lys Ile Val Leu Lys Val Val
1 5 10
aaa cag tgt tgt ggg aca gat ggt gta gaa gca aac tac att aaa aca 158
Lys Gln Cys Cys Gly Thr Asp Gly Val Glu Ala Asn Tyr Ile Lys Thr
15 20 25
gag att ctt cct ccc ttt ttt aaa cac ttc tgg cag cac agg atg gct 206
Glu Ile Leu Pro Pro Phe Phe Lys His Phe Trp Gln His Arg Met Ala
30 35 40
ttg gat aga aga aat tac cga cag tta gtt gat act act gtg gag ttg 254
Leu Asp Arg Arg Asn Tyr Arg Gln Leu Val Asp Thr Thr Val Glu Leu
45 50 55 60
gca aac aaa gta ggt gca gca gaa att ata tcc agg att gtg gat gat 302
Ala Asn Lys Val Gly Ala Ala Glu Ile Ile Ser Arg Ile Val Asp Asp
65 70 75
ctg aaa gat gaa gcc caa ca 322
Leu Lys Asp Glu Ala Gln
80

<210> 3226
<211> 386
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 51..386

<400> 3226
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Met Val
1
atg cac aat tat gag tct tca ggt ata rat ata rca aag gga aca gaa 104
Met His Asn Tyr Glu Ser Ser Gly Ile Xaa Ile Xaa Lys Gly Thr Glu
5 10 15
ctt cag ata gct gta gtg tca ccg tta gtt ctg tca gag gtc aaa aca 152
Leu Gln Ile Ala Val Val Ser Pro Leu Val Leu Ser Glu Val Lys Thr

20	25	30	
ttg tct gtc aaa gga ata aca cct gca gtg tta cct gaa aca gtg tat			200
Leu Ser Val Lys Gly Ile Thr Pro Ala Val Leu Pro Glu Thr Val Tyr			
35	40	45	50
ccc gtt att aaa gaa ggc agt gtt tgt agt tta caa aat caa ttg gca			248
Pro Val Ile Lys Glu Gly Ser Val Cys Ser Leu Gln Asn Gln Leu Ala			
	55	60	65
gaa aat gca aag gca act gct gct ttg aaa gtt gat gtt agt gga cca			296
Glu Asn Ala Lys Ala Thr Ala Ala Leu Lys Val Asp Val Ser Gly Pro			
	70	75	80
gta gca agt aca gca aca tca acc aag att ttt cca cta rct cag aag			344
Val Ala Ser Thr Ala Thr Ser Thr Lys Ile Phe Pro Leu Xaa Gln Lys			
	85	90	95
gaa aag cag aat gag tca act aat ggt aat tca gaa gtc aca			386
Glu Lys Gln Asn Glu Ser Thr Asn Gly Asn Ser Glu Val Thr			
100	105	110	

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 <222> 106..402

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ggctggttcg gacgtgggtc gacgctgtag caggactcca ggaag atg tta ccg agt	117
	Met Leu Pro Ser
	1
act tca gtg aat tcc tta gtg cag ggg aac gga gtc ttg aat tcc agg	165
Thr Ser Val Asn Ser Leu Val Gln Gly Asn Gly Val Leu Asn Ser Arg	
5	10
gat gcg gca aga cac aca gcc gga gcg aaa cgc tac aaa tat ctg aga	213
Asp Ala Ala Arg His Thr Ala Gly Ala Lys Arg Tyr Lys Tyr Leu Arg	
	25
agg ctt ttc cgc ttt cgg caa atg gac ttt gaa ttt gct gcc tgg cag	261
Arg Leu Phe Arg Phe Arg Gln Met Asp Phe Glu Phe Ala Ala Trp Gln	
	40
atg ctc tac ctg ttc aca tcc cca cag aga gtt tac aga aat ttt cat	309
Met Leu Tyr Leu Phe Thr Ser Pro Gln Arg Val Tyr Arg Asn Phe His	
	55
tat cga aaa cag acg aag gac cag tgg gcc aga gat gac cct gct ttc	357
Tyr Arg Lys Gln Thr Lys Asp Gln Trp Ala Arg Asp Asp Pro Ala Phe	
	70
ttg gtc ctg tta agt atc tgg ctc tgt gtg tcc act ata gga ttt	402
Leu Val Leu Leu Ser Ile Trp Leu Cys Val Ser Thr Ile Gly Phe	
85	90

<210> 3228
 <211> 264
 <212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 65..262

<400> 3228

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acgt atg ttt att gcg gca gta ttc aca ata gca aag act tgg aac caa      109
      Met Phe Ile Ala Ala Val Phe Thr Ile Ala Lys Thr Trp Asn Gln
      1           5           10          15
ccc aaa tgc cca tcg atg ata gac tgg ata aag wwa atg tgg cat ata      157
Pro Lys Cys Pro Ser Met Ile Asp Trp Ile Lys Xaa Met Trp His Ile
      20           25           30
tat acc atg gaa tac tct gca gcc ata aaa aag gat gag ttc atg tcc      205
Tyr Thr Met Glu Tyr Ser Ala Ala Ile Lys Lys Asp Glu Phe Met Ser
      35           40           45
ttg gca ggg aca tgg atg aag ctg gaa acc gtc att ctc agc aaa cta      253
Leu Ala Gly Thr Trp Met Lys Leu Glu Thr Val Ile Leu Ser Lys Leu
      50           55           60
aca cag gac ca      264
Thr Gln Asp
      65
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<210> 3229

<211> 283

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 12..281

<400> 3229

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aagtgtcagt t atg ggt ggt gac aat cct gaa gtg ggc aag aaa gct aga      50
      Met Gly Gly Asp Asn Pro Glu Val Gly Lys Lys Ala Arg
      1           5           10
aac tca agc aaa ttt gag ctg agg aaa agc cca gtt ttc agt gat gag      98
Asn Ser Ser Lys Phe Glu Leu Arg Lys Ser Pro Val Phe Ser Asp Glu
      15           20           25
gat tct gac ctt gac ttt gat atc agc aaa ttg gaa cag cag agc aag      146
Asp Ser Asp Leu Asp Phe Asp Ile Ser Lys Leu Glu Gln Gln Ser Lys
      30           35           40           45
tca ggt aaa agt tcc aga aat gtg aac aac aaa gat ttt ttt gat cca      194
Ser Gly Lys Ser Ser Arg Asn Val Asn Asn Lys Asp Phe Phe Asp Pro
      50           55           60
gtt gaa agt gat gaa gac ata gca agt gat cat gat gat gag ctg ggt      242
Val Glu Ser Asp Glu Asp Ile Ala Ser Asp His Asp Asp Glu Leu Gly
      65           70           75
tca aac aag atg atg aaa ttg ctg aag aag aag cag aga ga      283
Ser Asn Lys Met Met Lys Leu Leu Lys Lys Lys Gln Arg
      80           85           90
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	35		40		45	
gca	aca	ggt	ctt	gct	gaa	gca
Ala	Thr	Val	Leu	Ala	Glu	Ala
	50		55		60	
att	att	aat	cta	aaa	gaa	tat
Ile	Ile	Asn	Leu	Lys	Glu	Tyr
	65		70		75	
gtg	act	agt	aaa	aat	gtc	tgt
Val	Thr	Ser	Lys	Asn	Val	Cys
80			85		90	

312

360

409

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<220>
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 <222> 110..316

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tggtgaaaaa gagcccttga aaggctggaa gacgggagag gacaaaagc atg tct tcc	118
	Met Ser Ser
	1
ctt cct ggg tgc att ggt ttg gat gca gca aca gct aca gtg gag tct	166
Leu Pro Gly Cys Ile Gly Leu Asp Ala Ala Thr Ala Thr Val Glu Ser	
5 10 15	
gaa gag att gca gag ctg caa cag gca gtg gtt gag kad ntg ggt atc	214
Glu Glu Ile Ala Glu Leu Gln Gln Ala Val Val Glu Xaa Xaa Gly Ile	
20 25 30 35	
tct atg gag gaa ctt cgg cat ttc atc gat gwk gaa ctg gag aag atg	262
Ser Met Glu Glu Leu Arg His Phe Ile Asp Xaa Glu Leu Glu Lys Met	
40 45 50	
gat tgt gta cag caa cgc aag aag cag cta gca gag tta gag aca tgg	310
Asp Cys Val Gln Gln Arg Lys Lys Gln Leu Ala Glu Leu Glu Thr Trp	
55 60 65	
gta ata ca	318
Val Ile	

<210> 3233
 <211> 295
 <212> DNA
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<220>
 <221> CDS
 <222> 54..293

<400> 3233	
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	Met

aaa ata aag atg aca gct cca gtg aca agc tac gtg gag cct ggt tca	1	104
Lys Ile Lys Met Thr Ala Pro Val Thr Ser Tyr Val Glu Pro Gly Ser		
5 10 15		
ggt cct ttt agt gag tct acc att acc att tcc ctg tat att ccc tct	152	
Gly Pro Phe Ser Glu Ser Thr Ile Thr Ile Ser Leu Tyr Ile Pro Ser		
20 25 30		
gaa cag caa ttt gat cca ccc agg cct tta gag tca gat gtc ttc att	200	
Glu Gln Gln Phe Asp Pro Pro Arg Pro Leu Glu Ser Asp Val Phe Ile		
35 40 45		
gaa gat aga gcc gaa atg act gtg ttt gta cgg tct ttc gat gga ttt	248	
Glu Asp Arg Ala Glu Met Thr Val Phe Val Arg Ser Phe Asp Gly Phe		
50 55 60 65		
tct agt gcc caa aag aat caa gaa caa ctt ttg aca tta gca agc ca	295	
Ser Ser Ala Gln Lys Asn Gln Glu Gln Leu Leu Thr Leu Ala Ser		
70 75 80		

<210> 3234
 <211> 215
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 13..213

<400> 3234	
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Met Ala Gly Pro Leu Ser Pro Ser Phe Arg Ala Ala Leu	
1 5 10	
tgc cgc aac ctg gag tct ccc tcc tcc aga ttg tgt ggg ggt gtt ggg	99
Cys Arg Asn Leu Glu Ser Pro Ser Ser Arg Leu Cys Gly Gly Val Gly	
15 20 25	
agt gtc ata dga cgg gaa ttc tca ttt agg gtc tgc agt tcc tcc gtg	147
Ser Val Ile Xaa Arg Glu Phe Ser Phe Arg Val Xaa Ser Ser Ser Val	
30 35 40 45	
gaa gaa gca gtg ggc cgt ggg gtc cct agt ccc tcc ttt ctg ctt tta	195
Glu Glu Ala Val Gly Arg Gly Val Pro Ser Pro Ser Phe Leu Leu Leu	
50 55 60	
aaa ata aaa tca tgg cca cc	215
Lys Ile Lys Ser Trp Pro	
65	

<210> 3235
 <211> 292
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 54..290

<400> 3235

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Met
1
aaa ata aga aaa aat att tct gaa att cgg gaa ctt gag aac ata gaa 104
Lys Ile Arg Lys Asn Ile Ser Glu Ile Arg Glu Leu Glu Asn Ile Glu
5 10 15
gaa cac cag tct gta gat att gca act ttg gaa gat gaa gct cag gaa 152
Glu His Gln Ser Val Asp Ile Ala Thr Leu Glu Asp Glu Ala Gln Glu
20 25 30
aat aaa agc aaa atg aaa atg gtt gag gaa cat atg gag caa caa aaa 200
Asn Lys Ser Lys Met Lys Met Val Glu Glu His Met Glu Gln Gln Lys
35 40 45
gaa aat atg gag cat ctt aaa agt ctg aaa ata gaa gca gaa aat aag 248
Glu Asn Met Glu His Leu Lys Ser Leu Lys Ile Glu Ala Glu Asn Lys
50 55 60 65
tat gat gca att aaa ttc aaa att aat caa cta tcg gag cca gc 292
Tyr Asp Ala Ile Lys Phe Lys Ile Asn Gln Leu Ser Glu Pro
70 75

<210> 3236

<211> 308

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 28..306

<400> 3236

gaggagcttg aggaagcagg cagggaa atg tct gcc gcc gcc agc tct cgg gag 54
Met Ser Ala Ala Ala Ser Ser Arg Glu
1 5
cgc aac act gca ggt ggt tct aac ttt gat ggt ttg aga cca aat ggg 102
Arg Asn Thr Ala Gly Gly Ser Asn Phe Asp Gly Leu Arg Pro Asn Gly
10 15 20 25
aag gga gtg cct atg gac caa agc tcc agg ggt caa gat aaa cca gaa 150
Lys Gly Val Pro Met Asp Gln Ser Ser Arg Gly Gln Asp Lys Pro Glu
30 35 40
agc ttg caa cca wga cak mat aaa tcc aag tcc gaa att act gac atg 198
Ser Leu Gln Pro Xaa Xaa Xaa Lys Ser Lys Ser Glu Ile Thr Asp Met
45 50 55
gtt cgc tcc tcc act atc aca gtg tcg gac aag gct cat att tta tcc 246
Val Arg Ser Ser Thr Ile Thr Val Ser Asp Lys Ala His Ile Leu Ser
60 65 70
atg cag aag ttt gga ctg cga gat aca att gtg aaa tca cat cta cta 294
Met Gln Lys Phe Gly Leu Arg Asp Thr Ile Val Lys Ser His Leu Leu
75 80 85
cag aaa gaa gag ga 308
Gln Lys Glu Glu
90

<210> 3237

<211> 340
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 153..338

<400> 3237
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 tatgtgtgtc ctggctttgt ttgctgagaa ggtgtaagag catcaacagc ccagctgttg 120
 aaagtatcac tatctactaa aaggaaccag gg atg ctt gga gaa atg gtg gac 173
 Met Leu Gly Glu Met Val Asp
 1 5
 tcc agg gat ggg gca gtg aaa cca cac wgt aag cct ggm cca tct gat 221
 Ser Arg Asp Gly Ala Val Lys Pro His Xaa Lys Pro Gly Pro Ser Asp
 10 15 20
 tgc act gaa gtg aag aag tgc ttg aag aat gat gac aac atg tca caa 269
 Cys Thr Glu Val Lys Lys Cys Leu Lys Asn Asp Asp Asn Met Ser Gln
 25 30 35
 gga cac ata agt gag ctt gaa gat gtt ccc act ggc caa acc tgg gac 317
 Gly His Ile Ser Glu Leu Glu Asp Val Pro Thr Gly Gln Thr Trp Asp
 40 45 50 55
 aac tgg agt atc aaa gtc aat at 340
 Asn Trp Ser Ile Lys Val Asn
 60

<210> 3238
 <211> 366
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 73..366

<400> 3238
 agtttttcaa ggcgggctgt aactggtggc atttgtcccg ggaccaggctc cacagtttta 60
 tgtgtgagca ag atg gag gct gac ctg tct ggc ttt aac atc gat gcc ccc 111
 Met Glu Ala Asp Leu Ser Gly Phe Asn Ile Asp Ala Pro
 1 5 10
 cgt tgg gac cag cgc acc ttc ctg ggg aga gtg aag cac ttc cta aac 159
 Arg Trp Asp Gln Arg Thr Phe Leu Gly Arg Val Lys His Phe Leu Asn
 15 20 25
 atc acg gac ccc cgc act gtc ttt gta tct gag cgg gag ctg gac tgg 207
 Ile Thr Asp Pro Arg Thr Val Phe Val Ser Glu Arg Glu Leu Asp Trp
 30 35 40 45
 gcc aag gtg atg gtg gag aag agc agg atg ggg gtt gtg ccc cca ggc 255
 Ala Lys Val Met Val Glu Lys Ser Arg Met Gly Val Val Pro Pro Gly
 50 55 60
 acc caa gtg gag cag ctg ctg tat gcc aag aag ctg tat gac tcg gcc 303
 Thr Gln Val Glu Gln Leu Leu Tyr Ala Lys Lys Leu Tyr Asp Ser Ala

15	20	25	
cag ctg tat ggc atc aaa acc	cgg gat gca ata ctt	cag ttg aga agg	146
Gln Leu Tyr Gly Ile Lys Thr	Arg Asp Ala Ile Leu	Gln Leu Arg Arg	
30	35	40	
gat gga ttt cga aat ttg tat	cgt gga atc ctt ccc	cca ttg atg cag	194
Asp Gly Phe Arg Asn Leu Tyr	Arg Gly Ile Leu Pro	Pro Leu Met Gln	
45	50	55	60
aag aca act acg ctt gca ctt	atg ttt ggt ctg tat	gag gat tta tcc	242
Lys Thr Thr Thr Leu Ala Leu	Met Phe Gly Leu Tyr	Glu Asp Leu Ser	
65	70	75	
tgc ctt ctc cac aag cat gtc	agt gct cca gag ttt	gca acc agt ggc	290
Cys Leu Leu His Lys His Val	Ser Ala Pro Glu Phe	Ala Thr Ser Gly	
80	85	90	
gtg gcg gca gc			301
Val Ala Ala			
95			

<210> 3241
 <211> 404
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 143..403

<400> 3241	
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gtcctgccaa gaaagaaaca atggccttaga tgacgtctat tctaaggcct caaggcttgc	120
acccctgccca tgctaaatac ag atg cgc tcc tcc acc aag aga atc ccc tct	172
Met Arg Ser Ser Thr Lys Arg Ile Pro Ser	
1 5 10	
gcc ctc tgc cat ctc agc ccc gag cca gct cag ctg ccc atg acc tgt	220
Ala Leu Cys His Leu Ser Pro Glu Pro Ala Gln Leu Pro Met Thr Cys	
15 20 25	
gtg caa agc agg ggg cgg gac aaa cag cta tcg cct ttg gcc ttc cct	268
Val Gln Ser Arg Gly Arg Asp Lys Gln Leu Ser Pro Leu Ala Phe Pro	
30 35 40	
ttg ctc ctg aca gcg gtc tca aac ctg gag gag tca aag gtc caa gat	316
Leu Leu Leu Thr Ala Val Ser Asn Leu Glu Glu Ser Lys Val Gln Asp	
45 50 55	
gcc ttt gtt cac tat gaa cct ggt gtc agc tct agc gtc ctc agc arc	364
Ala Phe Val His Tyr Glu Pro Gly Val Ser Ser Ser Val Leu Ser Xaa	
60 65 70	
agg gca gcg tgg agc agg gcc agc cct ctg gca ctt gtg t	404
Arg Ala Ala Trp Ser Arg Ala Ser Pro Leu Ala Leu Val	
75 80 85	

<210> 3242
 <211> 439
 <212> DNA
 <213> Homo sapiens

004220" 666E7560

<220>
 <221> CDS
 <222> 278..439

<400> 3242
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 aaggaaataa gaacaattcc ccaacaatgt tttaaagtct tcattttcta ttatctttgt 120
 tttatgtaaa ctttactcat ttcgtataaa tttcattcat ttttgaggtc ctgctttctg 180
 tcagggttttg tgttgggcac tagagtaaga cttggggcatc ttgtcaggaa gctgctctgt 240
 gattaaagag atagatgtat gaacaagcaa tbataat atg gtt agt aag tcc tac 295
 Met Val Ser Lys Ser Tyr
 1 5
 agt aaa ggt act ctc tac agt aga ggg cct ggg aaa ctg cct ttt ttt 343
 Ser Lys Gly Thr Leu Tyr Ser Arg Gly Pro Gly Lys Leu Pro Phe Phe
 10 15 20
 ttc ttt gag aca ggg tct cca tca ccc aga cct cat ggg ctc aag cga 391
 Phe Phe Glu Thr Gly Ser Pro Ser Pro Arg Pro His Gly Leu Lys Arg
 25 30 35
 tcc tcc cac ctc agc ctc ctg agt agc ttg gac tac agg cat gca cca 439
 Ser Ser His Leu Ser Leu Leu Ser Ser Leu Asp Tyr Arg His Ala Pro
 40 45 50

<210> 3243
 <211> 297
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 141..296

<400> 3243
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 cattagtaga atgcatatcc atagagctaa tttagattga ccagttatgc aggtactcat 120
 ttgtgtgtgt atatgtgtgc atg tgt agc tct acg caa ttt tat cat aag tgt 173
 Met Cys Ser Ser Thr Gln Phe Tyr His Lys Cys
 1 5 10
 agc ttc atg aaa cca caa cca cta tca aga tac ttc act gtc cca tca 221
 Ser Phe Met Lys Pro Gln Pro Leu Ser Arg Tyr Phe Thr Val Pro Ser
 15 20 25
 tca gag act ccc tca tgc tac ccc tgt aga gtc aac acc tat tcc cta 269
 Ser Glu Thr Pro Ser Cys Tyr Pro Cys Arg Val Asn Thr Tyr Ser Leu
 30 35 40
 ccc cat tct gaa caa cta gcc acc act a 297
 Pro His Ser Glu Gln Leu Ala Thr Thr
 45 50

<210> 3244
 <211> 311
 <212> DNA
 <213> Homo sapiens

<220>

<221> CDS

<222> 23..310

<400> 3244

tatatgtytt gaattagggtt at atg ttc tgc att tac aag cac ata cag gat 52
Met Phe Cys Ile Tyr Lys His Ile Gln Asp
1 5 10
tct tac ttc cag caa ctt ggc agt aaa asa ata agt aga ctc ttt agg 100
Ser Tyr Phe Gln Gln Leu Gly Ser Lys Xaa Ile Ser Arg Leu Phe Arg
15 20 25
agc caa agt caa gct tgg gaa ctg ttg cta ggt ggt ata tat ttc ata 148
Ser Gln Ser Gln Ala Trp Glu Leu Leu Leu Gly Gly Ile Tyr Phe Ile
30 35 40
gtt tat gtt tgt ttc caa gac aag gtc tca ctc cat cgc cca ggc tgg 196
Val Tyr Val Cys Phe Gln Asp Lys Val Ser Leu His Arg Pro Gly Trp
45 50 55
agt gca gtg gca cga tca cag ttc act gca act ttg acc ttc tgg gny 244
Ser Ala Val Ala Arg Ser Gln Phe Thr Ala Thr Leu Thr Phe Trp Xaa
60 65 70
caa gtg acc ctc cca cct cag cct ccc aag ttg ctg gga ctt agg cac 292
Gln Val Thr Leu Pro Pro Gln Pro Pro Lys Leu Leu Gly Leu Arg His
75 80 85 90
ccg cca cca cgc ccc gta s 311
Pro Pro Pro Arg Pro Val
95

<210> 3245

<211> 279

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 36..278

<400> 3245

tgccccgagca caaccctggc aatttgggag gaaca atg aga ctg gga ata aga 53
Met Arg Leu Gly Ile Arg
1 5
aga act gtt ttc aaa act gaa aat tca ata tta agg aaa ctt tat ggt 101
Arg Thr Val Phe Lys Thr Glu Asn Ser Ile Leu Arg Lys Leu Tyr Gly
10 15 20
gat gtt cct ttt ata gaa gaa aga cac aga cat cgg ttc gag gta aac 149
Asp Val Pro Phe Ile Glu Glu Arg His Arg His Arg Phe Glu Val Asn
25 30 35
cct aac ctg atc aaa caa ttt gag cag aat gac tta agt ttt gta ggt 197
Pro Asn Leu Ile Lys Gln Phe Glu Gln Asn Asp Leu Ser Phe Val Gly
40 45 50
cag gat gtt gat gga gac agg atg gaa atc att gaa ctg gca aat cat 245
Gln Asp Val Asp Gly Asp Arg Met Glu Ile Ile Glu Leu Ala Asn His
55 60 65 70

cct tat ttt gtt ggt gtc cag ttc cat cct gag t 279
 Pro Tyr Phe Val Gly Val Gln Phe His Pro Glu
 75 80

<210> 3246
 <211> 390
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 95..388

<400> 3246
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 tgaggactcc ctgtcctccc aggtccggac tcag atg gag ctg gaa gag gat gtg 115
 Met Glu Leu Glu Glu Asp Val
 1 5
 aaa atc tac ctc gac gag aac tac gag cgc atc aac gtg cct gtg ccc 163
 Lys Ile Tyr Leu Asp Glu Asn Tyr Glu Arg Ile Asn Val Pro Val Pro
 10 15 20
 cag ttt ggc ggc ggt gwc cct gca gac atc atc cat gac ttc cag cgg 211
 Gln Phe Gly Gly Gly Xaa Pro Ala Asp Ile Ile His Asp Phe Gln Arg
 25 30 35
 ggt ctg act gcg tac cat gat atc tcc ctg gac aag tgc tat gtc atc 259
 Gly Leu Thr Ala Tyr His Asp Ile Ser Leu Asp Lys Cys Tyr Val Ile
 40 45 50 55
 gaa ctc aac acc acc att gtg ccc ccc tcg caa ctt ctg gga gct cct 307
 Glu Leu Asn Thr Thr Ile Val Pro Pro Ser Gln Leu Leu Gly Ala Pro
 60 65 70
 cat gaa cgt gaa gag ggg gac tac ctg ccg cag acg tac atc atc cag 355
 His Glu Arg Glu Glu Gly Asp Tyr Leu Pro Gln Thr Tyr Ile Ile Gln
 75 80 85
 gag gag atg gtg gtc acg gag cat gtc agt gac aa 390
 Glu Glu Met Val Val Thr Glu His Val Ser Asp
 90 95

<210> 3247
 <211> 302
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 100..300

<400> 3247
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 ttcacccagg ctgtagtgca gtggtgcaat ctgctccct atg gcc tca acc tcc 114
 Met Ala Ser Thr Ser
 1 5
 ctg gcc cat gct atc ctc tta ggc ggg tgc cac cat ggc tgg cta gat 162

Leu	Ala	His	Ala	Ile	Leu	Leu	Gly	Gly	Cys	His	His	Gly	Trp	Leu	Asp	
				10					15					20		
ttt	act	ttt	tat	ttt	gta	gag	aca	ggg	tat	ccc	tgt	gtt	gcc	cag	gct	210
Phe	Thr	Phe	Tyr	Phe	Val	Glu	Thr	Gly	Tyr	Pro	Cys	Val	Ala	Gln	Ala	
			25					30					35			
ggg	ctc	aaa	ctc	ctg	tcc	tca	agt	gat	cct	cct	gcc	ttg	gcc	acc	cat	258
Gly	Leu	Lys	Leu	Leu	Ser	Ser	Ser	Asp	Pro	Pro	Ala	Leu	Ala	Thr	His	
		40					45					50				
agt	gct	ggg	att	aca	ggg	gtg	ggc	cac	ctc	act	cag	tgc	cac	cc		302
Ser	Ala	Gly	Ile	Thr	Gly	Val	Gly	His	Leu	Thr	Gln	Cys	His			
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 <212> DNA
 <213> Homo sapiens

<220>
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 <222> 42..308

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					Met	Arg	Leu	Asn	Gln							
					1				5							
aac	acc	ttg	ctg	ctg	ggg	aag	aag	gtg	gtc	ctt	gta	ccc	tac	acc	tcg	104
Asn	Thr	Leu	Leu	Leu	Gly	Lys	Lys	Val	Val	Leu	Val	Pro	Tyr	Thr	Ser	
				10					15					20		
gag	cat	gtg	ccc	agg	tac	cac	gag	tgg	atg	aaa	tca	gag	gag	ctg	cag	152
Glu	His	Val	Pro	Arg	Tyr	His	Glu	Trp	Met	Lys	Ser	Glu	Glu	Leu	Gln	
			25					30					35			
cgt	ttg	aca	gcc	tcg	gag	ccg	ctg	acc	ctg	gag	cag	gag	tat	gcc	atg	200
Arg	Leu	Thr	Ala	Ser	Glu	Pro	Leu	Thr	Leu	Glu	Gln	Glu	Tyr	Ala	Met	
		40					45				50					
cag	tgc	agc	tgg	cag	gaa	gat	gca	gac	aag	tgt	acc	ttc	att	gtg	ctg	248
Gln	Cys	Ser	Trp	Gln	Glu	Asp	Ala	Asp	Lys	Cys	Thr	Phe	Ile	Val	Leu	
	55					60					65					
gat	gcc	gag	aag	tgg	cag	gcc	cag	cca	ggc	gcc	acc	gaa	gag	agc	tgc	296
Asp	Ala	Glu	Lys	Trp	Gln	Ala	Gln	Pro	Gly	Ala	Thr	Glu	Glu	Ser	Cys	
	70				75				80					85		
atg	gtg	gga	gct													308
Met	Val	Gly	Ala													

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 <213> Homo sapiens

<220>
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 <222> 29..316

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                                Met Asp Val Ile Glu Lys Pro Glu
                                1           5

aat gac cca gag tgg tgg aaa tgc agg aag atc aat ggt atg gtt ggt      100
Asn Asp Pro Glu Trp Trp Lys Cys Arg Lys Ile Asn Gly Met Val Gly
10           15           20

cta gta cca aaa aac tat gtt acc gtt atg cak wat aat cca tta act      148
Leu Val Pro Lys Asn Tyr Val Thr Val Met Xaa Xaa Asn Pro Leu Thr
25           30           35           40

tca ggt ttg gaa cca tca cct cca cag tgt gat tac att agg cct tca      196
Ser Gly Leu Glu Pro Ser Pro Pro Gln Cys Asp Tyr Ile Arg Pro Ser
45           50           55

ctc act gga aag ttt gct ggc aat cct tgg tat tat ggc aaa gtc acc      244
Leu Thr Gly Lys Phe Ala Gly Asn Pro Trp Tyr Tyr Gly Lys Val Thr
60           65           70

agg cat caa gca gaa atg gca tta aat gaa aga gga cat gaa ggg gat      292
Arg His Gln Ala Glu Met Ala Leu Asn Glu Arg Gly His Glu Gly Asp
75           80           85

ttc ctc att cgt gat agt gaa tct tc      318
Phe Leu Ile Arg Asp Ser Glu Ser
90           95

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<211> 394
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<220>
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<222> 178..393

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ttattggtac taaagaaatc agtcaatatt tacatgtatg catagtatat taattcagat      120
tgtaatatat gtgtagcctg ctagtagctt ttcaatggaa aaagtgaaaa gagcttc      177
atg tta act ttt tta att tta ata ggt tgc ttc ttc aag tgg aag aag      225
Met Leu Thr Phe Leu Ile Leu Ile Gly Cys Phe Phe Lys Trp Lys Lys
1           5           10           15

tat ttg act ggg ggt cag aag acc tgg gtt gga atc cta gtt cca tct      273
Tyr Leu Thr Gly Gly Gln Lys Thr Trp Val Gly Ile Leu Val Pro Ser
20           25           30

ttc tgt aat aat gta ggt ctg ctc tgc cca tcc tct gcc ctc ctc cct      321
Phe Cys Asn Asn Val Gly Leu Leu Cys Pro Ser Ser Ala Leu Leu Pro
35           40           45

cag aaa aat ctc tgc aaa ccc atg atg tcc aac aga cat agc tca tat      369
Gln Lys Asn Leu Cys Lys Pro Met Met Ser Asn Arg His Ser Ser Tyr
50           55           60

tgg tca cag cta acg gag tta act a      394
Trp Ser Gln Leu Thr Glu Leu Thr
65           70

<210> 3251

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Ala	Glu	Ile	Glu	Ala	Glu	Leu	Asp	Lys	Leu	Ser	Ile	Ser	Ser	Leu	Glu	
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aaa	gaa	gac	att	gag	agt	gat	gca	aaa	tca	gaa	acc	cag	agt	gat	gat	207
Lys	Glu	Asp	Ile	Glu	Ser	Asp	Ala	Lys	Ser	Glu	Thr	Gln	Ser	Asp	Asp	
			30					35					40			
agt	gat	aca	gat	dca	gtt	gaa	tta	cca	gaa	tca	gtt	ctt	cac	t		250
Ser	Asp	Thr	Asp	Xaa	Val	Glu	Leu	Pro	Glu	Ser	Val	Leu	His			
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tcagcaaaaag	cccttgctcag	tttaaaagaa	ggaagcttat	ctaacacgtg	gaatgaaaag											120
tacagttcctt	tacagaaaac	acctgtttgg	aaaggcagga	atacaagctc	tgctgtggaa											180
atg	cct	ttc	aga	aat	tca	aaa	cga	agt	cga	ttt	ttt	tct	gat	gaa	gat	228
Met	Pro	Phe	Arg	Asn	Ser	Lys	Arg	Ser	Arg	Phe	Phe	Ser	Asp	Glu	Asp	
1			5						10				15			
gat	agg	caa	ata	aat	aca	agg	tca	cct	aaa	aga	aac	cag	agg	gtt	gca	276
Asp	Arg	Gln	Ile	Asn	Thr	Arg	Ser	Pro	Lys	Arg	Asn	Gln	Arg	Val	Ala	
			20					25				30				
atg	gtt	cca	cag	aaa	ttt	aca	gca	aca	atg	tca	aca	nba	gat	aag	aaa	324
Met	Val	Pro	Gln	Lys	Phe	Thr	Ala	Thr	Met	Ser	Thr	Xaa	Asp	Lys	Lys	
			35				40					45				
gct	tca	cag	aag	att	ggc	ttt	cga	tta	cgt	aat	ctg	ctc	aag	ctt	cct	372
Ala	Ser	Gln	Lys	Ile	Gly	Phe	Arg	Leu	Arg	Asn	Leu	Leu	Lys	Leu	Pro	
			50				55				60					
aaa	gca	cat	aaa	tgg	tgt	ata	tac	gag	t							400
Lys	Ala	His	Lys	Trp	Cys	Ile	Tyr	Glu								
65							70									

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 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 25..396

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			Met	Ala	Thr	Glu	Gly	Met	Ile	Leu	Thr					
			1				5									
aac	cac	gac	cat	caa	atc	cgt	gtc	gga	gtc	ctt	aca	gtg	agt	gat	agt	99

Asn His Asp His Gln Ile Arg Val Gly Val Leu Thr Val Ser Asp Ser	
10 15 20 25	
tgc ttc agg aat ctt gca gaa gac cgc agt ggg ata aat ctc aaa gat	147
Cys Phe Arg Asn Leu Ala Glu Asp Arg Ser Gly Ile Asn Leu Lys Asp	
30 35 40	
ctc gta caa gat cct tct ttg ttg ggt ggg act ata tca gca tac aag	195
Leu Val Gln Asp Pro Ser Leu Leu Gly Gly Thr Ile Ser Ala Tyr Lys	
45 50 55	
ata gta cca gat gaa ata gaa gaa atc aag gaa acc ctg ata gat tgg	243
Ile Val Pro Asp Glu Ile Glu Glu Ile Lys Glu Thr Leu Ile Asp Trp	
60 65 70	
tgt gat gaa aag gaa ctt aat ttg ata tta aca act gga gga aca gga	291
Cys Asp Glu Lys Glu Leu Asn Leu Ile Leu Thr Thr Gly Gly Thr Gly	
75 80 85	
ttt gca cca cga gat gtc act cca gag gcc aca aaa gaa gta ata gaa	339
Phe Ala Pro Arg Asp Val Thr Pro Glu Ala Thr Lys Glu Val Ile Glu	
90 95 100 105	
cgg gaa gca cca ggg atg gcc ctg gca atg ctg atg gga tca ctt aat	387
Arg Glu Ala Pro Gly Met Ala Leu Ala Met Leu Met Gly Ser Leu Asn	
110 115 120	
gtt aca cct ct	398
Val Thr Pro	
<210> 3255	
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<212> DNA	
<213> Homo sapiens	
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acatgtttgca gaaaagcaca ktkacagcct a atg cct tta ctt tta gaa gcc	112
Met Pro Leu Leu Leu Glu Ala	
1 5	
cag tca aca cca ttt cag gtc aca cct tca act atg gca aat att gtg	160
Gln Ser Thr Pro Phe Gln Val Thr Pro Ser Thr Met Ala Asn Ile Val	
10 15 20	
aaa ggc ctg tat acc ctc aga cca gag tgg gtt cag atg gct cca act	208
Lys Gly Leu Tyr Thr Leu Arg Pro Glu Trp Val Gln Met Ala Pro Thr	
25 30 35	
cta ttt tct aaa ttt att cca aac att ctc cct ccg gcg gtg gaa tct	256
Leu Phe Ser Lys Phe Ile Pro Asn Ile Leu Pro Pro Ala Val Glu Ser	
40 45 50 55	
gaa ctt tct gaa tat gct gct caa gat cag aaa ttt caa aga gac tta	304
Glu Leu Ser Glu Tyr Ala Ala Gln Asp Gln Lys Phe Gln Arg Asp Leu	
60 65 70	
tac aga atg gtt tta caa ggg gtg acc agt ccc gga aga gag ctg ggg	352
Tyr Arg Met Val Leu Gln Gly Val Thr Ser Pro Gly Arg Glu Leu Gly	
75 80 85	
atg agt tgg ctt ata ata gct cgt cag cat gtg c	386

Met Ser Trp Leu Ile Ile Ala Arg Gln His Val
 90 95

<210> 3256
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 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 96..362

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 cccaggactg ctactccggc gttatatcca ccacc atg ggc ccc aag gac cac 113
 Met Gly Pro Lys Asp His
 1 5
 atg gta acc agc tcc ttc tgc tgc cag agc gac ggc tgc aac agt gcc 161
 Met Val Thr Ser Ser Phe Cys Cys Gln Ser Asp Gly Cys Asn Ser Ala
 10 15 20
 ttt ttg tct gtt ccc ttg acc aat ctt act gag aat ggc ctg atg tgc 209
 Phe Leu Ser Val Pro Leu Thr Asn Leu Thr Glu Asn Gly Leu Met Cys
 25 30 35
 ccc gcc tgc act gcg agc ttc agg gac aaa tgc atg ggc ccc atg acc 257
 Pro Ala Cys Thr Ala Ser Phe Arg Asp Lys Cys Met Gly Pro Met Thr
 40 45 50
 cac tgt act gga aag gaa aac cac tgc gtc tcc tta tct gga cac gtg 305
 His Cys Thr Gly Lys Glu Asn His Cys Val Ser Leu Ser Gly His Val
 55 60 65 70
 cag gct ggt ant ttc aaa ccc aga ttt gct atg cgg ggc tgt gct aca 353
 Gln Ala Gly Xaa Phe Lys Pro Arg Phe Ala Met Arg Gly Cys Ala Thr
 75 80 85
 gag agt atg t 363
 Glu Ser Met

<210> 3257
 <211> 331
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 81..329

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 aaacagctgt gtggagagtg atg agc atg tyc ctg gra gag ctg gaa aca gaa 113
 Met Ser Met Xaa Leu Xaa Glu Leu Glu Thr Glu
 1 5 10
 ggg gag agg cag ctg ana agc ctc ctt cag cat caa ctt gat act tct 161
 Gly Glu Arg Gln Leu Xaa Ser Leu Leu Gln His Gln Leu Asp Thr Ser
 15 20 25

gtc tcc att gag gaa tgt atg tct aag aaa gag agc ttt gct cct ggt	209
Val Ser Ile Glu Glu Cys Met Ser Lys Lys Glu Ser Phe Ala Pro Gly	
30 35 40	
act atg tac aag ccc ttt ggg aag gaa gca gct ggg act atg act ttg	257
Thr Met Tyr Lys Pro Phe Gly Lys Glu Ala Ala Gly Thr Met Thr Leu	
45 50 55	
tcc caa ttc cag aca ctg cat gag aag gac cag gaa act gct tct ctc	305
Ser Gln Phe Gln Thr Leu His Glu Lys Asp Gln Glu Thr Ala Ser Leu	
60 65 70 75	
agg gaa tta ggg ctt aat gaa aca ga	331
Arg Glu Leu Gly Leu Asn Glu Thr	
80	

<210> 3258
 <211> 314
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 36..314

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Met Glu Glu Ile Tyr Ala	
1 5	
aag ttt gtg tcc cag aaa atc ags aaa acc cgc tgg cga ccg ctg cct	101
Lys Phe Val Ser Gln Lys Ile Xaa Lys Thr Arg Trp Arg Pro Leu Pro	
10 15 20	
ccg gga agt tta cag acc gcg gag acg ttc gst aca gga tct tkg grc	149
Pro Gly Ser Leu Gln Thr Ala Glu Thr Phe Xaa Thr Gly Ser Xaa Xaa	
25 30 35	
aat krg gra aat taw rwt tca ctg tgg tct att gga gat ttt gga aac	197
Asn Xaa Xaa Asn Xaa Xaa Ser Leu Trp Ser Ile Gly Asp Phe Gly Asn	
40 45 50	
ttg gac tct gat gga ggg ttt kaa ggr gac cat cag kta ttg tgt gat	245
Leu Asp Ser Asp Gly Gly Phe Xaa Gly Asp His Gln Xaa Leu Cys Asp	
55 60 65 70	
atc aga cac cat ggt gat gta atg gat tta cag ttt ttt gac cag gaa	293
Ile Arg His His Gly Asp Val Met Asp Leu Gln Phe Phe Asp Gln Glu	
75 80 85	
aga att gtc gct gct tca tca	314
Arg Ile Val Ala Ala Ser Ser	
90	

<210> 3259
 <211> 327
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 64..327

<400> 3259
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 att atg gat gga ggg gat gat ggt aac ctt att atc aaa aag agg ttt 108
 Met Asp Gly Gly Asp Asp Gly Asn Leu Ile Ile Lys Lys Arg Phe
 1 5 10 15
 gtg tct gag gca gaa cta gat gaa cgg cgc aaa agg agg caa gaa gaa 156
 Val Ser Glu Ala Glu Leu Asp Glu Arg Arg Lys Arg Arg Gln Glu Glu
 20 25 30
 tgg gag aaa gtt cga aaa cct gaa gat cca gaa gaa tgt cca gag gag 204
 Trp Glu Lys Val Arg Lys Pro Glu Asp Pro Glu Glu Cys Pro Glu Glu
 35 40 45
 gtt tat gac cct cga tct cta tat gaa agg cta cag gaa cag aag gac 252
 Val Tyr Asp Pro Arg Ser Leu Tyr Glu Arg Leu Gln Glu Gln Lys Asp
 50 55 60
 agg aag cag cag gag tac gag gaa cag ttc aaa ttc aaa aac atg gta 300
 Arg Lys Gln Gln Glu Tyr Glu Glu Gln Phe Lys Phe Lys Asn Met Val
 65 70 75
 aga ggc tta gat gaa gat aag acc aac 327
 Arg Gly Leu Asp Glu Asp Lys Thr Asn
 80 85

<210> 3260
 <211> 236
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 65..235

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 tacc atg ctt atg tta ttg tgg gaa gga gtt ctg gaa tca gat aga cat 109
 Met Leu Met Leu Leu Trp Glu Gly Val Leu Glu Ser Asp Arg His
 1 5 10 15
 gga cct caa atg gga gag cag ctg tta aag tct caa tca gct gac cca 157
 Gly Pro Gln Met Gly Glu Gln Leu Leu Lys Ser Gln Ser Ala Asp Pro
 20 25 30
 ttt ttg aac ctt gag atg gat gct ggc atc tcc aac atc cag cga agt 205
 Phe Leu Asn Leu Glu Met Asp Ala Gly Ile Ser Asn Ile Gln Arg Ser
 35 40 45
 cag agc tgg ctc agc aac att ggc ccc acc c 236
 Gln Ser Trp Leu Ser Asn Ile Gly Pro Thr
 50 55

<210> 3261
 <211> 195
 <212> DNA
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<220>

<221> CDS
 <222> 12..194

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 Met Phe Ser Val Ser Lys Leu Ile Ala Gln Glu Thr Ile
 1 5 10
 atg gaa tct ttg gat ggc tta cat ctt cct gaa tcg agc aga gaa act 98
 Met Glu Ser Leu Asp Gly Leu His Leu Pro Glu Ser Ser Arg Glu Thr
 15 20 25
 act gca atg att ctt atg aat gtg tat tgc aat aag att ttg aag cct 146
 Thr Ala Met Ile Leu Met Asn Val Tyr Cys Asn Lys Ile Leu Lys Pro
 30 35 40 45
 gta gat ggg tcc tgt tgt caa cct cgg cct cct gtt act ctc ata caa a 195
 Val Asp Gly Ser Cys Cys Gln Pro Arg Pro Pro Val Thr Leu Ile Gln
 50 55 60

<210> 3262
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 <212> DNA
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<220>
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 acgaagtctc gctctgtcac ccagggtgga gtgcagtggc atg atc tct gct cac 115
 Met Ile Ser Ala His
 1 5
 tac aac ctc cgc ctc cng ggt tcc agc gat tct cct gcc tca gcc tcc 163
 Tyr Asn Leu Arg Leu Xaa Gly Ser Ser Asp Ser Pro Ala Ser Ala Ser
 10 15 20
 cga gtg gct ggg act aca ggc gtg cgc cac cac gcc tgg cta att ttt 211
 Arg Val Ala Gly Thr Thr Gly Val Arg His His Ala Trp Leu Ile Phe
 25 30 35
 tgt att ttt ggt aga gac ggg gtt tcg cca tgt tgg tca ggc tgg tct 259
 Cys Ile Phe Gly Arg Asp Gly Val Ser Pro Cys Trp Ser Gly Trp Ser
 40 45 50
 cga act cct gac ctc gtg gtc tgc cct cct cga cct ccc aaa gtg ccg 307
 Arg Thr Pro Asp Leu Val Val Cys Pro Pro Arg Pro Pro Lys Val Pro
 55 60 65

<210> 3263
 <211> 365
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 181..363

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tgggctgggt ggtctgagga cctgaggtca taggtggatc tcctcacgga gtgagngcaa      120
ggacaggggg ctggtctccc aaaggagtcc cctgtcccg ggtcttcggc accaaatgtc      180
atg cac gtc cat ttg aag aga gtc cac caa cag gct ttg tgt gag caa      228
Met His Val His Leu Lys Arg Val His Gln Gln Ala Leu Cys Glu Gln
1          5          10          15
caa ggc tgt tta ttt cac ctg ggt gca ggt tgg ctg agt ctg aaa aag      276
Gln Gly Cys Leu Phe His Leu Gly Ala Gly Trp Leu Ser Leu Lys Lys
20          25          30
gag tca gca aat ttt ggt ggg att atc att agt tct tat agv ntt ggg      324
Glu Ser Ala Asn Phe Gly Gly Ile Ile Ile Ser Ser Tyr Xaa Xaa Gly
35          40          45
ata ggt ggg cca ggg gtg gat ctc aca aag tac att ctc aa      365
Ile Gly Gly Pro Gly Val Asp Leu Thr Lys Tyr Ile Leu
50          55          60

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<222> 130..414

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gattgagaaa ctgcttttac tctcccgact actgtactcc caggcagaaa cccacggctg      120
aagcccacg atg ccc atg tgt aac ttg gtt twy tac aca cac gtt tgg agc      171
Met Pro Met Cys Asn Leu Val Xaa Tyr Thr His Val Trp Ser
1          5          10
cca gtg tgc aga ccc gca gcg cag agg agg cgg cgg aac acc ccg ggt      219
Pro Val Cys Arg Pro Ala Ala Gln Arg Arg Arg Arg Asn Thr Pro Gly
15          20          25          30
tgg tcg ggt ttc caa ggg ctg acc cga gct cca gca ctt ttt ccg cgc      267
Trp Ser Gly Phe Gln Gly Leu Thr Arg Ala Pro Ala Leu Phe Pro Arg
35          40          45
ctg att ttt cag gtc att ttc gaa tgg gct atc ttt gct tac att ttg      315
Leu Ile Phe Gln Val Ile Phe Glu Trp Ala Ile Phe Ala Tyr Ile Leu
50          55          60
agc ttg gat cct ctc cag aaa gca tta cta cct tct aaa agg aaa aac      363
Ser Leu Asp Pro Leu Gln Lys Ala Leu Leu Pro Ser Lys Arg Lys Asn
65          70          75
atc tcg tat ttg cag aca gtg ctg agg gag caa agt tca ttt tct cgg      411
Ile Ser Tyr Leu Gln Thr Val Leu Arg Glu Gln Ser Ser Phe Ser Arg
80          85          90
agc tc      416
Ser
95

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<210> 3265
 <211> 364
 <212> DNA
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<220>
 <221> CDS
 <222> 73..363

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 gggaagagac gg atg atg aac aag ctt tac atc ggg aac ctg agc ccc gcc 111
 Met Met Asn Lys Leu Tyr Ile Gly Asn Leu Ser Pro Ala
 1 5 10
 gtc acc gcc gac gac ctc cgg cag ctc ttt ggg gac agg aag ctg ccc 159
 Val Thr Ala Asp Asp Leu Arg Gln Leu Phe Gly Asp Arg Lys Leu Pro
 15 20 25
 ctg gcg gga cag gtc ctg ctg aag tcc ggc tac gcc ttc gtg gac tac 207
 Leu Ala Gly Gln Val Leu Leu Lys Ser Gly Tyr Ala Phe Val Asp Tyr
 30 35 40 45
 ccc gac cag aac tgg gcc atc cgc gcc atc gag acc ctc tcg ggt aaa 255
 Pro Asp Gln Asn Trp Ala Ile Arg Ala Ile Glu Thr Leu Ser Gly Lys
 50 55 60
 gtg gaa ttg cat ggg aaa atc atg gaa gtt gat tac tca gtc tct aaa 303
 Val Glu Leu His Gly Lys Ile Met Glu Val Asp Tyr Ser Val Ser Lys
 65 70 75
 aag cta agg agc agg aaa att cag att cga aac atc cct cct cac ctg 351
 Lys Leu Arg Ser Arg Lys Ile Gln Ile Arg Asn Ile Pro Pro His Leu
 80 85 90
 cag tgg gag gtg t 364
 Gln Trp Glu Val
 95

<210> 3266
 <211> 276
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 93..275

<400> 3266
 cccttggttac tgctacccat cctacctgca ccctgctttt tccctcttgs cacgcttttt 60
 ttcctctccc tcttaccccc accctgtaca aa atg cat aaa gga tgg aaa aac 113
 Met His Lys Gly Trp Lys Asn
 1 5
 tac tgc agc cag aag tct ttg aat gag gca tca atg gat gaa tat tta 161
 Tyr Cys Ser Gln Lys Ser Leu Asn Glu Ala Ser Met Asp Glu Tyr Leu
 10 15 20
 ggc agc tta ggg ctg ttt cga aag ctg act gcc aag gat gcc tct tgc 209
 Gly Ser Leu Gly Leu Phe Arg Lys Leu Thr Ala Lys Asp Ala Ser Cys

25	30	35	
ctc ttt cgg gcc att tcg	gag cag ttg ttt tgc	agc cag gtc cat cat	257
Leu Phe Arg Ala Ile Ser	Glu Gln Leu Phe Cys	Ser Gln Val His His	
40	45	50	55
ttg gaa atc agg aag gca a			276
Leu Glu Ile Arg Lys Ala			
60			

<210> 3267
 <211> 328
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 154..327

<400> 3267	
tgaaaaatgta aattagtgc gttattatgg magtcagtat ggaacttcct caaaaaacta	60
acaataaaaac tcccatatga tccagcaatc ctaccactgr atatttatcc aaaggaaagg	120
aagtcggtat atttaacagg catctgcacc ccc atg ttt att gca gca cta ttc	174
Met Phe Ile Ala Ala Leu Phe	
1 5	
aca gta gcc aag ata tgg aat caa cct aaa tgt cca tca acg gat gaa	222
Thr Val Ala Lys Ile Trp Asn Gln Pro Lys Cys Pro Ser Thr Asp Glu	
10 15 20	
tgg ata aat aaa atg tgg tac ata tac aca atg gag tac tat cca gac	270
Trp Ile Asn Lys Met Trp Tyr Ile Tyr Thr Met Glu Tyr Tyr Pro Asp	
25 30 35	
ata aaa aag aat gga att ctg aca ttt aag gca aca agg atg aac cgg	318
Ile Lys Lys Asn Gly Ile Leu Thr Phe Lys Ala Thr Arg Met Asn Arg	
40 45 50 55	
aag aca tta t	328
Lys Thr Leu	

<210> 3268
 <211> 334
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 157..333

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ctgctggcag acgagtacac cttcgcttc cgcggccaac acgacacgat caagaaggag	120
tgcctggcct gcagagggggc cgccgctgtg tttgac atg tcc tac ttc ggg aag	174
Met Ser Tyr Phe Gly Lys	
1 5	
ttc tac ctg gtg ggg ctg gat gca agg aag gct gcc gac tgg ctc ttc	222
Phe Tyr Leu Val Gly Leu Asp Ala Arg Lys Ala Ala Asp Trp Leu Phe	

	10		15		20		
tcc gca gat gtc agc cga ccc cca ggc tcc acc gtg tac acg tgc atg							270
Ser Ala Asp Val Ser Arg Pro Pro Gly Ser Thr Val Tyr Thr Cys Met							
	25		30		35		
ctc aac cac cat ggg ggc acc gag agt gac ctg act gtc agc cgc ctg							318
Leu Asn His His Gly Gly Thr Glu Ser Asp Leu Thr Val Ser Arg Leu							
	40		45		50		
gca ccc agc cam cag t							334
Ala Pro Ser Xaa Gln							
55							

<210> 3269
 <211> 351
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 92..349

<400> 3269	
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tggcagcaag aattcccttc tgaaggatgc c atg gct cca ggc acc cca aag	112
Met Ala Pro Gly Thr Pro Lys	
	1 5
tcc ctc ctg ttg tct gct tcc atc aag agg gaa gga gag kst csr acg	160
Ser Leu Leu Leu Ser Ala Ser Ile Lys Arg Glu Gly Glu Xaa Xaa Thr	
	10 15 20
gca tca ccc cac tca tct gcc acc gat gac ctc cac cat tca gac aga	208
Ala Ser Pro His Ser Ser Ala Thr Asp Asp Leu His His Ser Asp Arg	
	25 30 35
tac cag acc ttt ctg cga gta cga gcc aac cgg cag acc cga ctg aat	256
Tyr Gln Thr Phe Leu Arg Val Arg Ala Asn Arg Gln Thr Arg Leu Asn	
	40 45 50 55
gct cgg att ggg ara atg aaa cgg agg aag caa gat gaa ggg cag agg	304
Ala Arg Ile Gly Xaa Met Lys Arg Arg Lys Gln Asp Glu Gly Gln Arg	
	60 65 70
gaa ggc tcc tgc atg gct gag gat gat gct gtg gac atc gag cat ga	351
Glu Gly Ser Cys Met Ala Glu Asp Asp Ala Val Asp Ile Glu His	
	75 80 85

<210> 3270
 <211> 168
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 8..166

<400> 3270	
gggggaa atg cgg gag aga ggg aga gag cga ggc aac ccg ggg ctc aaa	49

	Met	Arg	Glu	Arg	Gly	Arg	Glu	Arg	Gly	Asn	Pro	Gly	Leu	Lys	
	1				5					10					
aca	gtc	aaa	ttc	aaa	tta	aaa	ggt	cga	gac	acg	aat	cag	gga	ata	ttc
Thr	Val	Lys	Phe	Lys	Leu	Lys	Gly	Arg	Asp	Thr	Asn	Gln	Gly	Ile	Phe
15					20					25				30	
cgg	gaa	aga	aag	agg	gaa	cct	gcg	gas	ctc	ggt	cag	ttt	gga	gga	gtc
Arg	Glu	Arg	Lys	Arg	Glu	Pro	Ala	Xaa	Leu	Gly	Gln	Phe	Gly	Gly	Val
				35					40					45	
acg	tat	cac	acg	gga	aac	cag	ca								
Thr	Tyr	His	Thr	Gly	Asn	Gln									
			50												

<210> 3271

<211> 360

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 26..358

<400> 3271

aaatgaacta	gaaaatctag	aagaa	atg	gat	aaa	ttc	ctg	gac	aga	tac	acc				
			Met	Asp	Lys	Phe	Leu	Asp	Arg	Tyr	Thr				
			1				5								
ctc	cca	aga	cta	aac	cag	gaa	aaa	ggt	gaa	tcc	ctg	aat	aga	cca	ata
Leu	Pro	Arg	Leu	Asn	Gln	Glu	Lys	Val	Glu	Ser	Leu	Asn	Arg	Pro	Ile
10				15					20					25	
aca	ggc	tct	gaa	att	gag	gca	ata	att	aat	agc	cta	cca	act	aaa	aaa
Thr	Gly	Ser	Glu	Ile	Glu	Ala	Ile	Ile	Asn	Ser	Leu	Pro	Thr	Lys	Lys
				30					35					40	
agc	cca	gga	cca	gat	gga	ttc	aca	gcc	aaa	ttc	tac	cag	agg	tac	aaa
Ser	Pro	Gly	Pro	Asp	Gly	Phe	Thr	Ala	Lys	Phe	Tyr	Gln	Arg	Tyr	Lys
			45					50					55		
gat	ggg	ctg	gta	cca	ttc	ctt	ctg	aaa	cta	ttc	caa	tca	ata	gaa	aaa
Asp	Gly	Leu	Val	Pro	Phe	Leu	Leu	Lys	Leu	Phe	Gln	Ser	Ile	Glu	Lys
	60					65					70				
gag	gga	atc	ctc	cct	aac	tca	ttt	ttt	gag	gcc	agt	atc	atc	ctg	ata
Glu	Gly	Ile	Leu	Pro	Asn	Ser	Phe	Phe	Glu	Ala	Ser	Ile	Ile	Leu	Ile
	75				80						85				
cca	aag	ccg	ggc	aga	gac	aca	aca	aaa	ama	gag	aat	ttt	aga	cca	ata
Pro	Lys	Pro	Gly	Arg	Asp	Thr	Thr	Lys	Xaa	Glu	Asn	Phe	Arg	Pro	Ile
90				95					100					105	
tcc	ctg	atg	aca	tcg	atg	ca									
Ser	Leu	Met	Thr	Ser	Met										
					110										

<210> 3272

<211> 270

<212> DNA

<213> Homo sapiens

<220>

<221> CDS
<222> 67..270

<400> 3272
aagcacagat ggcagtcctat tcattgaaga tgggtttttt caagggtgagt gttgggtcttt 60
tgcaca atg ctt gag atg gaa atg act tgg ctg aga cta tgt gat gag 108
Met Leu Glu Met Glu Met Thr Trp Leu Arg Leu Cys Asp Glu
1 5 10
tgc tcc aga tgg ggc atg gca tcg gca tgg ggt agg ggt gga aag ctt 156
Cys Ser Arg Trp Gly Met Ala Ser Ala Trp Gly Arg Gly Gly Lys Leu
15 20 25 30
ctt gga gct caa gta gcc ctt cat cct aga aac tgc agc aaa gct aag 204
Leu Gly Ala Gln Val Ala Leu His Pro Arg Asn Cys Ser Lys Ala Lys
35 40 45
atc ttc ctg ttc agt att tta tta atg tct tta aga act ttt cac tgt 252
Ile Phe Leu Phe Ser Ile Leu Leu Met Ser Leu Arg Thr Phe His Cys
50 55 60
aat tat ttc aga ggc aat 270
Asn Tyr Phe Arg Gly Asn
65

<210> 3273
<211> 285
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 40..285

<400> 3273
acagctgctg agggaccact ctgctcccc gcctaagcc atg cac ctc tgt ggg 54
Met His Leu Cys Gly
1 5
ggc aat ggg ctg ctg acc cag aca gac ccc aag gag caa caa agg cag 102
Gly Asn Gly Leu Leu Thr Gln Thr Asp Pro Lys Glu Gln Gln Arg Gln
10 15 20
ctg aag aag cag aag aac cgg gca gcc gcc cag cga asc ggc aga agc 150
Leu Lys Lys Gln Lys Asn Arg Ala Ala Gln Arg Xaa Gly Arg Ser
25 30 35
aca cag aca agg cag acg ccc tgc acc agg tgt gga caa ccc cta acc 198
Thr Gln Thr Arg Gln Thr Pro Cys Thr Arg Cys Gly Gln Pro Leu Thr
40 45 50
cct ttc ctt gtc tct ggc tcc act tac tgg ccc agc cac ctc ttc tcc 246
Pro Phe Leu Val Ser Gly Ser Thr Tyr Trp Pro Ser His Leu Xaa Ser
55 60 65
atc cca cck ktg agc aga cct ccc cca aac tcc tgt aag 285
Ile Pro Pro Xaa Ser Arg Pro Pro Pro Asn Ser Cys Lys
70 75 80

<210> 3274
<211> 280

<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 111..278

<400> 3274
caattaattt ttcataaacc ttctacagct tgtcttttaa ccctccaaac tttggcaaga 60
aatccatatt ctcatgcctt ttaccaaaaa gtacattcta ctttttttac atg aat 116
Met Asn
1
cct ttt cac gac tta cac aga cct tct atg aca tgc ctg gac ttt ctg 164
Pro Phe His Asp Leu His Arg Pro Ser Met Thr Cys Leu Asp Phe Leu
5 10 15
act tgt cct aaa cat ccc tct tta aac aac cat tca ttt aac ttt agg 212
Thr Cys Pro Lys His Pro Ser Leu Asn Asn His Ser Phe Asn Phe Arg
20 25 30
gca aga att tac cat aca gga tcc tgt ctc ata caa aat tat tat tgc 260
Ala Arg Ile Tyr His Thr Gly Ser Cys Leu Ile Gln Asn Tyr Tyr Cys
35 40 45 50
tac atc ctt ccc tac caa ga 280
Tyr Ile Leu Pro Tyr Gln
55

<210> 3275
<211> 231
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 72..230

<400> 3275
aattggggcg cgggcctgtg agccagttgg agttgcggcg gcggaacga ttgggctgag 60
cagaggacga c atg ttg ctt ttc gtg gag cag gta gca tct aaa gga act 110
Met Leu Leu Phe Val Glu Gln Val Ala Ser Lys Gly Thr
1 5 10
ggt tta aat cct aat gcc aaa gta tgg caa gaa att gct cct gga aat 158
Gly Leu Asn Pro Asn Ala Lys Val Trp Gln Glu Ile Ala Pro Gly Asn
15 20 25
act gat gcc acc cca gta act cat gga mct gaa rgc tct tgg cat gaa 206
Thr Asp Ala Thr Pro Val Thr His Gly Xaa Glu Xaa Ser Trp His Glu
30 35 40 45
ata gca gcw aca tca ggt gct cat c 231
Ile Ala Ala Thr Ser Gly Ala His
50

<210> 3276
<211> 329
<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 28..327

<400> 3276

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catggataca aagaatcaat tattaata atg gct gta ctg ccc aaa gga atg tac      54
                               Met Ala Val Leu Pro Lys Gly Met Tyr
                               1               5
aga ttc aat gtt att cct atc aaa cta cca atg aga ttc ttc aca gaa      102
Arg Phe Asn Val Ile Pro Ile Lys Leu Pro Met Arg Phe Phe Thr Glu
10               15               20               25
ctg gaa aaa ttt att tta caa ttt ata tgg aac caa aaa aga gcc cta      150
Leu Glu Lys Phe Ile Leu Gln Phe Ile Trp Asn Gln Lys Arg Ala Leu
               30               35               40
ata gtt aaa gta ata cta agt gaa aac aac aga gct aac aaa gct aga      198
Ile Val Lys Val Ile Leu Ser Glu Asn Asn Arg Ala Asn Lys Ala Arg
               45               50               55
gga atc aca tta ccc aac ttc aaa cta tgt tac aga gct aca gtg abc      246
Gly Ile Thr Leu Pro Asn Phe Lys Leu Cys Tyr Arg Ala Thr Val Xaa
               60               65               70
aat ata gca tgg tac tgg cat aaa aac agg tac ata cac caa tgg mac      294
Asn Ile Ala Trp Tyr Trp His Lys Asn Arg Tyr Ile His Gln Trp Xaa
               75               80               85
aga rta gag atc cca gah ata rgg cac aca ttt at      329
Arg Xaa Glu Ile Pro Xaa Ile Xaa His Thr Phe
90               95               100

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<210> 3277

<211> 311

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 39..311

<400> 3277

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ctttcctatt ttaagaatcc tcttattagt gctgtggc atg aat act tgt cca tct      56
                               Met Asn Thr Cys Pro Ser
                               1               5
gtc tat cca tct atc ccc gag cac ctg cat cct tct cag caa aag cca      104
Val Tyr Pro Ser Ile Pro Glu His Leu His Pro Ser Gln Gln Lys Pro
               10               15               20
gaa ccc kgt cct cac aga gct ccc aag ctg ctg tca aaa ggt gaa cag      152
Glu Pro Xaa Pro His Arg Ala Pro Lys Leu Leu Ser Lys Gly Glu Gln
               25               30               35
agg ctt gat gca gcc agg aaa aca tcc atg agt gca tgt cag gga aag      200
Arg Leu Asp Ala Ala Arg Lys Thr Ser Met Ser Ala Cys Gln Gly Lys
               40               45               50
gct cag cac agc cac ctg ctc cct cat cat ggc cct ccc tgc tcc agg      248

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Ala Gln His Ser His Leu Leu Pro His His Gly Pro Pro Cys Ser Arg
 55 60 65 70
 cag ggt gtt cca tcc aga aga gga gcc tgc acg aag gca agc tgt tca 296
 Gln Gly Val Pro Ser Arg Arg Gly Ala Cys Thr Lys Ala Ser Cys Ser
 75 80 85
 ggg cga aga gca gtc 311
 Gly Arg Arg Ala Val
 90

<210> 3278
 <211> 271
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 27..269

<400> 3278
 agttgtaaac ccaaggccaa gagacc atg gcc acg tta gcc cgg ctg caa gct 53
 Met Ala Thr Leu Ala Arg Leu Gln Ala
 1 5
 agg tcg tcg act gta gga aat cag tac tac ttt agg aac agt gtt gta 101
 Arg Ser Ser Thr Val Gly Asn Gln Tyr Tyr Phe Arg Asn Ser Val Val
 10 15 20 25
 gat cca ttt aga aaa aag gag aat gat gca gca gtt aaa atc caa agc 149
 Asp Pro Phe Arg Lys Lys Glu Asn Asp Ala Ala Val Lys Ile Gln Ser
 30 35 40
 tgg ttt cga gga tgt caa gtt cgg gca tat atc agg cat tta aac agg 197
 Trp Phe Arg Gly Cys Gln Val Arg Ala Tyr Ile Arg His Leu Asn Arg
 45 50 55
 att gta aca att att caa aaa tgg tgg aga agt ttc tta ggc aga aag 245
 Ile Val Thr Ile Ile Gln Lys Trp Trp Arg Ser Phe Leu Gly Arg Lys
 60 65 70
 caa tat caa cta act gtg cag gta aa 271
 Gln Tyr Gln Leu Thr Val Gln Val
 75 80

<210> 3279
 <211> 206
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 20..205

<400> 3279
 atttattctg cccagctg atg ttt gag cca gca tgt cgc gga gga agc aag 52
 Met Phe Glu Pro Ala Cys Arg Gly Gly Ser Lys
 1 5 10
 cga asc tca aca ttt cca atc cga ccc cga agt ggs ctc gct ccc ccs 100

Arg	Xaa	Ser	Thr	Phe	Pro	Ile	Arg	Pro	Arg	Ser	Gly	Leu	Ala	Pro	Pro	
			15					20					25			
ggc	gag	atg	gag	aca	cag	aaa	agg	gtc	aac	cga	gtc	gcc	cta	cta	aga	148
Gly	Glu	Met	Glu	Thr	Gln	Lys	Arg	Val	Asn	Arg	Val	Ala	Leu	Leu	Arg	
		30					35					40				
gca	agg	atg	ccc	acg	tct	gtg	gcc	ggg	gct	gtg	ccg	agt	tct	ttg	aat	196
Ala	Arg	Met	Pro	Thr	Ser	Val	Ala	Gly	Ala	Val	Pro	Ser	Ser	Leu	Asn	
		45				50					55					
tat	cag	atc	t													206
Tyr	Gln	Ile														
60																

<210> 3280
 <211> 345
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 35..343

<400> 3280																
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Met Ala Phe Ser Gln Ile Leu																
1 5																
act	gga	aga	aga	ttt	att	tca	ggc	acc	agc	caa	gtg	sgc	tgt	tyc	tgc	103
Thr	Gly	Arg	Arg	Phe	Ile	Ser	Gly	Thr	Ser	Gln	Val	Xaa	Cys	Xaa	Cys	
		10					15					20				
tct	gga	agc	tgc	tat	tgc	ccg	gta	aga	aac	cag	tat	ctg	gaa	aag	gag	151
Ser	Gly	Ser	Cys	Tyr	Cys	Pro	Val	Arg	Asn	Gln	Tyr	Leu	Glu	Lys	Glu	
		25				30					35					
cag	cgt	cgt	cag	tac	ctc	cta	cgt	ttg	aaa	aac	agc	cag	ctg	gag	aag	199
Gln	Arg	Arg	Gln	Tyr	Leu	Leu	Arg	Leu	Lys	Asn	Ser	Gln	Leu	Glu	Lys	
		40			45				50					55		
acc	tac	ggg	gag	atg	gcc	aag	atc	gtg	gat	gtc	ccc	acc	aag	cag	ctt	247
Thr	Tyr	Gly	Glu	Met	Ala	Lys	Ile	Val	Asp	Val	Pro	Thr	Lys	Gln	Leu	
			60					65					70			
aga	gct	gcc	aac	ccc	ata	gac	tcc	atg	ctc	tgc	cac	ttc	tgc	cac	aat	295
Arg	Ala	Ala	Asn	Pro	Ile	Asp	Ser	Met	Leu	Cys	His	Phe	Cys	His	Asn	
			75				80					85				
gtc	agc	ttt	ccc	tgt	acc	aga	aat	ggc	tgt	ggt	gac	atg	gag	cac	ttc	343
Val	Ser	Phe	Pro	Cys	Thr	Arg	Asn	Gly	Cys	Val	Asp	Met	Glu	His	Phe	
		90					95					100				
aa																345

<210> 3281
 <211> 453
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 7..453

<400> 3281

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      Met Ser Lys Ser Leu Gly Asn Val Leu Asp Pro Arg Asp Ile
          1             5             10
atc agt ggg gtg gag atg cag ttg ctg cag gaa aag ctg aga agc gga      96
Ile Ser Gly Val Glu Met Gln Leu Leu Gln Glu Lys Leu Arg Ser Gly
15             20             25             30
aat ttg gac cct gca gag ctg gcc att gtg gct gca gca cag aaa aag      144
Asn Leu Asp Pro Ala Glu Leu Ala Ile Val Ala Ala Ala Gln Lys Lys
          35             40             45
gac ttt cct cac ggg atc cct gag tgt ggg aca gat gcc ctg aga ttc      192
Asp Phe Pro His Gly Ile Pro Glu Cys Gly Thr Asp Ala Leu Arg Phe
          50             55             60
aca ctc tgc tcc cat gga gtt cag gcg ggc gac ttg cac ctg tca gtc      240
Thr Leu Cys Ser His Gly Val Gln Ala Gly Asp Leu His Leu Ser Val
          65             70             75
tct gag gtc cag agc tgc cga cat ttc tgc aac aag atc tgg aat gct      288
Ser Glu Val Gln Ser Cys Arg His Phe Cys Asn Lys Ile Trp Asn Ala
          80             85             90
ctt cgc ttt atc ctc aat gct tta ggg gag aaa ttt gtg cca cag ccg      336
Leu Arg Phe Ile Leu Asn Ala Leu Gly Glu Lys Phe Val Pro Gln Pro
          95             100             105             110
gct gag gag ctg tct ccc tcc tcc ccg atg gat gcc tgg atc ctg agc      384
Ala Glu Glu Leu Ser Pro Ser Ser Pro Met Asp Ala Trp Ile Leu Ser
          115             120             125
cgc ctt gcc ctg gct gcc cag gag tgt gag cgg ggc ttc ctc asc cga      432
Arg Leu Ala Leu Ala Ala Gln Glu Cys Glu Arg Gly Phe Leu Xaa Arg
          130             135             140
gag ctc tgc ctc gtc act cat      453
Glu Leu Ser Leu Val Thr His
          145

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<210> 3282

<211> 262

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 69..260

<400> 3282

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aaccggaggg aaactcaatg cacagaccct gatttgcaac ttgtaatgta aatcaactca      60
actgcatc atg tac tta cca gcc acc ttc tcc caa ctg tgg ccg ggg ccg      110
      Met Tyr Leu Pro Ala Thr Phe Ser Gln Leu Trp Pro Gly Pro
          1             5             10
aga agc agc atg ttc tgt cca tct gta aaa ggc ctt ctt tct ctc tta      158
Arg Ser Ser Met Phe Cys Pro Ser Val Lys Gly Leu Leu Ser Leu Leu
15             20             25             30
aga cgt cac aac tgg ttg tta ctg aga act tta gaa rha cga cta gat      206
Arg Arg His Asn Trp Leu Leu Leu Arg Thr Leu Glu Xaa Arg Leu Asp

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Leu	Gly	Ser	Leu	Phe	Gln	Asn	Val	Thr	Glu	Glu	Lys	Ala	Asn	Ile	Ile	
	20						25					30				
gct	tca	gcc	ctt	gcc	cag	atc	cca	cag	aag	gtg	tta	tgg	agg	tac	aaa	261
Ala	Ser	Ala	Leu	Ala	Gln	Ile	Pro	Gln	Lys	Val	Leu	Trp	Arg	Tyr	Lys	
	35						40				45					
gga	aaa	aaa	cca	tcc	aca	tta	gga	gcc	aat	act	cgg	ctg	tat	gat	tgg	309
Gly	Lys	Lys	Pro	Ser	Thr	Leu	Gly	Ala	Asn	Thr	Arg	Leu	Tyr	Asp	Trp	
50					55					60					65	
ata	ccc	cag	aat	gat	ctt	ctt	ggg	cat	ccc	aaa	acc	aaa	gc			350
Ile	Pro	Gln	Asn	Asp	Leu	Leu	Gly	His	Pro	Lys	Thr	Lys				
			70						75							

<210> 3285
 <211> 411
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 142..411

<400> 3285																
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tgacttgctg	gtgaagg	gtggagg	gttggtgt	ggacaagctc	tttgatttgg	atgagaaact										120
aatgttaaga	atgggtcaga	a	atg	ggg	ctg	ctc	agc	ctc	tgg	acc	aac	ccc				171
			Met	Gly	Leu	Leu	Ser	Leu	Trp	Thr	Asn	Pro				
			1				5					10				
agg	aag	agt	ctg	aag	agc	agc	cag	tgt	ttc	ggc	ttg	tgc	cct	gta	tac	219
Arg	Lys	Ser	Leu	Lys	Ser	Ser	Gln	Cys	Phe	Gly	Leu	Cys	Pro	Val	Tyr	
			15				20							25		
ttg	aag	ctg	cca	aac	aag	tac	ggt	ctg	aaa	atc	cag	aat	ggc	ttg	atg	267
Leu	Lys	Leu	Pro	Asn	Lys	Tyr	Val	Leu	Lys	Ile	Gln	Asn	Gly	Leu	Met	
			30				35						40			
ttt	aca	tgc	aca	ttt	tac	aac	tgc	tta	cta	cag	tgg	atg	atg	gaa	ttc	315
Phe	Thr	Cys	Thr	Phe	Tyr	Asn	Cys	Leu	Leu	Gln	Trp	Met	Met	Glu	Phe	
		45					50					55				
aag	caa	ttg	tac	att	gtc	ctg	aca	ctg	gaa	aag	aca	ttt	gga	att	tac	363
Lys	Gln	Leu	Tyr	Ile	Val	Leu	Thr	Leu	Glu	Lys	Thr	Phe	Gly	Ile	Tyr	
		60					65				70					
ttt	ttg	acc	tgg	tct	gcc	atg	aat	tct	gcc	agt	ctg	atg	atc	cag	ccc	411
Phe	Leu	Thr	Trp	Ser	Ala	Met	Asn	Ser	Ala	Ser	Leu	Met	Ile	Gln	Pro	
					80					85					90	

<210> 3286
 <211> 412
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 209..412

<400> 3286

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catcttatat ggggtgcaatt catgatatcc caaaacaatt acaatagtaa tatcaaagat      60
tactgaccac agatgaccat aatagatata ataataatga gaaagtttga aatattgtgg      120
agaawtamcc acaatgtgac agagacacaa agtgagcaca ggctgttgga aaaatgggtgc      180
tgatagtctt gcctaataa ggattgct atg aac ctt cca ttc gta agc atc      232
                Met Asn Leu Pro Phe Val Ser Ile
                1                5
aca gta tct gca aga tgc aat aag gtg atg ctc aat aaa aca tgg tat      280
Thr Val Ser Ala Arg Cys Asn Lys Val Met Leu Asn Lys Thr Trp Tyr
                10                15                20
cta tat ttg cat atg gct tac cag ttg agc atc act aat cta aaa atc      328
Leu Tyr Leu His Met Ala Tyr Gln Leu Ser Ile Thr Asn Leu Lys Ile
                25                30                35                40
caa aac ttg aaa tgc tcc ctt gag cat ttg agt atc ata ttg tca scc      376
Gln Asn Leu Lys Cys Ser Leu Glu His Leu Ser Ile Ile Leu Ser Xaa
                45                50                55
aaa agt ttt cag rtt tta gra cat ttt gca ttt tca      412
Lys Ser Phe Gln Xaa Leu Xaa His Phe Ala Phe Ser
                60                65

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<210> 3287

<211> 340

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 183..338

<400> 3287

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gactctcgga gcgcgcacag tcggctcgca gcgcggcact acagcggccc cggcgcaggg      60
agttcagatt aaagaagcta attgatcaag aaatcaagtc tcaggaggag aaggagcaag      120
aaaaggagaa aagggtcacc accctgaaag aggagstrcc caagctgaag tcttttgctt      180
tg atg gtg gtg gat gaa cag caa agg ctg acg gca cag ctc acc ctt      227
    Met Val Val Asp Glu Gln Gln Arg Leu Thr Ala Gln Leu Thr Leu
    1                5                10                15
caa aga cag aaa atc caa gag ctg acc aca aat gca aag gaa aca cat      275
Gln Arg Gln Lys Ile Gln Glu Leu Thr Thr Asn Ala Lys Glu Thr His
                20                25                30
acc aaa cta gcc ctt gct gaa gcc aga gtt cag gag gaa gag cag aag      323
Thr Lys Leu Ala Leu Ala Glu Ala Arg Val Gln Glu Glu Glu Gln Lys
                35                40                45
gca acc aga cta gag gt      340
Ala Thr Arg Leu Glu
                50

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<210> 3288

<211> 247

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 32..247

<400> 3288

ttttatatct gcacaaaaag aaaccacgga a atg gaa gac aca gac att gaa 52
Met Glu Asp Thr Asp Ile Glu
1 5
gac tcc ttg tat aag gat gta gac tat ggg aca gaa gtt tta caa atc 100
Asp Ser Leu Tyr Lys Asp Val Asp Tyr Gly Thr Glu Val Leu Gln Ile
10 15 20
gaa cat tct tac tgc aga caa gat ata aat aag gaa cat ctt tgg cag 148
Glu His Ser Tyr Cys Arg Gln Asp Ile Asn Lys Glu His Leu Trp Gln
25 30 35
aaa gtc tct aag cta cat tca aag ata act ctt cta gag tta aaa gag 196
Lys Val Ser Lys Leu His Ser Lys Ile Thr Leu Leu Glu Leu Lys Glu
40 45 50 55
caa caa act cta ggt aga ttg aag tct ttg gaa gct ctt ata agg caa 244
Gln Gln Thr Leu Gly Arg Leu Lys Ser Leu Glu Ala Leu Ile Arg Gln
60 65 70
cat 247
His

<210> 3289

<211> 384

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 116..382

<400> 3289

gcggggcaag atggcggcgc ccagacaggc ctggagcacg gatgaataag agggaacccc 60
cacacggaga cactgctgga gagagtcgta ctggggaggc agctggagca gcaag atg 118
Met
1
ctg tcg aga ccg aag cca ggg gag tcc gag gtg gac ctg ctg cac ttc 166
Leu Ser Arg Pro Lys Pro Gly Glu Ser Glu Val Asp Leu Leu His Phe
5 10 15
cag agt cag ttt ctc gca gct ggt gca gcc cca gca gtg cag ctg gtg 214
Gln Ser Gln Phe Leu Ala Ala Gly Ala Ala Pro Ala Val Gln Leu Val
20 25 30
aag aaa gga aat agg ggc ggt ggt gat gcc aac tca gac cgg cct ccg 262
Lys Lys Gly Asn Arg Gly Gly Asp Ala Asn Ser Asp Arg Pro Pro
35 40 45
ctc cag gac cat cgg gat gtg gtg atg ttg gac aat ctc cca gat ttg 310
Leu Gln Asp His Arg Asp Val Val Met Leu Asp Asn Leu Pro Asp Leu
50 55 60 65
ccc cca gct ttg gtc cct tct cct cca aag aga gcc agg ccc agc cct 358
Pro Pro Ala Leu Val Pro Ser Pro Pro Lys Arg Ala Arg Pro Ser Pro
70 75 80
ggc cac tgc ctg cct gag gat gag ga 384
Gly His Cys Leu Pro Glu Asp Glu

004220"666F550

<210> 3290
 <211> 355
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 137..355

<400> 3290
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 ggctctgtga gcgcccctga gcgcccgcag cggccgcggt gggttcttca ggttatctta 120
 tgatgaggct tttgct atg gct aat gat ccc ttg gaa ggc ttc cat gaa gta 172
 Met Ala Asn Asp Pro Leu Glu Gly Phe His Glu Val
 1 5 10
 aac ctt gct tca cct act tct ccg gac ctt ctt ggt gtg tat gaa tca 220
 Asn Leu Ala Ser Pro Thr Ser Pro Asp Leu Leu Gly Val Tyr Glu Ser
 15 20 25
 gga act caa gag cag act acc tca cca agt gtc atc tac cgg cca cac 268
 Gly Thr Gln Glu Gln Thr Thr Ser Pro Ser Val Ile Tyr Arg Pro His
 30 35 40
 cct tca gct tta tcc tct gta cct atc cag gca aat gca tta gat gtt 316
 Pro Ser Ala Leu Ser Ser Val Pro Ile Gln Ala Asn Ala Leu Asp Val
 45 50 55 60
 tct gaa ctt cct aca caa ccc gtg tat tca tcc ccc agc 355
 Ser Glu Leu Pro Thr Gln Pro Val Tyr Ser Ser Pro Ser
 65 70

<210> 3291
 <211> 205
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 48..203

<400> 3291
 aattcagccc tgacgacagc agtgggttga gccatcaagg tgagtgg atg gaa act 56
 Met Glu Thr
 1
 tgg aag gga aca act gag tca agg aat gga aat cca aat att cca tgg 104
 Trp Lys Gly Thr Thr Glu Ser Arg Asn Gly Asn Pro Asn Ile Pro Trp
 5 10 15
 gag gcc ggg ttt gat ttt gtt tgt tgg tgg tgg tgt aag aac gag ggc 152
 Glu Ala Gly Phe Asp Phe Val Cys Trp Trp Trp Cys Lys Asn Glu Gly
 20 25 30 35
 tgt gac ctt ttc agc tgc gcc tgt gtg atc cca tct tac ttc ttt ttt 200
 Cys Asp Leu Phe Ser Ser Ala Cys Val Ile Pro Ser Tyr Phe Phe Phe
 40 45 50

ttt tt
Phe

205

<210> 3292
<211> 410
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 125..409

<400> 3292
cttaactgtc actgtggaga ggagagagag aggacagaga gcaagtcact cccggctgcc 60
tttttcacct ctgacagagc ccagacacca tgaacgcaag tgaattccga agagagggaa 120
ggag atg gtg gat tac gtg gcc aac tac atg gaa ggc att gag gga cgc 169
Met Val Asp Tyr Val Ala Asn Tyr Met Glu Gly Ile Glu Gly Arg
1 5 10 15
cag gtc tac cct gac gtg gag ccc ggg tac ctg cgg ccg ctg atc cct 217
Gln Val Tyr Pro Asp Val Glu Pro Gly Tyr Leu Arg Pro Leu Ile Pro
20 25 30
gcc gct gcc cct cag gag cca gac acg ttt gag gac atc atc aac gac 265
Ala Ala Ala Pro Gln Glu Pro Asp Thr Phe Glu Asp Ile Ile Asn Asp
35 40 45
gtt gag aag ata atc atg cct ggg gtg acg cac tgg cac agc ccc tac 313
Val Glu Lys Ile Ile Met Pro Gly Val Thr His Trp His Ser Pro Tyr
50 55 60
ttc ttc gcc tac ttc ccc act gcc agc tcg tac ccg gcc atg ctt gcg 361
Phe Phe Ala Tyr Phe Pro Thr Ala Ser Ser Tyr Pro Ala Met Leu Ala
65 70 75
gac atg ctg tgc ggg gcc att ggc tgc atc ggc ttc tcc tgg ggc tgc t 410
Asp Met Leu Cys Gly Ala Ile Gly Cys Ile Gly Phe Ser Trp Gly Cys
80 85 90 95

<210> 3293
<211> 478
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 257..478

<400> 3293
gatggcagta ttcctgagaa ctttgtgtag atgtccaaat gtatgaggaa agactaggaa 60
aatatccaga aaataccaca gtgatgaatg tggataaatt tttgctcaga actctgtcct 120
aattcagcat cagaaattca cactgggtgag gaattcctak gaatgtaaca agtatgggaa 180
agcctttact caggagtgtg ggcttcatgc aaataagata attcacactg gagttagata 240
tataaatgag aagaat atg gga aag ctt tca gtg caa aca ctg gac tca ttc 292
Met Gly Lys Leu Ser Val Gln Thr Leu Asp Ser Phe
1 5 10
atc gtt aag aga atc cat act gga gag aga ccc tat aat aaa tgt gac 340

Ile	Val	Lys	Arg	Ile	His	Thr	Gly	Glu	Arg	Pro	Tyr	Asn	Lys	Cys	Asp	
	15						20					25				
aag	tgc	aac	aaa	gcc	ttt	ggc	cag	tgg	tca	gtc	ctc	aac	cag	cac	cag	388
Lys	Cys	Asn	Lys	Ala	Phe	Gly	Gln	Trp	Ser	Val	Leu	Asn	Gln	His	Gln	
	30					35				40						
agg	ctt	cac	acc	agg	gag	ata	tgt	tac	tac	cag	tgt	aac	aag	tgt	ggc	436
Arg	Leu	His	Thr	Arg	Glu	Ile	Cys	Tyr	Tyr	Gln	Cys	Asn	Lys	Cys	Gly	
45					50				55						60	
aag	ttc	aca	gtc	aga	att	cag	ctt	ttt	cat	cat	atc	aga	atc			478
Lys	Phe	Thr	Val	Arg	Ile	Gln	Leu	Phe	His	His	Ile	Arg	Ile			
				65					70							

<210> 3294
 <211> 246
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 17..244

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		Met	Val	Val	Val	Thr	Gly	Arg	Glu	Pro	Asp	Ser	Arg				
		1				5					10						
cgt	cag	gac	ggc	gcc	atg	tcc	agc	tct	gac	gcc	gaa	gac	gac	ttt	ctg	100	
Arg	Gln	Asp	Gly	Ala	Met	Ser	Ser	Ser	Asp	Ala	Glu	Asp	Asp	Phe	Leu		
		15				20					25						
gag	ccg	gcc	acg	ccg	acg	gcc	acg	cag	gcg	ggg	cac	gcg	stg	ccc	cct	148	
Glu	Pro	Ala	Thr	Pro	Thr	Ala	Thr	Gln	Ala	Gly	His	Ala	Xaa	Pro	Pro		
		30				35				40							
gct	gcc	aca	gga	agt	ttc	ctg	agg	ttg	ttc	ccc	kka	aca	tcg	gag	ggg	196	
Ala	Ala	Thr	Gly	Ser	Phe	Leu	Arg	Leu	Phe	Pro	Xaa	Thr	Ser	Glu	Gly		
45					50				55						60		
ctc	act	tca	cta	cac	gcc	tgt	cca	cac	tgc	ggc	gct	acg	aag	aca	cca	244	
Leu	Thr	Ser	Leu	His	Ala	Cys	Pro	His	Cys	Gly	Ala	Thr	Lys	Thr	Pro		
				65					70					75			
tt																246	

<210> 3295
 <211> 363
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 160..363

<400> 3295																	
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agtggagaca	gggtttcacc	gtcttgcca	ggctggtgtt	gaactcctga	cctcgtgatc											120	
caccggcttc	agcctcccaa	aagtgctggg	attacaggc	atg	agc	cac	cgt	gcc								174	

	Met	Ser	His	Arg	Ala	
	1				5	
cgg cca cct caa ttt ttt ttt tct gag ttt cat gtt aca cag aac ata						222
Arg Pro Pro Gln Phe Phe Phe Ser Glu Phe His Val Thr Gln Asn Ile						
	10				20	
cct ttt tgt ttt gga gct agc tac agg gaa gca cag gct tct cta gag						270
Pro Phe Cys Phe Gly Ala Ser Tyr Arg Glu Ala Gln Ala Ser Leu Glu						
	25				35	
tgg aat gta caa ttc tta tca adg caa aaa gtt aaa gac tac ttg ctt						318
Trp Asn Val Gln Phe Leu Ser Xaa Gln Lys Val Lys Asp Tyr Leu Leu						
	40				50	
ttt aaa att agg gag aat gaa aaa tmt vca gca ctt ttc ccc agc						363
Phe Lys Ile Arg Glu Asn Glu Lys Xaa Xaa Ala Leu Phe Pro Ser						
	55				65	

<210> 3296

<211> 324

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 128..322

<400> 3296

agaaagtcaa tattgtgtaa agttgagaga aaagtcttca cagcggaga agaaatcact	60
ttttgtccc gaatcagtggt gtggaggcaa aacccttcag caagaagaga agcaacttca	120
gccgtgt atg caa atg gat aac cgg ttg cct ccc aaa aaa gtt cca ggt	169
Met Gln Met Asp Asn Arg Leu Pro Pro Lys Lys Val Pro Gly	
	10
ttc tgt tcc ttt cgc tat gga ttg tct ttc ctt gtg cac tgt tgt aat	217
Phe Cys Ser Phe Arg Tyr Gly Leu Ser Phe Leu Val His Cys Cys Asn	
	30
gtt ata ata aca gca cag cgt gcg tgc ctg aac ctc aca atg gta gtc	265
Val Ile Ile Thr Ala Gln Arg Ala Cys Leu Asn Leu Thr Met Val Val	
	45
atg gtg aat agc aca gat cca cat ggt ttg ccc aac acc tcc aca aag	313
Met Val Asn Ser Thr Asp Pro His Gly Leu Pro Asn Thr Ser Thr Lys	
	60
aag ctc ctg ga	324
Lys Leu Leu	
	65

<210> 3297

<211> 356

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 76..354

<400> 3297
gaagaaggat taaaagatgg tcatacagagc tcccatggag acattttttc acactttcttt 60
ggggattttg gtttc atg ttt gga gga acc cct cgt cag caa gac aga aat 111
Met Phe Gly Gly Thr Pro Arg Gln Gln Asp Arg Asn
1 5 10
att cca aga gga agt gat att att gta gat cta gaa gtc act ttg gaa 159
Ile Pro Arg Gly Ser Asp Ile Ile Val Asp Leu Glu Val Thr Leu Glu
15 20 25
gaa gta tat gca gga aat ynt gtg gaa gta gtt aga aac aaa cct gtg 207
Glu Val Tyr Ala Gly Asn Xaa Val Glu Val Val Arg Asn Lys Pro Val
30 35 40
gca agg cag gct cct ggc aaa cgg aag tgc aat tgt cgg caa gag atg 255
Ala Arg Gln Ala Pro Gly Lys Arg Lys Cys Asn Cys Arg Gln Glu Met
45 50 55 60
cgg acc acc cag ctg ggc cct ggg cgc ttc caa atg acc cag gag gtg 303
Arg Thr Thr Gln Leu Gly Pro Gly Arg Phe Gln Met Thr Gln Glu Val
65 70 75
gtc tgc gac gaa tgc cct aat gtc aaa cta gtg aat gaa gaa cga acg 351
Val Cys Asp Glu Cys Pro Asn Val Lys Leu Val Asn Glu Glu Arg Thr
80 85 90
ctg gt 356
Leu

<210> 3298
<211> 307
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 143..307

<400> 3298
cactttctac cattgagttc cagagagaag ccctggagaa ctcacacacc aacactgagg 60
tgttgaggaa catgggcttt gcagcaaaag cgatgaaatc tgttcatgaa aacatggatc 120
tgracaaaat wagrwtgwt kg atg caa gag atc aca gag caa cag gat atc 172
Met Gln Glu Ile Thr Glu Gln Gln Asp Ile
1 5 10
gcc caa gaa atc tca gaa gca ttt tct caa cgg gtt ggc ttt ggt gat 220
Ala Gln Glu Ile Ser Glu Ala Phe Ser Gln Arg Val Gly Phe Gly Asp
15 20 25
gac ttt gat gag gat gag ttg atg gca gaa ctt gaa gaa ttg gaa cag 268
Asp Phe Asp Glu Asp Glu Leu Met Ala Glu Leu Glu Glu Leu Glu Gln
30 35 40
gag gaa tta aat aag aag atg aca aat atc cgc ctt ccc 307
Glu Glu Leu Asn Lys Lys Met Thr Asn Ile Arg Leu Pro
45 50 55

<210> 3299
<211> 445
<212> DNA
<213> Homo sapiens

<220>

<221> CDS

<222> 261..443

<400> 3299

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aatcaaagcc acaatgacac cagtcagcat ggggtgttatt aagaagtcag aaaatcacag      60
atgctggcga ggttgtggag aaaaaggaat gcttatacgc agttggtggg agtgtaaatt      120
agttcaactg ttgtkgaaag actgtgtgga aattcctcaa agatctaaag atagaaatac      180
cattcaaccc ataaatctca ttagtgggta tataacccaaa ggaatataaa tcaactctatt      240
ataaagacac atgcacatgt atg ttc att gca gca ctc ttc acg gta gca gag      293
                        Met Phe Ile Ala Ala Leu Phe Thr Val Ala Glu
                        1           5           10
aca tgg aat cag tct aaa tgc ctg tca ata ata gac tgg rta aag aaa      341
Thr Trp Asn Gln Ser Lys Cys Leu Ser Ile Ile Asp Trp Xaa Lys Lys
                        15           20           25
atg tgg tac ata tat acc atg gaa tac tat gca gcc att aaa aag rac      389
Met Trp Tyr Ile Tyr Thr Met Glu Tyr Tyr Ala Ala Ile Lys Lys Xaa
                        30           35           40
aag att atg tcc ttt gcg ggg aca tgg atg aag gtg gaa gct att atc      437
Lys Ile Met Ser Phe Ala Gly Thr Trp Met Lys Val Glu Ala Ile Ile
                        45           50           55
ctc agc aa      445
Leu Ser
60
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<210> 3300

<211> 302

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 53..301

<400> 3300

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gacaactcgc gccagctacg gggcctcaga gaagccggac ttcgcaagca cc atg cag      58
                        Met Gln
                        1
tgg ata agg ggc gga tcg gga atg ctg atc act gga gat tcc atc gtt      106
Trp Ile Arg Gly Gly Ser Gly Met Leu Ile Thr Gly Asp Ser Ile Val
                        5           10           15
agt gct gag gca gtt aaw tgg gat cac gtc acc atg gcc aac cgg gag      154
Ser Ala Glu Ala Val Xaa Trp Asp His Val Thr Met Ala Asn Arg Glu
                        20           25           30
ttg gca ttt aaa gct ggc gac gtc atc aaa gtc ttg gat gct tcc aac      202
Leu Ala Phe Lys Ala Gly Asp Val Ile Lys Val Leu Asp Ala Ser Asn
                        35           40           45           50
aag gat tgg tgg tgg ggc cag atc gac gat gag gag gga tgg ttt cct      250
Lys Asp Trp Trp Trp Gly Gln Ile Asp Asp Glu Glu Gly Trp Phe Pro
                        55           60           65
gcc agc ttt gtg agg ctc tgg gtg aac cag gag gat gag gtg gag gag      298
Ala Ser Phe Val Arg Leu Trp Val Asn Gln Glu Asp Glu Val Glu Glu
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004220"066T550

70 75 80 302
gga t
Gly

<210> 3301
<211> 254
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 96..254

<400> 3301
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caggatcaga caaccggaaa tgatccctcg gatta atg ctg aac tgt tgt ttc 113
Met Leu Asn Cys Cys Phe
1 5
ggc caa ctg ctc ttt caa mtt cma agc ttt tct tct cck aag gaa agt 161
Gly Gln Leu Leu Phe Gln Xaa Xaa Ser Phe Ser Ser Pro Lys Glu Ser
10 15 20
gtt cca aga aga cat ctt tca gaa gga aca aat tct tat gcg aca aga 209
Val Pro Arg Arg His Leu Ser Glu Gly Thr Asn Ser Tyr Ala Thr Arg
25 30 35
ctt cta aat aat cat caa gtt cca cct cag tct gaa cct gtg agc 254
Leu Leu Asn Asn His Gln Val Pro Pro Gln Ser Glu Pro Val Ser
40 45 50

<210> 3302
<211> 177
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 19..177

<400> 3302
tagggatgta gtttcacc atg tca ccg agg ctg gtc tca aac tcc tgg gca 51
Met Ser Pro Arg Leu Val Ser Asn Ser Trp Ala
1 5 10
caa gcg att tcg ccc act tca gcc tcc caa aat att ggg att aca ggc 99
Gln Ala Ile Ser Pro Thr Ser Ala Ser Gln Asn Ile Gly Ile Thr Gly
15 20 25
gtt asc acy aca ctc ggc cca tat ttg gtt ttg agg ata agt tgg gra 147
Val Xaa Thr Thr Leu Gly Pro Tyr Leu Val Leu Arg Ile Ser Trp Xaa
30 35 40
cam ytt ggr aat ctt ttc agc aga ggg gtg 177
Xaa Xaa Gly Asn Leu Phe Ser Arg Gly Val
45 50

<210> 3303

SECRET

SECRET

[illegible][illegible]

SECRET

SECRET

ctc atg cag act aac aaa atg agc aat tta cat tta aga raa atc tac	275
Leu Met Gln Thr Asn Lys Met Ser Asn Leu His Leu Arg Xaa Ile Tyr	
20 25 30	
aac aca aac ata ctt agt ttc tat ttg tat aca aga gaa cga atg cat	323
Asn Thr Asn Ile Leu Ser Phe Tyr Leu Tyr Thr Arg Glu Arg Met His	
35 40 45	
gaa ctc att tac tca ttt aac aaa cgt ttg ttg acc ccc ta	364
Glu Leu Ile Tyr Ser Phe Asn Lys Arg Leu Leu Thr Pro	
50 55 60	

<210> 3305
 <211> 374
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 156..374

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gttgtcttac cgcagtgagt accacgcggt actacagaga cgggtgccc gtgtgcccgg	120
caggtgggag csgcccgcac cagcggcctc gggga atg gaa gcg gag aac gcg	173
Met Glu Ala Glu Asn Ala	
1 5	
ggc agc tat tcc ctt cag caa gct caa gct ttt tat acg ttt cca ttt	221
Gly Ser Tyr Ser Leu Gln Gln Ala Gln Ala Phe Tyr Thr Phe Pro Phe	
10 15 20	
caa caa ctg atg gct gaa gct cct aat atg gca gtt gtg aat gaa cag	269
Gln Gln Leu Met Ala Glu Ala Pro Asn Met Ala Val Val Asn Glu Gln	
25 30 35	
can atg cca gaa gaa gtt cca gcc cca gct cct gct cag gaa cca gtg	317
Xaa Met Pro Glu Glu Val Pro Ala Pro Ala Pro Ala Gln Glu Pro Val	
40 45 50	
caa gag gct cca aaa gga aga aaa aga aaa ccc aga aca aca gaa cca	365
Gln Glu Ala Pro Lys Gly Arg Lys Arg Lys Pro Arg Thr Thr Glu Pro	
55 60 65 70	
aaa caa ccc	374
Lys Gln Pro	

<210> 3306
 <211> 237
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> 48..236

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Met Glu Phe	

	10		15		20	
gac tat aaa cag tac gtg ttt ggc ggc tgg gcc tkg ggc ttg gtg gtg						149
Asp Tyr Lys Gln Tyr Val Phe Gly Gly Trp Ala Xaa Gly Leu Val Val						
	25		30		35	
tat ctc cga cac tca gag gat ttc cct aga gat tat gac gtt gca gcc						197
Tyr Leu Arg His Ser Glu Asp Phe Pro Arg Asp Tyr Asp Val Ala Ala						
	40		45		50	
ccg ctg cga gga cgt aga gac ggc cga ggg ggt agc ttt aac tgc gac						245
Pro Leu Arg Gly Arg Arg Asp Gly Arg Gly Gly Ser Phe Asn Cys Asp						
55	60		65		70	
ggt						248
Gly						

<210> 3309
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<220>
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Met Ala Ala Ala Ala Leu Gly Ser Ser	
	1 5
tca ggc tcg gcg tcc ccg gwc gtg gct gag ctc tgc cag aac acc ccg	99
Ser Gly Ser Ala Ser Pro Xaa Val Ala Glu Leu Cys Gln Asn Thr Pro	
10 15 20 25	
gag acc ttt ttg gag gcc tcc aag ctg ctg ctc acc tat gct gac aac	147
Glu Thr Phe Leu Glu Ala Ser Lys Leu Leu Leu Thr Tyr Ala Asp Asn	
	30 35 40
atc ctc aga aac cct aat gat gaa aaa tat aga tcc atc cgg att gga	195
Ile Leu Arg Asn Pro Asn Asp Glu Lys Tyr Arg Ser Ile Arg Ile Gly	
	45 50 55
aac aca gcc ttt tct act aga ctc ttg cct gtc aga gga gct gtt gaa	243
Asn Thr Ala Phe Ser Thr Arg Leu Leu Pro Val Arg Gly Ala Val Glu	
	60 65 70
tgt tta ttt gaa atg ggc ttt gaa gag gga gaa amc atc tca tct ttc	291
Cys Leu Phe Glu Met Gly Phe Glu Glu Gly Glu Xaa Ile Ser Ser Phe	
	75 80 85
cta aaa aag ctt cvr tgg agc agc tgc aaa aaa att cgt gas mt	335
Leu Lys Lys Leu Xaa Trp Ser Ser Cys Lys Lys Ile Arg Xaa	
90 95 100	

<210> 3310
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 <212> DNA
 <213> Homo sapiens

<220>
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 <222> 254..406

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gtacgtgtgt ctgctgttag aatataaaac tagactctaa gcgtgctcat tttatttttc 120
cattgccttt gatatacatat gaatttagtt atacagaygg agcatccgaa atgcttgagg 180
tcagtaatgt ttcagatttt ggggtttttt ggatttttga atatttgcac atatacaatg 240
agatatcttg ggg atg aga ccg aat act aaa cac gaa att gat tca tgt 289
          Met Arg Pro Asn Thr Lys His Glu Ile Asp Ser Cys
              1             5             10
gca cat agc ctg aag gta gtt tca tac agt att tta aat ttt gtg cac 337
Ala His Ser Leu Lys Val Val Ser Tyr Ser Ile Leu Asn Phe Val His
          15             20             25
gma caa agt ttg tgt ata ttg act atc aaa ggg caa ggg tgt cga cac 385
Xaa Gln Ser Leu Cys Ile Leu Thr Ile Lys Gly Gln Gly Cys Arg His
          30             35             40
agg tat gca gtt tta cac tgc 406
Arg Tyr Ala Val Leu His Cys
          45             50

<210> 3311
<211> 357
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 34..357

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          Met Asp His Leu Glu Ser Phe
              1             5
att gct gaa tgt gat cgg aga act gag ctg gcc aag aag cgg ctg gca 102
Ile Ala Glu Cys Asp Arg Arg Thr Glu Leu Ala Lys Lys Arg Leu Ala
          10             15             20
gaa aca cag gag gaa atc agt gcg vna gtt tct gca aag gca gaa aaa 150
Glu Thr Gln Glu Glu Ile Ser Ala Xaa Val Ser Ala Lys Ala Glu Lys
          25             30             35
gta cat gag tta aat gaa gaa ata gga aaa ctg ctt gct aaa gcc gaa 198
Val His Glu Leu Asn Glu Glu Ile Gly Lys Leu Leu Ala Lys Ala Glu
          40             45             50             55
cag cta ggg gct gaa ggt aat gtg gat gaa tcc cag aag att ctt atg 246
Gln Leu Gly Ala Glu Gly Asn Val Asp Glu Ser Gln Lys Ile Leu Met
          60             65             70
gaa gtg gaa aaa gtt cgt gcg aag aaa aaa gaa gct gag gaa gaa tac 294
Glu Val Glu Lys Val Arg Ala Lys Lys Lys Glu Ala Glu Glu Glu Tyr
          75             80             85
aga aat tcc atg cct gca tcc agt ttt cag cag caa aag ctg cgt gtc 342
Arg Asn Ser Met Pro Ala Ser Ser Phe Gln Gln Gln Lys Leu Arg Val
          90             95             100
tgc gag gtc tgt tca 357
Cys Glu Val Cys Ser

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105

<210> 3312
<211> 486
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 311..484

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aaactcgcc ttgctgaaga gacaggcatt tgtgggagct gtgtgtgttt gttgtgtgtg 120
ttgtgtgtgt tgtgtgtgtt ttttcatgtg ctggaaatat ggcttgtaat gttctaatat 180
ttttctaatt tagtcttttt gcttttagact catttagact tccggtgact atcgagagg 240
gtacaacttt atggatctaa attatcagga gaataaaaa gattagaaaa aaacttttagt 300
ttttcaagtt atg gag tat cat tca agt ctg gtt ttg att aag gct acc 349
Met Glu Tyr His Ser Ser Leu Val Leu Ile Lys Ala Thr
1 5 10
agt ttt cta gga att gtg gtt tct gtc aaa tgc atg cgg aag gca ctg 397
Ser Phe Leu Gly Ile Val Val Ser Val Lys Cys Met Arg Lys Ala Leu
15 20 25
att ggg gtt ctg gtt gga gtt ctg gtt tcc chb cag aaa act gca gaa 445
Ile Gly Val Leu Val Gly Val Leu Val Ser Xaa Gln Lys Thr Ala Glu
30 35 40 45
aca ctc ttt gat gtt att tgt gca aat gca tta aca tct ca 486
Thr Leu Phe Asp Val Ile Cys Ala Asn Ala Leu Thr Ser
50 55

<210> 3313
<211> 462
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 131..460

<400> 3313
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ccatagggct agcaggggtg gcagcttctt ctttttcccc ccaaccatcc tcaggctggg 120
tttcttcttc atg gtc tca aaa gnk ggt tgc ttg acc ttg gga atg atg 169
Met Val Ser Lys Xaa Gly Cys Leu Thr Leu Gly Met Met
1 5 10
cct acc ttc cag gcc aga aac gga ttg gct ggc ttc tcc tat ctg ctt 217
Pro Thr Phe Gln Ala Arg Asn Gly Leu Ala Gly Phe Ser Tyr Leu Leu
15 20 25
ctg cat ttg gtg tgt ttt aat acg tat cag att tcc ttt grc ctc gct 265
Leu His Leu Val Cys Phe Asn Thr Tyr Gln Ile Ser Phe Xaa Leu Ala
30 35 40 45
gag tac act gcg gac gtt kwc gga gtt ggc act cta cga ctt cta gat 313

Glu	Tyr	Thr	Ala	Asp	Val	Xaa	Gly	Val	Gly	Thr	Leu	Arg	Leu	Leu	Asp	
				50					55					60		
gca	gtt	aag	act	tgt	ggc	ctt	atc	arc	tct	gtg	aag	ttc	tac	caa	gcc	361
Ala	Val	Lys	Thr	Cys	Gly	Leu	Ile	Xaa	Ser	Val	Lys	Phe	Tyr	Gln	Ala	
			65				70					75				
tav	baa	agt	gra	ctt	tat	ggg	aaa	gtg	cag	gaa	ata	ccc	cag	aag	gag	409
Xaa	Xaa	Ser	Xaa	Leu	Tyr	Gly	Lys	Val	Gln	Glu	Ile	Pro	Gln	Lys	Glu	
		80				85					90					
acc	anc	cct	ttc	tat	ccc	ggg	cac	cta	tgg	ggc	agc	aaa	act	cta	tgc	457
Thr	Xaa	Pro	Phe	Tyr	Pro	Gly	His	Leu	Trp	Gly	Ser	Lys	Thr	Leu	Cys	
	95				100				105							
cta	tt															462
Leu																
110																

<210> 3314
 <211> 366
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 212..364

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caaacaatcc	cagtggctca	atgtctttcg	cagatcgag	acctcggcct	tgctctcttt		120										
aagatgtgga	gssaaackga	ataatgaaga	gcacaatgag	ctgaggggaag	tggaaggcac		180										
cgctaagaag	aatggcggca	ccctctacta	c atg gcg ccc	gag cac ctg	aat		232										
			Met Ala Pro	Glu His Leu	Asn												
			1		5												
gac gtc aac	gca aag ccc	aca gag aag	tcg gat gtg	tac agc nnt	gcw		280										
Asp Val Asn	Ala Lys Pro	Thr Glu Lys	Ser Asp Val	Tyr Ser Xaa	Ala												
	10		15		20												
gta gta ctc	tgg gcg ata	ttt gca aat	aag gag cca	tat gaa agt	aag		328										
Val Val Leu	Trp Ala Ile	Phe Ala Asn	Lys Glu Pro	Tyr Glu Ser	Lys												
	25		30		35												
gca tta ctt	act ttc cac	tgc cgt ccc	ctc agc ata	cc			366										
Ala Leu Leu	Thr Phe His	Cys Arg Pro	Leu Ser Ile														
40		45		50													

<210> 3315
 <211> 414
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 172..414

<400>	3315																
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ctgtacagag acttgaagaa aggtcttgaa ggacttggtc ttgaaagcct tcttcatcta 120
atctacctaa caacccccta tgatctgggt tcacagtgtg accctgattg g atg ata 177
Met Ile

1

tac ttc agg cag ttt agc caa ctc agt cca gca gaa caa aat gta gct 225
Tyr Phe Arg Gln Phe Ser Gln Leu Ser Pro Ala Glu Gln Asn Val Ala
5 10 15

gcc att ctt gga gtc tct gaa agc ttt att ggg aag aaa gca tca ggc 273
Ala Ile Leu Gly Val Ser Glu Ser Phe Ile Gly Lys Lys Ala Ser Gly
20 25 30

caa gcc atc gga aag ctt aat gct ttt aaa aaa gtg atc cag tat caa 321
Gln Ala Ile Gly Lys Leu Asn Ala Phe Lys Lys Val Ile Gln Tyr Gln
35 40 45 50

cat gca gaa tat gta act cat aca tcc ttc aat ttg tca cca agg tgg 369
His Ala Glu Tyr Val Thr His Thr Ser Phe Asn Leu Ser Pro Arg Trp
55 60 65

aca aga acg ttg tca aca ggc tat atc tgt ctt ttg ttc ttt ata 414
Thr Arg Thr Leu Ser Thr Gly Tyr Ile Cys Leu Leu Phe Phe Ile
70 75 80

<210> 3316

<211> 211

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 21..209

<400> 3316

acttcctgct tcttacctac atg gtc aag cag ttt gct gtt tcc tct ggc tct 53
Met Val Lys Gln Phe Ala Val Ser Ser Gly Ser
1 5 10

gag aaa ctt ttc agc tgc aag tcc aat gct caa ttc aaa atg tat aaa 101
Glu Lys Leu Phe Ser Ser Lys Ser Asn Ala Gln Phe Lys Met Tyr Lys
15 20 25

acg ccc att ttc ctg aat gaa gtc ttg gtg aaa ctg ccc aca gac cct 149
Thr Pro Ile Phe Leu Asn Glu Val Leu Val Lys Leu Pro Thr Asp Pro
30 35 40

tcc agc gat gag cct gtc ttc cac att tcc cac att gat cgg gtc tac 197
Ser Ser Asp Glu Pro Val Phe His Ile Ser His Ile Asp Arg Val Tyr
45 50 55

acc ctc cga aca gc 211
Thr Leu Arg Thr
60

<210> 3317

<211> 295

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 13..294

<400> 3317

gtgttgaggc ta atg gcg gtg ccc acg gaa ctg gat gga ggg agt gtt aag	51
Met Ala Val Pro Thr Glu Leu Asp Gly Gly Ser Val Lys	
1 5 10	
gag acc gca gcg gaa gag gaa tcg cga gtt ctg gca cct ggc gcc gcc	99
Glu Thr Ala Ala Glu Glu Glu Ser Arg Val Leu Ala Pro Gly Ala Ala	
15 20 25	
ccg ttc gga aat ttt cct cat tat tct cgc ttc cac cct ccg gag caa	147
Pro Phe Gly Asn Phe Pro His Tyr Ser Arg Phe His Pro Pro Glu Gln	
30 35 40 45	
cgg ctc cgc ctc ctg ccc ccg gag ctg ctt cga cag ctc ttt cct gag	195
Arg Leu Arg Leu Leu Pro Pro Glu Leu Leu Arg Gln Leu Phe Pro Glu	
50 55 60	
agt ccc gag aac ggg ccg att ctg ggg ctc gac gtg ggg tgt aac tcc	243
Ser Pro Glu Asn Gly Pro Ile Leu Gly Leu Asp Val Gly Cys Asn Ser	
65 70 75	
ggg gat ctg agt gtg gct cta tac aaa cac ttc ctc tcc cta cct gac	291
Gly Asp Leu Ser Val Ala Leu Tyr Lys His Phe Leu Ser Leu Pro Asp	
80 85 90	
gga c	295
Gly	

<210> 3318

<211> 201

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 1..201

<400> 3318

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Met Leu Phe Ile Arg Leu Arg Phe Leu Leu Phe Ile Tyr Phe Asn Phe	
1 5 10 15	
tta ttt ttt cat tat tat act tta agt ttt agg gta cat gtg cac aat	96
Leu Phe Phe His Tyr Tyr Thr Leu Ser Phe Arg Val His Val His Asn	
20 25 30	
gtg cag gtt agt gac ata tgt ata cat gtg aca tgc tgg tgc act gca	144
Val Gln Val Ser Asp Ile Cys Ile His Val Thr Cys Trp Cys Thr Ala	
35 40 45	
ccc act aac tcg tca tct agc att agg tat atc tcc caa tgc tat ccc	192
Pro Thr Asn Ser Ser Ser Ser Ile Arg Tyr Ile Ser Gln Cys Tyr Pro	
50 55 60	
tcc ccc ctc	201
Ser Pro Leu	
65	

<210> 3319

<211> 265

<212> DNA
 <213> Homo sapiens
 <220>
 <221> CDS
 <222> 94..264

<400> 3319
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 acaatcacag ttatatattt tttctggggt cat atg ttg ctt aga aca ctt ccc 114
 Met Leu Leu Arg Thr Leu Pro
 1 5
 tat acg aaa aac atg aaa att ttt ttt cat att ttc ttt cat aag tgt 162
 Tyr Thr Lys Asn Met Lys Ile Phe Phe His Ile Phe Phe His Lys Cys
 10 15 20
 cta ttt aca tat agg tta ttt att act ctt gcg tta att ttg tgg tat 210
 Leu Phe Thr Tyr Arg Leu Phe Ile Thr Leu Ala Leu Ile Leu Trp Tyr
 25 30 35
 agt gac ata gag gag tct acc ttt ccc cct cta atg agg tat tgt ccc 258
 Ser Asp Ile Glu Glu Ser Thr Phe Pro Pro Leu Met Arg Tyr Cys Pro
 40 45 50 55
 aac act t 265
 Asn Thr

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 <212> DNA
 <213> Homo sapiens
 <220>
 <221> CDS
 <222> 81..473

<400> 3320
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 Met Lys Val Ala Gly Ala Cys Pro Gly Gln Trp
 1 5 10
 gtc cca gct gag gct gct kga cwt act ctc cga gcc tcg gca gta ttc 161
 Val Pro Ala Glu Ala Ala Xaa Xaa Thr Leu Arg Ala Ser Ala Val Phe
 15 20 25
 cct agc cga gac ttt ttt tgt ggt tgt tat tct gct gat tgt aga tat 209
 Pro Ser Arg Asp Phe Phe Cys Gly Cys Tyr Ser Ala Asp Cys Arg Tyr
 30 35 40
 ctt tgc ttt gct gac atc ctg ttt tgt ttt tgg ttt tta cat ccc att 257
 Leu Cys Phe Ala Asp Ile Leu Phe Cys Phe Trp Phe Leu His Pro Ile
 45 50 55
 tgt ttc ttt tta tca cag aaa cgc ttc gtt aag gga ctc agg cag tac 305
 Cys Phe Phe Leu Ser Gln Lys Arg Phe Val Lys Gly Leu Arg Gln Tyr
 60 65 70 75
 ggg aag aac ttc ttc agw wtt aga aag gag ctg ctt ccc aat aag gaa 353
 Gly Lys Asn Phe Phe Xaa Xaa Arg Lys Glu Leu Leu Pro Asn Lys Glu

	80	85	90	
aca ggg gag ctg atc acc ttc tat tac tat tgg aag aag acc ccc gaa				401
Thr Gly Glu Leu Ile Thr Phe Tyr Tyr Tyr Trp Lys Lys Thr Pro Glu				
	95	100	105	
gca gcc agc tcc cga gcc cat cgt agg cac cgc agc agg ccg tgt tca				449
Ala Ala Ser Ser Arg Ala His Arg Arg His Arg Ser Arg Pro Cys Ser				
	110	115	120	
gga gga tta aga ctc gca ccg cgt cc				475
Gly Gly Leu Arg Leu Ala Pro Arg				
	125	130		

<210> 3321
 <211> 318
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 158..316

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ggaggggacaa attgccaatg tttggagtct ggtttccagg ttgccgtttt tgggggcttt	120
gggtgtggcg gttgccgtag ctgaaattgg ctgcacc atg tcg gcc ttc gag aag	175
	Met Ser Ala Phe Glu Lys
	1 5
cct cag atc atc gcc cat atc cag aag ggc ttc aac tac acg gtg ttt	223
Pro Gln Ile Ile Ala His Ile Gln Lys Gly Phe Asn Tyr Thr Val Phe	
	10 15 20
gac tgt aag tgg gtg ccc tgc agc gcc aaa ttt gtg acc atg ggc aac	271
Asp Cys Lys Trp Val Pro Cys Ser Ala Lys Phe Val Thr Met Gly Asn	
	25 30 35
ttc gca cgg ggc acc ggc gtc att cag ctg tac gag atc cgg cac gg	318
Phe Ala Arg Gly Thr Gly Val Ile Gln Leu Tyr Glu Ile Arg His	
	40 45 50

<210> 3322
 <211> 182
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 24..182

<400> 3322	
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	Met Lys Gln Ile Leu Val Lys Met His Ser
	1 5 10
aaa cat tct gag aac agc tta ctt ctc act aaa aca gaa cca aaa cat	101
Lys His Ser Glu Asn Ser Leu Leu Leu Thr Lys Thr Glu Pro Lys His	
	15 20 25

gtg aca gaa aat cag aaa tca aag act ttg aat gtg cct aaa gag cat 149
 Val Thr Glu Asn Gln Lys Ser Lys Thr Leu Asn Val Pro Lys Glu His
 30 35 40

gaa gac aat ata ttt aca cct aaa cca aca cca 182
 Glu Asp Asn Ile Phe Thr Pro Lys Pro Thr Pro
 45 50

<210> 3323

<211> 303

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 142..303

<400> 3323

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 gtccagtttg gacctctgac ccttgggcag cacctccga cagccggctc gggrmccaam 120
 ttcytcgcaa gccaggtgaa a atg agn tct tca gta aga aga aaa ggc aag 171
 Met Xaa Ser Ser Val Arg Arg Lys Gly Lys
 1 5 10

cca ggc aaa gga ggt gga aaa ggg tct tct aga gga gga aga gga ggc 219
 Pro Gly Lys Gly Gly Gly Lys Gly Ser Ser Arg Gly Gly Arg Gly Gly
 15 20 25

agg agt cac gcc agt aaa tct cat ggg agt ggt ggc ggt ggc ggt ggt 267
 Arg Ser His Ala Ser Lys Ser His Gly Ser Gly Gly Gly Gly Gly Gly
 30 35 40

ggg ggt ggt gga ggt ggc ggc aac aga aag gcc tct 303
 Gly Gly Gly Gly Gly Gly Gly Asn Arg Lys Ala Ser
 45 50

<210> 3324

<211> 287

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 63..287

<400> 3324

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 gc atg tgg gct gct gag cag aac caa gta ttg tca ttg tgg cag tta 107
 Met Trp Ala Ala Glu Gln Asn Gln Val Leu Ser Leu Trp Gln Leu
 1 5 10 15

cag ttt tta ttt aac aaa cat ata gaa aat tta agc agt nta cat att 155
 Gln Phe Leu Phe Asn Lys His Ile Glu Asn Leu Ser Ser Xaa His Ile
 20 25 30

aaa cca ttt gah ctc ata aca tct tta tgt ggg agg tac tgt agt agt 203
 Lys Pro Phe Xaa Leu Ile Thr Ser Leu Cys Gly Arg Tyr Cys Ser Ser
 35 40 45

ccc atc ttt ggc cgg gcg cag tgg ctc atg cct gta gtc cca gca ctt	251
Pro Ile Phe Gly Arg Ala Gln Trp Leu Met Pro Val Val Pro Ala Leu	
50 55 60	
tgg aag gca ggg akg gtg gat cac ttg agg ctg gga	287
Trp Lys Ala Gly Xaa Val Asp His Leu Arg Leu Gly	
65 70 75	

<210> 3325
 <211> 485
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 41..484

<400> 3325	
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Met Tyr Leu Pro Asp	
1 5	
gta gat cag aaa gag agc gac ggc gga gca gat ctc act cta ggt ctg	103
Val Asp Gln Lys Glu Ser Asp Gly Gly Ala Asp Leu Thr Leu Gly Leu	
10 15 20	
aga gag gct cta gaa cta att taw tcc tat tcc agg tca gaa cga tct	151
Arg Glu Ala Leu Glu Leu Ile Xaa Ser Tyr Ser Arg Ser Glu Arg Ser	
25 30 35	
cat tat tat gac tct gat cgt cgc tac cat agg agc tcc cct tat cga	199
His Tyr Tyr Asp Ser Asp Arg Arg Tyr His Arg Ser Ser Pro Tyr Arg	
40 45 50	
gag agg acg cgc tat tct cgg cca tac aca gat aac aga gca cga gag	247
Glu Arg Thr Arg Tyr Ser Arg Pro Tyr Thr Asp Asn Arg Ala Arg Glu	
55 60 65	
agt tct gac tca gaa gaa gag tat aag aag aca tac tca agg cgt acc	295
Ser Ser Asp Ser Glu Glu Glu Tyr Lys Lys Thr Tyr Ser Arg Arg Thr	
70 75 80 85	
tca tct cat tcc tct tct tac aga gac cta agg aca tca tcc tat tct	343
Ser Ser His Ser Ser Ser Tyr Arg Asp Leu Arg Thr Ser Ser Tyr Ser	
90 95 100	
aaa tct gat cgg gac tgt aaa act gag acc tct tac tta gag atg gra	391
Lys Ser Asp Arg Asp Cys Lys Thr Glu Thr Ser Tyr Leu Glu Met Xaa	
105 110 115	
aga aga ggc aag tat tct tca aaa cta gaa aga gaa tct aaa agg act	439
Arg Arg Gly Lys Tyr Ser Ser Lys Leu Glu Arg Glu Ser Lys Arg Thr	
120 125 130	
tca gaa aat gaa gca att aaa aga tgt tgt tct cct cct ggg ggw c	485
Ser Glu Asn Glu Ala Ile Lys Arg Cys Cys Ser Pro Pro Gly Gly	
135 140 145	

<210> 3326
 <211> 239
 <212> DNA
 <213> Homo sapiens

<220>

<221> CDS

<222> 20..238

<400> 3326

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taccaaacag actactgta atg tcc aca agc aca ttc atc tca ccc gct cag      52
                        Met Ser Thr Ser Thr Phe Ile Ser Pro Ala Gln
                        1           5           10
ctg aaa gag agc tgt aac act gca act tca agt gca tgg ccc atc tgc      100
Leu Lys Glu Ser Cys Asn Thr Ala Thr Ser Ser Ala Trp Pro Ile Cys
                        15           20           25
tca gtg aga aca cgc cca gga gcg aga gtg ggg cag gaa agt gaa cct      148
Ser Val Arg Thr Arg Pro Gly Ala Arg Val Gly Gln Glu Ser Glu Pro
                        30           35           40
gct gtc aac tcc cta ccc atc caa cgg gat ccc agt gtt caa ggg cct      196
Ala Val Asn Ser Leu Pro Ile Gln Arg Asp Pro Ser Val Gln Gly Pro
                        45           50           55
gtg ttc cac tca cag ccc agc ccc gaa agc tgt gcc ggc caa c          239
Val Phe His Ser Gln Pro Ser Pro Glu Ser Cys Ala Gly Gln
                        60           65           70
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<210> 3327

<211> 414

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 242..412

<400> 3327

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atgatccgcc cgccttggcc tcccaaagtg ctgggattac tggcatgagc caccaagccc      120
ggccttaaaa tagtattttt aataacagaa gcattcacag aaactccagt tcatttaatt      180
tgcttattgt tcttccactc tggggacagt aaccattggt ctctttattt tgcacttaca      240
c atg agc caa cgt aca aga tcc tta ttt atg gat gca cac ctt acg tgt      289
  Met Ser Gln Arg Thr Arg Ser Leu Phe Met Asp Ala His Leu Thr Cys
    1           5           10           15
gaa aaa cct acc cct tgt ctc caa atg aaa gac tgc atc tct ttc atc      337
Glu Lys Pro Thr Pro Cys Leu Gln Met Lys Asp Cys Ile Ser Phe Ile
                        20           25           30
ctg ctt cct act ggt gac tcc ctc cca ctt act cct ttc ctc ttg ctg      385
Leu Leu Pro Thr Gly Asp Ser Leu Pro Leu Thr Pro Phe Leu Leu Leu
                        35           40           45
cct gct gtg gsc ttt tat ttc ttc tca gt          414
Pro Ala Val Xaa Phe Tyr Phe Phe Ser
    50           55
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<210> 3328

<211> 354

<212> DNA

<213> Homo sapiens

<220>
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 <222> 72..353

<400> 3328
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 tttgagaaag a atg aca ata tca gta ggt aaa acc aac atc aac agt tac 110
 Met Thr Ile Ser Val Gly Lys Thr Asn Ile Asn Ser Tyr
 1 5 10
 aag acc atc ctt ccm agc cca agt aag gca gtc aaa aga ggt gta gat 158
 Lys Thr Ile Leu Pro Ser Pro Ser Lys Ala Val Lys Arg Gly Val Asp
 15 20 25
 ctg gta gca gaa act ggg tcc ata att atc aaa gtg gaa gtt cac aga 206
 Leu Val Ala Glu Thr Gly Ser Ile Ile Ile Lys Val Glu Val His Arg
 30 35 40 45
 gca att ata act gag aag ata aaa act cat gta act tcc att cag tac 254
 Ala Ile Ile Thr Glu Lys Ile Lys Thr His Val Thr Ser Ile Gln Tyr
 50 55 60
 tgc aat tta aaa ata gat ttt ttt cac aat aac tat ata cag ata ata 302
 Cys Asn Leu Lys Ile Asp Phe Phe His Asn Asn Tyr Ile Gln Ile Ile
 65 70 75
 tat tta aca cat aaa aca aaa gag aaa aat aac aad dct ttc tca tca 350
 Tyr Leu Thr His Lys Thr Lys Glu Lys Asn Asn Xaa Xaa Phe Ser Ser
 80 85 90
 caa c 354
 Gln

<210> 3329
 <211> 465
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 290..463

<400> 3329
 gaattcagat gtgcctcagc aacgcccag tgtagttgtc tcaccacatt ctacaacctc 60
 tgttatacag ggacatcaaa tcatagcagt tcccgactca ggatcaaaag tatcccatc 120
 tcctgcccta tcatctgacg ttcggtctac aaatggcaca gcagaatgca aaactgtaa 180
 gaggccagca gaggatactg atagggaaac agtcgcagga attccaaata aagtaggagt 240
 tagaattggt acaatcagtg accccaacaa tgctggctgc agcgcaaca atg gtt gct 298
 Met Val Ala
 1
 gtg cca gca gga gca gat cca agc act gta gct aaa gta gca ata gaa 346
 Val Pro Ala Gly Ala Asp Pro Ser Thr Val Ala Lys Val Ala Ile Glu
 5 10 15
 agt gct gtt cag caa aag caa cag cat cca cca aca tat gta cag aat 394
 Ser Ala Val Gln Gln Lys Gln Gln His Pro Pro Thr Tyr Val Gln Asn
 20 25 30 35
 gtg gtc cgc aga aca ctc cta tgc cac ctt cac cag ctg tac aag tgc 442

Val Val Arg Arg Thr Leu Leu Cys His Leu His Gln Leu Tyr Lys Cys
 40 45 50
 agg gcc agc cta aca ggt ctc ar
 Arg Ala Ser Leu Thr Gly Leu
 55

465

<210> 3330
 <211> 370
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 24..368

<400> 3330
 cgggctgccc tcgcctcgtc gct atg gcg ccc acc atc cag acc cag gcc cag 53
 Met Ala Pro Thr Ile Gln Thr Gln Ala Gln
 1 5 10
 cgg gag gat ggc cac agg ccc aat tcc cac cgg act ctg cct grg agk 101
 Arg Glu Asp Gly His Arg Pro Asn Ser His Arg Thr Leu Pro Xaa Xaa
 15 20 25
 tct gga gtg gtc tgc cga gtc aag tac tgc aat agc ctc cct gat atc 149
 Ser Gly Val Val Cys Arg Val Lys Tyr Cys Asn Ser Leu Pro Asp Ile
 30 35 40
 ccc ttc gac ccc aag ttc atc acc tac ccc ttc gac cag aac agg ttc 197
 Pro Phe Asp Pro Lys Phe Ile Thr Tyr Pro Phe Asp Gln Asn Arg Phe
 45 50 55
 gtc cag tac aaa gcc act tcc ttg gag aaa cag cac aaa cat gac ctc 245
 Val Gln Tyr Lys Ala Thr Ser Leu Glu Lys Gln His Lys His Asp Leu
 60 65 70
 ctg act gag cca gac ctg ggg gtc acc atc gat ctc atc aat cct gac 293
 Leu Thr Glu Pro Asp Leu Gly Val Thr Ile Asp Leu Ile Asn Pro Asp
 75 80 85 90
 acc tac cgc atc gac ccc aat gtt ctt cta gat cca gct gat gag aaa 341
 Thr Tyr Arg Ile Asp Pro Asn Val Leu Leu Asp Pro Ala Asp Glu Lys
 95 100 105
 ctt ttg gaa grg gag att cag gsc ccc tc 370
 Leu Leu Glu Xaa Glu Ile Gln Xaa Pro
 110 115

<210> 3331
 <211> 384
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 67..384

<400> 3331
 catgttctcg gtgctgatat tctcaatagt tatgccggtc tagcctgtgt ggaagagccc 60

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aatgac atg att act gag agt tca ctg gat gtt gct gaa gaa gaa atc      108
      Met Ile Thr Glu Ser Ser Leu Asp Val Ala Glu Glu Glu Ile
        1              5              10
ata gac gat gat gat gat gac atc acc ctt aca gtt gaa gct tct tgt      156
Ile Asp Asp Asp Asp Asp Asp Ile Thr Leu Thr Val Glu Ala Ser Cys
15              20              25              30
cat gac ggg gat gaa aca att gaa act att gag gct gct gag gca ctc      204
His Asp Gly Asp Glu Thr Ile Glu Thr Ile Glu Ala Ala Glu Ala Leu
              35              40              45
ctc aat atg gat tcc cct ggc cct atg ctg gat gaa aaa cga ata aat      252
Leu Asn Met Asp Ser Pro Gly Pro Met Leu Asp Glu Lys Arg Ile Asn
              50              55              60
aat aat ata ttt agt tca cct gaa gat gac atg gtt gtt gcn cca gtc      300
Asn Asn Ile Phe Ser Ser Pro Glu Asp Asp Met Val Val Ala Pro Val
              65              70              75
acc cat gtg tcc gtc aca tta gat ggb wkt cct gaa gtg atg gaa aca      348
Thr His Val Ser Val Thr Leu Asp Gly Xaa Pro Glu Val Met Glu Thr
              80              85              90
cag cag gtg caa gaa aaa tat gca gac tca ccg gga      384
Gln Gln Val Gln Glu Lys Tyr Ala Asp Ser Pro Gly
95              100              105

<210> 3332
<211> 463
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 230..463

<400> 3332
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tgcattggttc tgttcaggat aaagctgcct tagagagttc ccagagatct cttgggctgg      120
gcacaatggc tcacagcctg taatcccagb actttgggag gctgagagta atcaagtcag      180
aggattatat gactttttatc tgcctagaga agaactatgg atctacaac atg gag act      238
                                   Met Glu Thr
                                   1
gga aga tgg aaa aaa atc aac act gaa ggt gat gtt cct cct tct atg      286
Gly Arg Trp Lys Lys Ile Asn Thr Glu Gly Asp Val Pro Pro Ser Met
              5              10              15
tca gga agc tgt gct gtg tgt gta gac agg gtg ctg tac ttg ttt gga      334
Ser Gly Ser Cys Ala Val Cys Val Asp Arg Val Leu Tyr Leu Phe Gly
20              25              30              35
gga cac cat tca aga ggc aat acc aat aag ttc tac atg ctg gat tca      382
Gly His His Ser Arg Gly Asn Thr Asn Lys Phe Tyr Met Leu Asp Ser
              40              45              50
agg tct aca gac aga gtg tta cag tgg gaa aga att gat tgc caa gga      430
Arg Ser Thr Asp Arg Val Leu Gln Trp Glu Arg Ile Asp Cys Gln Gly
              55              60              65
att cct cca tca tca aag grc aaa ctt ggt gtc      463
Ile Pro Pro Ser Ser Lys Xaa Lys Leu Gly Val
              70              75

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<210> 3333
 <211> 241
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 67..240

<400> 3333
 gaaaaggaaa cgccaagaca tagaaaacca cgcttttccc gtaggaagaa ccgatgatga 60
 gccctg atg aaa gaa gga aga aga ccc gct gtc tgc gaa ggc cta aag 108
 Met Lys Glu Gly Arg Arg Pro Ala Val Cys Glu Gly Leu Lys
 1 5 10
 gtt aga aat aca gca att ttt ctc atg ccg aar gaa aag gca aaa tgg 156
 Val Arg Asn Thr Ala Ile Phe Leu Met Pro Lys Glu Lys Ala Lys Trp
 15 20 25 30
 tct aag aaa ctg caa gag tgt gat aca agt ttt cct caa cag cga gct 204
 Ser Lys Lys Leu Gln Glu Cys Asp Thr Ser Phe Pro Gln Gln Arg Ala
 35 40 45
 ggg act ggc gac aat ttc tta act cac agc ctc cac a 241
 Gly Thr Gly Asp Asn Phe Leu Thr His Ser Leu His
 50 55

<210> 3334
 <211> 330
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 12..329

<400> 3334
 ttgagggggac t atg cgt aaa aag ctg agt ttg gat gag gaa tct tct ctc 50
 Met Arg Lys Lys Leu Ser Leu Asp Glu Glu Ser Ser Leu
 1 5 10
 ttt aaa caa aaa gcc caa cag aag cgg gta ttt gat acc gtc agg att 98
 Phe Lys Gln Lys Ala Gln Gln Lys Arg Val Phe Asp Thr Val Arg Ile
 15 20 25
 gcc aat gac aca cgg ggs cgc tct atc tca ttc cca gct ctg tta ncc 146
 Ala Asn Asp Thr Arg Gly Arg Ser Ile Ser Phe Pro Ala Leu Leu Xaa
 30 35 40 45
 att cca ggc tcc aac cgt tca agt gtc atc atg aca gca aaa cct ttt 194
 Ile Pro Gly Ser Asn Arg Ser Ser Val Ile Met Thr Ala Lys Pro Phe
 50 55 60
 gag tct ggt ctt cag caa aca gag gac aaa tca ctc ctg aac cag ggg 242
 Glu Ser Gly Leu Gln Gln Thr Glu Asp Lys Ser Leu Leu Asn Gln Gly
 65 70 75
 agc agc tca gag gag gtt gca ggg agc tcc cag aag atg ggc caa cca 290
 Ser Ser Ser Glu Glu Val Ala Gly Ser Ser Gln Lys Met Gly Gln Pro

	65		70		75	
gct cca gag ggc ttt gct gtg agg ctc gtc ttc cag gac ttc gac ctg						290
Ala Pro Glu Gly Phe Ala Val Arg Leu Val Phe Gln Asp Phe Asp Leu						
	80		85		90	
gag ccg tcc cag gac tgt gca ggg gac tct rwb aca atc tca ttc gtc						338
Glu Pro Ser Gln Asp Cys Ala Gly Asp Ser Xaa Thr Ile Ser Phe Val						
	95		100		105	
ggt tcg gat cca agc cag ttc tgt ggt cag caa ggc tcc cct ctg ggc						386
Gly Ser Asp Pro Ser Gln Phe Cys Gly Gln Gln Gly Ser Pro Leu Gly						
110		115		120		125
agg ccc cct ggt cag agg gag t						408
Arg Pro Pro Gly Gln Arg Glu						
	130					

<210> 3337
 <211> 250
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 46..249

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tcccgccttg gagcaagccg gggcctgggc ggcarctggg ccgcc atg gag tcc acg	57
	Met Glu Ser Thr
	1
ctg ggc gcg ggc atc gtg ata gcc gag gcg cta cag aac cag cta gcc	105
Leu Gly Ala Gly Ile Val Ile Ala Glu Ala Leu Gln Asn Gln Leu Ala	
5	10
15	20
tgg ctg gag aac gtg tgg ctc tgg rrt sac ctt tkc tng scg atc cca	153
Trp Leu Glu Asn Val Trp Leu Trp Xaa Xaa Leu Xaa Xaa Xaa Ile Pro	
	25
	30
	35
agk atc ctc ttt ctg ttc tac ttc ccc gcg gcn tac tac gcc tcc cgc	201
Xaa Ile Leu Phe Leu Phe Tyr Phe Pro Ala Ala Tyr Tyr Ala Ser Arg	
	40
	45
	50
cgt gtr ggc atc gcg gtg ctc tgg atc agc cts atc acc gag tgg ctc a	250
Arg Val Gly Ile Ala Val Leu Trp Ile Ser Leu Ile Thr Glu Trp Leu	
	55
	60
	65

<210> 3338
 <211> 418
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 231..416

<400> 3338	
aggtgcggaa gtgcgagggc ccaggtggct gaaggggccc ttaggaacat ccaagcgggtg	60
gggcacaggc agatccccga cctgacctgg accacccttc tcctcttggc ccgccccttc	120

aactcgctc cggcttnagg tctggattgg ccccgcccc tgacctgagc ctggtccttc 180
 ttcaggcact gacccttgac ctccggtggc tcccccatct ctcaggcgcg atg gct 236
 Met Ala

1
 acg ggc gcg gat gta cgg gac att cta raa ctc dkv ggt cca gaa ggg 284
 Thr Gly Ala Asp Val Arg Asp Ile Leu Xaa Leu Xaa Gly Pro Glu Gly
 5 10 15
 gat gca gcc tct ggg acc atc agc aag aag gac att atc aac ccg gac 332
 Asp Ala Ala Ser Gly Thr Ile Ser Lys Lys Asp Ile Ile Asn Pro Asp
 20 25 30
 aag aaa aaa tcc aag aag tcc tct gag aca ctg act ttc aag agg ccg 380
 Lys Lys Lys Ser Lys Lys Ser Ser Glu Thr Leu Thr Phe Lys Arg Pro
 35 40 45 50
 agg gca tgc acc ggg aag tct atg rct tgc tct act ct 418
 Arg Ala Cys Thr Gly Lys Ser Met Xaa Cys Ser Thr
 55 60

<210> 3339
 <211> 390
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 31..390

<400> 3339
 aaaaagagct gcgcgccgcg gcggcggaag atg gct gcg gcc gag gtg gcg gac 54
 Met Ala Ala Ala Glu Val Ala Asp
 1 5
 act cag ctg atg ctt gga gtc ggg ctg atc gaa aag gac aca aat gga 102
 Thr Gln Leu Met Leu Gly Val Gly Leu Ile Glu Lys Asp Thr Asn Gly
 10 15 20
 gaa gtt ctg tgg gtg tgg tgt tat cct tcc acg aca gcc aca tta agg 150
 Glu Val Leu Trp Val Trp Cys Tyr Pro Ser Thr Thr Ala Thr Leu Arg
 25 30 35 40
 aac ctg ctg ctg aga aaa tgc tgc ctt aca gat gaa aac aaa ctt ctc 198
 Asn Leu Leu Leu Arg Lys Cys Cys Leu Thr Asp Glu Asn Lys Leu Leu
 45 50 55
 cat ccc ttt gtc ttt ggt cag tac aga aga aca tgg ttt tat atc aca 246
 His Pro Phe Val Phe Gly Gln Tyr Arg Arg Thr Trp Phe Tyr Ile Thr
 60 65 70
 aca att gaa gtt cca gat tct tcc att ttg aaa aag gtg act cat ttt 294
 Thr Ile Glu Val Pro Asp Ser Ser Ile Leu Lys Lys Val Thr His Phe
 75 80 85
 tct att gtc ctg acc gcc aaa gat ttt arc cca gag aag tat gct gcc 342
 Ser Ile Val Leu Thr Ala Lys Asp Phe Xaa Pro Glu Lys Tyr Ala Ala
 90 95 100
 ttc act agg ata ttg tgt aga atg tac ctg aaa cat ggg agc cca gta 390
 Phe Thr Arg Ile Leu Cys Arg Met Tyr Leu Lys His Gly Ser Pro Val
 105 110 115 120

<210> 3340

<211> 425
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 59..424

<400> 3340
 acaataaaaat atcagatgca ccagagacac aaggcttgaa gctctgtcct gggaaaat 58
 atg gca aac agt gcc tct cct gaa cag aat caa aat cac tgt tca gcc 106
 Met Ala Asn Ser Ala Ser Pro Glu Gln Asn Gln Asn His Cys Ser Ala
 1 5 10 15
 atc aac aac agc atc cca ctg atg cag ggc aac ctc ccc act ctg acc 154
 Ile Asn Asn Ser Ile Pro Leu Met Gln Gly Asn Leu Pro Thr Leu Thr
 20 25 30
 ttg tct gga aag atc cga gtg acg gtt act ttc ttc ctt ttt ctg ctc 202
 Leu Ser Gly Lys Ile Arg Val Thr Val Thr Phe Phe Leu Phe Leu Leu
 35 40 45
 tct gcg acc ttt aat gct tct ttc ttg ttg aaa ctt cag aag tgg aca 250
 Ser Ala Thr Phe Asn Ala Ser Phe Leu Leu Lys Leu Gln Lys Trp Thr
 50 55 60
 cag aag aaa gag aaa ggg aaa aag ctc tca aga atg aag ctg ctc tta 298
 Gln Lys Lys Glu Lys Gly Lys Lys Leu Ser Arg Met Lys Leu Leu Leu
 65 70 75 80
 aaa cat ctg acc tta gcc aac ctg ttg gag act ctg att gtc atg cca 346
 Lys His Leu Thr Leu Ala Asn Leu Leu Glu Thr Leu Ile Val Met Pro
 85 90 95
 ctg gat ggg atg tgg aac att aba gtc caa tgg tat gct gga gag tta 394
 Leu Asp Gly Met Trp Asn Ile Xaa Val Gln Trp Tyr Ala Gly Glu Leu
 100 105 110
 ctc tgc aaa gtt ctc agt tat cta aag ctt t 425
 Leu Cys Lys Val Leu Ser Tyr Leu Lys Leu
 115 120

<210> 3341
 <211> 478
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 95..478

<400> 3341
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 tgcgtgtagg tgaagggggc ttctgaccg agac atg gat tta ggt gct att aca 115
 Met Asp Leu Gly Ala Ile Thr
 1 5
 aaa tac tca gca tta cac gcc aag ccc aat gga ctg knc ctk caa tac 163
 Lys Tyr Ser Ala Leu His Ala Lys Pro Asn Gly Leu Xaa Leu Gln Tyr
 10 15 20

ggg act gct gga ttt cga acg aag gca gaa cat ctt gat cat gtc atg	211
Gly Thr Ala Gly Phe Arg Thr Lys Ala Glu His Leu Asp His Val Met	
25 30 35	
ttt cgc atg gga tta tta gct gtc ctg agg tca aaa cag aca aaa tcc	259
Phe Arg Met Gly Leu Leu Ala Val Leu Arg Ser Lys Gln Thr Lys Ser	
40 45 50 55	
act ata gga gtc atg gta aca gcg tcc cac aat cct gag gaa gac aat	307
Thr Ile Gly Val Met Val Thr Ala Ser His Asn Pro Glu Glu Asp Asn	
60 65 70	
ggg gta aaa ttg gtt gat cct ttg ggt gaa atg ttg gca cca tcc tgg	355
Gly Val Lys Leu Val Asp Pro Leu Gly Glu Met Leu Ala Pro Ser Trp	
75 80 85	
gag gaa cat gcc acc tgt tta gca aat gct gag gaa caa gat atg cag	403
Glu Glu His Ala Thr Cys Leu Ala Asn Ala Glu Glu Gln Asp Met Gln	
90 95 100	
aga gtg ctt att gac atc agc gag aaa gaa gct gtg aat ctg caa caa	451
Arg Val Leu Ile Asp Ile Ser Glu Lys Glu Ala Val Asn Leu Gln Gln	
105 110 115	
gat gcc ttt gta gtt att ggt aga rwc	478
Asp Ala Phe Val Val Ile Gly Arg Xaa	
120 125	
<210> 3342	
<211> 484	
<212> DNA	
<213> Homo sapiens	
<220>	
<221> CDS	
<222> 178..483	
<400> 3342	
cagttggagg gagegcttgg tgagactgag tgtttacggt gcaggtcttc tcccctgtct	60
gcctcccgga gctaggactg cagaggggcc tatcatggtg cttgcaggcc ccttggtgtg	120
ctcgtgtgtg stggccagcc tcacaactgc tgggtgtccca cctctccagc tcccagg	177
atg tct cca gtg agc cca gca gtg agc agc agc tgt gcg ccc tta gca	225
Met Ser Pro Val Ser Pro Ala Val Ser Ser Cys Ala Pro Leu Ala	
1 5 10 15	
agc acc cca ccg tgg cct ttg aag acc tgc agc cgt ggg tct cta act	273
Ser Thr Pro Pro Trp Pro Leu Lys Thr Cys Ser Arg Gly Ser Leu Thr	
20 25 30	
tca cct acc ctg gag ccc ggg att tct csh agc tgg ctt tgg acc cct	321
Ser Pro Thr Leu Glu Pro Gly Ile Ser Xaa Ser Trp Leu Trp Thr Pro	
35 40 45	
ccg gga acc agc tca tcg tgg gag cca gga act acc tct tca gac tca	369
Pro Gly Thr Ser Ser Ser Trp Glu Pro Gly Thr Thr Ser Ser Asp Ser	
50 55 60	
gcc ttg cca atn nct ctc ttc ttc agg cca cag agt ggg cct cyw gtg	417
Ala Leu Pro Xaa Xaa Leu Phe Phe Arg Pro Gln Ser Gly Pro Xaa Val	
65 70 75 80	
agg aca cgc gcc gct cct gcc aaa gcr nag gga aga ctg agg avd agt	465
Arg Thr Arg Ala Ala Pro Ala Lys Ala Xaa Gly Arg Leu Arg Xaa Ser	
85 90 95	

gtc aga act acg tgc gag t
Val Arg Thr Thr Cys Glu
100

484

<210> 3343
<211> 263
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 84..263

<400> 3343
tctgcgtaga aatttcttcc accaaatacc ctaaatacatc tctctcaagt tcaaagtttc 60
acagatctct agggcagggt caa atg ctg cca gtc tca ttg cta aag cat aac 113
Met Leu Pro Val Ser Leu Leu Lys His Asn
1 5 10
agg agt cac ttt tac tcc att ttt ccc aac aag ttc ctc atc tcc atc 161
Arg Ser His Phe Tyr Ser Ile Phe Pro Asn Lys Phe Leu Ile Ser Ile
15 20 25
aga gac cac ctc agc ctg gac ttt att gtc cat atc att atc agc att 209
Arg Asp His Leu Ser Leu Asp Phe Ile Val His Ile Ile Ile Ser Ile
30 35 40
ttg gtc aaa gcc att caa caa ttc tct agg aag ttc caa act ttc cca 257
Leu Val Lys Ala Ile Gln Gln Phe Ser Arg Lys Phe Gln Thr Phe Pro
45 50 55
cat cag 263
His Gln
60

<210> 3344
<211> 426
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 209..424

<400> 3344
atttttcctt tttgtttttg ttgttgatgt gaccgcgtgt ccacaaccct gggattccct 60
cgccctcaga ttccagaatc caatttcttg gatttcagtg tttttaagggt gggaggtctc 120
gctatgcttc chaggctgga ctaaaattcc tgggctcaag tgattccccc gcctcagcct 180
cctgagtagc tgggactaca gatatggc atg tca gtc tgg tgg tct agc cag 232
Met Ser Val Trp Trp Ser Ser Gln
1 5
agg aag act cct gga gct ggt gaa ctg tgc atg gat atg cag tca cgg 280
Arg Lys Thr Pro Gly Ala Gly Glu Leu Cys Met Asp Met Gln Ser Arg
10 15 20
gca gcc cac ctc cta ctc ctc acc ckc cct gtg cct gtg agg gtc tgc 328
Ala Ala His Leu Leu Leu Leu Thr Xaa Pro Val Pro Val Arg Val Cys

25		30		35		40	
act cac cct acg	gag tct tgc tct	gtg gcc cag gct	gga gtg cag tgg				
Thr His Pro Thr	Glu Ser Cys Ser	Val Ala Gln Ala	Gly Val Gln Trp				
	45		50			55	
cat gat ctt ggc	tca ctg caa cct	ctg cct cct gag	ttc acg cca ttc				
His Asp Leu Gly	Ser Leu Gln Pro	Leu Pro Pro Glu	Phe Thr Pro Phe				
	60		65			70	
tc							

376
424
426

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<213> Homo sapiens

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<222> 15..200

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	Met Arg Arg Ile Trp Trp Pro Ile Trp Ser Leu Leu
	1 5 10
aat ggt aac tat	agt gcc tca cca ata tct ttc ttg cgc tat tcc aat
Asn Gly Asn Tyr	Ser Ala Ser Pro Ile Ser Phe Leu Arg Tyr Ser Asn
	15 20 25
tta tca atc att	att gga ccc aat atc ctg aat tac agt ctg att att
Leu Ser Ile Ile	Ile Gly Pro Asn Ile Leu Asn Tyr Ser Leu Ile Ile
	30 35 40
ttt cac caa tct	ttt atc ttt cat tta ccc aca ctg aaa ttc ttg agc
Phe His Gln Ser	Phe Ile Phe His Leu Pro Thr Leu Lys Phe Leu Ser
	45 50 55 60
cca act t	
Pro Thr	

50
98
146
194
201

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<220>
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<222> 195..455

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gatccgctgc taacacggga	gccagctggg tgttatttct caaactctga ggctgcggag
ttcacacatt gaaatctgtc	atctttttcm rgagagaaac ttycggtaat gtatgtamcc
ttctgtaatg gaag atg	att gaa gac aag ggg cct cgt gtt gct gac tac
	Met Ile Glu Asp Lys Gly Pro Arg Val Ala Asp Tyr
	1 5 10
ttt gtt gta gca gga	tta act gat gtt tca aag cct cta gaa gaa gaa
Phe Val Val Ala Gly	Leu Thr Asp Val Ser Lys Pro Leu Glu Glu Glu

60
120
180
230
278

15	20	25	
att cac ttc aat gat gct tgt cat aaa gta gct aaa cca aaa gaa cct			326
Ile His Phe Asn Asp Ala Cys His Lys Val Ala Lys Pro Lys Glu Pro			
30	35	40	
att aca gat gtt tca gtt att atc aaa tct ctt ggg gag gaa gtc cca			374
Ile Thr Asp Val Ser Val Ile Ile Lys Ser Leu Gly Glu Glu Val Pro			
45	50	55	60
cag gat tat atc tgt att gat gtt acc cca act gga ttg tca gct gat			422
Gln Asp Tyr Ile Cys Ile Asp Val Thr Pro Thr Gly Leu Ser Ala Asp			
65	70	75	
ctt aat aat gga gtc ttg tgg ggc aca gat tta			455
Leu Asn Asn Gly Val Leu Trp Gly Thr Asp Leu			
80	85		

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 <213> Homo sapiens

<220>
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 <222> 10..351

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Met Xaa Lys Asn His Arg Asn Lys Lys Ser Ile His Phe Pro	
1	5
ctg tgc acc att cca agt agm atg mtg aaa tct tgt act ctc cca ctt	99
Leu Cys Thr Ile Pro Ser Xaa Met Xaa Lys Ser Cys Thr Leu Pro Leu	
15	20
cag cgc acc tgg gac ats mat cct tcc ttt gtc cat tgg awc caa gcc	147
Gln Arg Thr Trp Asp Xaa Xaa Pro Ser Phe Val His Trp Xaa Gln Ala	
35	40
cgx cta caa tcc cca ccg yct agt cac tta gta scc ctc tcg gtg atc	195
Arg Leu Gln Ser Pro Pro Xaa Ser His Leu Val Xaa Leu Ser Val Ile	
50	55
aga tcg act ctc gtg cta tcc cag tgc ttg tgt tca agg mac cct tat	243
Arg Ser Thr Leu Val Leu Ser Gln Cys Leu Cys Ser Arg Xaa Pro Tyr	
65	70
ttt agt gca atg atg acc cca aag tgc aag agt att gmt gct ggc aat	291
Phe Ser Ala Met Met Thr Pro Lys Cys Lys Ser Ile Xaa Ala Gly Asn	
80	85
tca ggt atg cca aag aga aac tgt aaa gtg ctt cct tca agt gaa aag	339
Ser Gly Met Pro Lys Arg Asn Cys Lys Val Leu Pro Ser Ser Glu Lys	
95	100
atg maa gtt cac	
Met Xaa Val His	351

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<220>

<221> CDS

<222> 51..257

<400> 3348

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Met Glu
1
gga caa agg ctg atg ggg gca gat gtc aaa cag gcc aga ggc cca gtg 104
Gly Gln Arg Leu Met Gly Ala Asp Val Lys Gln Ala Arg Gly Pro Val
5 10 15
ggc tgg tgt agg cag cta gct cag cag agc tct gga gsc gra tty cgt 152
Gly Trp Cys Arg Gln Leu Ala Gln Gln Ser Ser Gly Xaa Xaa Phe Arg
20 25 30
ggg gtc tta tac caa gtg ttc cat gat acc att tgt gag aaa gaa gct 200
Gly Val Leu Tyr Gln Val Phe His Asp Thr Ile Cys Glu Lys Glu Ala
35 40 45 50
ccc aag tca tca tta ctc aga aag cag acc cag ccc cct aag aag cag 248
Pro Lys Ser Ser Leu Arg Lys Gln Thr Gln Pro Pro Lys Lys Gln
55 60 65
agt tct cct 257
Ser Ser Pro

<210> 3349

<211> 454

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 50..454

<400> 3349

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Met Ala Gly
1
gct ggt tcc gcc gct gta tcg ggg gca ggg acc ccg gtg gcg ggg ccc 106
Ala Gly Ser Ala Ala Val Ser Gly Ala Gly Thr Pro Val Ala Gly Pro
5 10 15
aca ggc cgc gac ctt ttc gcc gaa ggg ctg ctg gag ttc ctg cga ccc 154
Thr Gly Arg Asp Leu Phe Ala Glu Gly Leu Leu Glu Phe Leu Arg Pro
20 25 30 35
gct gtg cag cag ctc gac tct cac gta cac gcc gtc aga gag agc cag 202
Ala Val Gln Gln Leu Asp Ser His Val His Ala Val Arg Glu Ser Gln
40 45 50
gta gag ctc cgg gaa caa att gac aac cta gcc acw gaa ctg tgc cgc 250
Val Glu Leu Arg Glu Gln Ile Asp Asn Leu Ala Thr Glu Leu Cys Arg
55 60 65
ata aat gag gat cag aag gtg gcc ctg gat ctt gac ccc tat gtt aag 298
Ile Asn Glu Asp Gln Lys Val Ala Leu Asp Leu Asp Pro Tyr Val Lys
70 75 80
aag cta ctt aat gcc cgg cga cgc gtt gtc ttg gtt aac aac att cta 346

Lys	Leu	Leu	Asn	Ala	Arg	Arg	Arg	Val	Val	Leu	Val	Asn	Asn	Ile	Leu	
85						90					95					
cag	aat	gct	cag	gaa	cga	ctg	aga	cgg	cta	aac	cac	agt	gtt	gcc	aag	394
Gln	Asn	Ala	Gln	Glu	Arg	Leu	Arg	Arg	Leu	Asn	His	Ser	Val	Ala	Lys	
100					105					110					115	
gaa	aca	gcc	cgc	agg	mgr	gca	atg	ctg	gat	tcg	gga	att	tac	ccc	ctg	442
Glu	Thr	Ala	Arg	Arg	Arg	Ala	Met	Leu	Asp	Ser	Gly	Ile	Tyr	Pro	Leu	
				120					125					130		
gct	ccc	agg	tat													454
Ala	Pro	Arg	Tyr													
				135												

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<220>
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 <222> 11..310

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	Met	Asn	Gly	Asp	Leu	Glu	Glu	Glu	Gly	Gly	Arg	Glu	Ala				
	1				5					10							
aca	gat	gcc	cct	gag	caa	gtc	gag	gag	att	ctg	gat	cac	agt	gag	cag	97	
Thr	Asp	Ala	Pro	Glu	Gln	Val	Glu	Glu	Ile	Leu	Asp	His	Ser	Glu	Gln		
	15				20					25							
cag	gca	cgc	cct	gct	cgt	gta	aat	gga	ggc	acc	gat	gag	gag	aat	ggt	145	
Gln	Ala	Arg	Pro	Ala	Arg	Val	Asn	Gly	Gly	Thr	Asp	Glu	Glu	Asn	Gly		
	30				35				40					45			
gag	gag	ckg	cag	cag	gtt	aat	aat	gag	cgt	caa	ctg	gtc	cta	gac	aag	193	
Glu	Glu	Xaa	Gln	Gln	Val	Asn	Asn	Glu	Arg	Gln	Leu	Val	Leu	Asp	Lys		
				50				55						60			
gaa	aga	aag	tct	caa	gga	gct	ggc	agt	gga	caa	gat	gag	gct	gat	gta	241	
Glu	Arg	Lys	Ser	Gln	Gly	Ala	Gly	Ser	Gly	Gln	Asp	Glu	Ala	Asp	Val		
			65				70						75				
gac	cct	caa	aga	cca	cca	agg	cca	gaa	gta	aaa	att	acc	agt	cca	gaa	289	
Asp	Pro	Gln	Arg	Pro	Pro	Arg	Pro	Glu	Val	Lys	Ile	Thr	Ser	Pro	Glu		
		80					85					90					
gaa	aat	gaa	aac	aac	caa	caa	cc									312	
Glu	Asn	Glu	Asn	Asn	Gln	Gln											
		95				100											

<210> 3351
 <211> 358
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 <213> Homo sapiens

<220>
 <221> CDS
 <222> 162..356

<400> 3351

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gcttggccttg gcatttctgg cttggcggtc ctcctttcgc agattggaaa ccgcgggcta 120
tcctgctggg aggttgtggc cgaggcagta gctcgctact g atg gcc tcc tgg ggt 176
                               Met Ala Ser Trp Gly
                               1           5

gga gaa aag cgg gga ggc gct gag ggg tct ccg aag ctg gca gtc tac 224
Gly Glu Lys Arg Gly Gly Ala Glu Gly Ser Pro Lys Leu Ala Val Tyr
                               10           15           20

gcc acg agg aag acc cgt agc gtc agg agc cag gag gac cag tgg tac 272
Ala Thr Arg Lys Thr Arg Ser Val Arg Ser Gln Glu Asp Gln Trp Tyr
                               25           30           35

ttg ggc tac cgg ggg acc agt ggt cct cgg gct tct cct aca gct ggt 320
Leu Gly Tyr Arg Gly Thr Ser Gly Pro Arg Ala Ser Pro Thr Ala Gly
                               40           45           50

ggr aaa ata gcg tcg gca gcg aga caa gca cgg cga ga 358
Gly Lys Ile Ala Ser Ala Ala Arg Gln Ala Arg Arg
                               55           60           65

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<210> 3352

<211> 425

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 125..424

<400> 3352

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atctgaaaaaa gaaaaaaaaa tttcagaaga atggggcttt aaggatattt ctactgctca 120
gcaa atg ttg aag agg gca cag raa atg aaa tsg aag aaa cta aag aaa 169
Met Leu Lys Arg Ala Gln Xaa Met Lys Xaa Lys Lys Leu Lys Lys
1           5           10           15

aaa ata gat tcc act gtg cgt cta gcc tta ttc aaa aac aat gaa aat 217
Lys Ile Asp Ser Thr Val Arg Leu Ala Leu Phe Lys Asn Asn Glu Asn
                               20           25           30

aaa gtg tct ctt cca aaa tca cca aag atg gta cag ccc aga aga gat 265
Lys Val Ser Leu Pro Lys Ser Pro Lys Met Val Gln Pro Arg Arg Asp
                               35           40           45

ggt tac ttt gaa ggt ata gaa gaa gac cct atc cac aaa gat acc act 313
Gly Tyr Phe Glu Gly Ile Glu Glu Asp Pro Ile His Lys Asp Thr Thr
                               50           55           60

gca aat gaa aaa tta gaa cgg aat aga gaa tat aca tac caa tgg ctt 361
Ala Asn Glu Lys Leu Glu Arg Asn Arg Glu Tyr Thr Tyr Gln Trp Leu
                               65           70           75

cac aca cag gtt ggg gtt cat gaa acs gct agt tcc aga aat atg aaa 409
His Thr Gln Val Gly Val His Glu Thr Ala Ser Ser Arg Asn Met Lys
                               80           85           90           95

tgc aat cac ttt ttg c 425
Cys Asn His Phe Leu
                               100

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 agaccggtaa tccggggaga agagctgcac agagggctag actctcgaga tgggctgggg 120
 acctcagtgc tgaggtggga a atg acc aga aag gac tgg cdh tgt gcg gat 171
 Met Thr Arg Lys Asp Trp Xaa Cys Ala Asp
 1 5 10
 ctg gga gtc agg gtg tca ggc aga ggg cat agc aag tgc aga ggc cct 219
 Leu Gly Val Arg Val Ser Gly Arg Gly His Ser Lys Cys Arg Gly Pro
 15 20 25
 gag gca gga acc agc ttg gga cag aac ctg gca ggc cag cag cag gag 267
 Glu Ala Gly Thr Ser Leu Gly Gln Asn Leu Ala Gly Gln Gln Gln Glu
 30 35 40
 cca ggt cgc gtg gaa aca tct gcc ctc agg cta gga tgg aac att cag 315
 Pro Gly Arg Val Glu Thr Ser Ala Leu Arg Leu Gly Trp Asn Ile Gln
 45 50 55
 gtt tta twm nsa atg cag tgg gac acc gat t 346
 Val Leu Xaa Xaa Met Gln Trp Asp Thr Asp
 60 65

<210> 3354
 <211> 195
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 21..194

<400> 3354
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 Met His Phe Ser Phe Thr Ser Phe Phe Trp Asn
 1 5 10
 gcc ctt ttt gca gaa agc tac ggg ttt atg agg aac aca cac gca ggc 101
 Ala Leu Phe Ala Glu Ser Tyr Gly Phe Met Arg Asn Thr His Ala Gly
 15 20 25
 aca cac aca caa cgt gct gac aaa agg cat cca wtg tca ata agg tca 149
 Thr His Thr Gln Arg Ala Asp Lys Arg His Pro Xaa Ser Ile Arg Ser
 30 35 40
 tcc aac tca att aaa aac att ata aag aaa tca acc cct tca cac t 195
 Ser Asn Ser Ile Lys Asn Ile Ile Lys Lys Ser Thr Pro Ser His
 45 50 55

<210> 3355
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 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 231..425

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 ggacacagag agaatctgaa cacacagcct tggtaggatt ccttccgttt atcatcatta 120
 gatcataacc ccytgtgtcm agtcctatct ctccargact gcctccttct tcattaaacc 180
 ttgcataaaa actcacaat ttaaccattt atttggattc ttatttcctt atg aaa 236
 Met Lys
 1
 att cct gtg tgg cat aaa acg tgc ttt tta aaa tct gaa agt ttt tct 284
 Ile Pro Val Trp His Lys Thr Cys Phe Leu Lys Ser Glu Ser Phe Ser
 5 10 15
 cct gat aat tta tct gtt agt ttg cct tgt aga cct agc cag gta ccc 332
 Pro Asp Asn Leu Ser Val Ser Leu Pro Cys Arg Pro Ser Gln Val Pro
 20 25 30
 tca cag ggg caa gga aaa tct ttt ctc ctc cta caa ctt ata cat gag 380
 Ser Gln Gly Gln Gly Lys Ser Phe Leu Leu Leu Gln Leu Ile His Glu
 35 40 45 50
 gat aaa gcc atc cag aat gaa gct att ttc cag cct tct ctg cag ct 427
 Asp Lys Ala Ile Gln Asn Glu Ala Ile Phe Gln Pro Ser Leu Gln
 55 60 65

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 <212> DNA
 <213> Homo sapiens

<220>
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 <222> 19..435

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 Met Ala Lys Ser Leu Leu Lys Thr Ala Ser Leu
 1 5 10
 tct gga agg aca aaa ttg cta cat caa aca gga ttg tca ctt tat agt 99
 Ser Gly Arg Thr Lys Leu Leu His Gln Thr Gly Leu Ser Leu Tyr Ser
 15 20 25
 aca tcc cat gga ttt tat gag gaa gaa gtg aaa aaa aca ctt cag cag 147
 Thr Ser His Gly Phe Tyr Glu Glu Glu Val Lys Lys Thr Leu Gln Gln
 30 35 40
 ttt cct ggt gga tcc att gac ctt cag aag gaa gac aat ggc att ggc 195
 Phe Pro Gly Gly Ser Ile Asp Leu Gln Lys Glu Asp Asn Gly Ile Gly
 45 50 55
 att ctt act ctg aac aat cca agt aga atg aat gcc ttt tca ggt gtt 243

Ile	Leu	Thr	Leu	Asn	Asn	Pro	Ser	Arg	Met	Asn	Ala	Phe	Ser	Gly	Val		
60					65					70					75		
atg	atg	cta	caa	ctt	ctg	gaa	aaa	gta	att	gaa	ttg	gaa	aat	tgg	aca	291	
Met	Met	Leu	Gln	Leu	Leu	Glu	Lys	Val	Ile	Glu	Leu	Glu	Asn	Trp	Thr		
				80					85					90			
gag	ggg	aaa	ggc	ctc	att	gtc	cgt	ggg	gca	aaa	aat	act	ttc	tct	tca	339	
Glu	Gly	Lys	Gly	Leu	Ile	Val	Arg	Gly	Ala	Lys	Asn	Thr	Phe	Ser	Ser		
			95					100					105				
gga	tct	gat	ctg	aat	gct	gtg	aaa	tca	cta	gga	ctc	cag	aga	ctt	cct	387	
Gly	Ser	Asp	Leu	Asn	Ala	Val	Lys	Ser	Leu	Gly	Leu	Gln	Arg	Leu	Pro		
		110					115					120					
tta	ata	agt	gtt	gcg	ctg	gtt	caa	ggg	tgg	gca	ttg	ggg	gga	gga	gca	435	
Leu	Ile	Ser	Val	Ala	Leu	Val	Gln	Gly	Trp	Ala	Leu	Gly	Gly	Gly	Ala		
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gc																437	

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	Met	Pro	Ile	Ser	Ser	Gly	Gly	Ser	Val	Cys	Arg	Val	Arg			
	1				5					10						
gtc	gca	tgt	tgc	ttt	gca	aac	atg	ggt	ttc	aac	stt	cac	aat	cct	aag	158
Val	Ala	Cys	Cys	Phe	Ala	Asn	Met	Val	Phe	Asn	Xaa	His	Asn	Pro	Lys	
	15				20					25						
agc	ttc	ctt	tgt	tgt	ccc	cat	ttt	aaa	aac	aag	gaa	gtg	aga	tat	gga	206
Ser	Phe	Leu	Cys	Cys	Pro	His	Phe	Lys	Asn	Lys	Glu	Val	Arg	Tyr	Gly	
	30				35				40					45		
gag	ttg	gca	ctt	ggc	cta	aac	cac	att	tca	cat	aca	gca	g			246
Glu	Leu	Ala	Leu	Gly	Leu	Asn	His	Ile	Ser	His	Thr	Ala				
				50					55							

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 <222> 168..416

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aattcattta	cttaaataaa	atctgaatct	cagcccaaac	ctgggagatt	caaacctga											120

gagcgggtctt accaaagacg cccgtatgtc kkggtgaagt cagttgg atg caa gca	176
Met Gln Ala	
1	
ggt tgt gct ggt acc agg gcc cca gct act gat gaa gtg gca gga gtc	224
Val Cys Ala Gly Thr Arg Ala Pro Ala Thr Asp Glu Val Ala Gly Val	
5 10 15	
cac aga agc cta ctt cga agt tcc cgg ggc ttc cag ggg aga ttg acg	272
His Arg Ser Leu Leu Arg Ser Ser Arg Gly Phe Gln Gly Arg Leu Thr	
20 25 30 35	
aga ttc ctg ggg agg cga ttc atg aca gct gag ttc ctt ttg gag gat	320
Arg Phe Leu Gly Arg Arg Phe Met Thr Ala Glu Phe Leu Leu Glu Asp	
40 45 50	
ccg tct tca ggc agt ctg atc ccc cag gaa agc agc tgg aaa aca aga	368
Pro Ser Ser Gly Ser Leu Ile Pro Gln Glu Ser Ser Trp Lys Thr Arg	
55 60 65	
gca tgt gaa gga agc gca sag ctc ctc gcc agc cag aca gcc agc cga c	417
Ala Cys Glu Gly Ser Ala Xaa Leu Leu Ala Ser Gln Thr Ala Ser Arg	
70 75 80	

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 <213> Homo sapiens

<220>
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 <222> 163..363

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gggaatggat gattttccaa aagagaaaac acttgacctg ggtctgaaag gctgggtatg	120
atttaaggca ggcactattg ttcacttggt agccccaggg cc atg cta ctc cac	174
Met Leu Leu His	
1	
ttc ctt caa gga aac aga ggg aag ccg gca agt ggc tgc ctg ggg tgt	222
Phe Leu Gln Gly Asn Arg Gly Lys Pro Ala Ser Gly Cys Leu Gly Cys	
5 10 15 20	
gtg tcc aca cac cat ata gag gca gtt ctt cag ctc tgt cag cca tgg	270
Val Ser Thr His His Ile Glu Ala Val Leu Gln Leu Cys Gln Pro Trp	
25 30 35	
cca aag cag gca gta ttt gaa cca cct tgg acc act cct gag ggg cag	318
Pro Lys Gln Ala Val Phe Glu Pro Pro Trp Thr Thr Pro Glu Gly Gln	
40 45 50	
cat cag aca cca ggc atc ctt tca gac acc att ctt gga gtc tct t	364
His Gln Thr Pro Gly Ile Leu Ser Asp Thr Ile Leu Gly Val Ser	
55 60 65	

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 <212> DNA
 <213> Homo sapiens

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<221> CDS
<222> 92..277

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 Met Arg Leu Gly Ala Val Ala
 1 5
 cac gcc tgt aat ccc agc act ttg gga ggc caa gac ggg cga atc acg 160
 His Ala Cys Asn Pro Ser Thr Leu Gly Gly Gln Asp Gly Arg Ile Thr
 10 15 20
 agc cag gag ttc aag acc agc ctg acc aac atg agg aaa ccc ttg tct 208
 Ser Gln Glu Phe Lys Thr Ser Leu Thr Asn Met Arg Lys Pro Leu Ser
 25 30 35
 cta ctg gaa atg caa aga att ggc tgg gca tgg tgg tgg gca cct gtg 256
 Leu Leu Glu Met Gln Arg Ile Gly Trp Ala Trp Trp Trp Ala Pro Val
 40 45 50 55
 atc cca gct act cga aag gct 277
 Ile Pro Ala Thr Arg Lys Ala
 60

<210> 3361
 <211> 177
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 16..177

<400> 3361
 ggttcgggat gagcg atg gca tcg gtc aag gtg gcc gtg agg gtc cgg ccc 51
 Met Ala Ser Val Lys Val Ala Val Arg Val Arg Pro
 1 5 10
 atg aat cgc agg gaa aag gnn ttg gag gcc aag ttc att att cag atg 99
 Met Asn Arg Arg Glu Lys Xaa Leu Glu Ala Lys Phe Ile Ile Gln Met
 15 20 25
 gag aaa agc aaa acg aca atc asa aac tta aag ata cca gaa gga ggc 147
 Glu Lys Ser Lys Thr Thr Ile Xaa Asn Leu Lys Ile Pro Glu Gly Gly
 30 35 40
 act ggg gac tca ggm aga gaa cgg ryc grc 177
 Thr Gly Asp Ser Gly Arg Glu Arg Xaa Xaa
 45 50

<210> 3362
 <211> 296
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 143..295

004220" 6666T560

<400> 3362

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cctagaatat gagtcaagaa taaactcctt ccctctcagc ttctttttcca tctaaaccac      60
tatttttcatt cattatatca ccaccccaaa tcttttcctt tgttttaact ggccaaattg      120
cacttcagat aagctagtta ga atg tct ctt twa ata gar tca gct ctg gct      172
                Met Ser Leu Xaa Ile Glu Ser Ala Leu Ala
                    1             5             10
cac aca acc agg aag aaa aac acc tgg cca gtg gca tct gag cct cac      220
His Thr Thr Arg Lys Lys Asn Thr Trp Pro Val Ala Ser Glu Pro His
                    15             20             25
atc cca gga gat tca cgc ttc tct cta agg aaa ccc ttc cgg atg atg      268
Ile Pro Gly Asp Ser Arg Phe Ser Leu Arg Lys Pro Phe Arg Met Met
                    30             35             40
ggg atc cat cat caa ctt cgt gtg gcg t      296
Gly Ile His His Gln Leu Arg Val Ala
                    45             50

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<210> 3363

<211> 361

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 188..361

<400> 3363

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acttaacggt ggtggctggt tctgcgccgg atccgggaga ggggcgggcg ccattgtgct      60
tcgctgccga ctgcatttcc tcagtcacgg gcctagaact ccaaggagaa aggcggcggt      120
gcgtgttgct gcgagtggga cgcgcaactgg tcggtgccgg ctcaggagcc gggaaaaatc      180
tttaaga atg gag tct aaa cct tca agg att cca aga aga att tct gtt      229
                Met Glu Ser Lys Pro Ser Arg Ile Pro Arg Arg Ile Ser Val
                    1             5             10
caa cct tcc agc tcc tta agt gct agg atg atg tct gga agc aga gga      277
Gln Pro Ser Ser Ser Leu Ser Ala Arg Met Met Ser Gly Ser Arg Gly
                    15             20             25             30
agt agt tta aat gat acc tat cac tca aga gac tct tca ttt aga ttg      325
Ser Ser Leu Asn Asp Thr Tyr His Ser Arg Asp Ser Ser Phe Arg Leu
                    35             40             45
gat tct gaa tat cag tct aca tca gca tca gca acc      361
Asp Ser Glu Tyr Gln Ser Thr Ser Ala Ser Ala Thr
                    50             55

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<210> 3364

<211> 298

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 113..298


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<400> 3364
ggctcatttc ctggccgctc ctgggcttcg cggaaagaag agattactca cactccttcg      60
caagcacaga accagttgta ctgagctttt tgctaagctg tttcagccaa ga atg gct      118
                                   Met Ala
                                   1

gtg gaa tct gga gtg att tca acc ctg ata cct cag gat cct ccg gaa      166
Val Glu Ser Gly Val Ile Ser Thr Leu Ile Pro Gln Asp Pro Pro Glu
      5              10              15

caa gaa cta ata cta gtg aaa gta gaa gat aac ttt tcc tgg gat gag      214
Gln Glu Leu Ile Leu Val Lys Val Glu Asp Asn Phe Ser Trp Asp Glu
      20              25              30

aaa ttt aag cag aat ggg agt act caa tcc tgc caa gaa ttg ttt cgt      262
Lys Phe Lys Gln Asn Gly Ser Thr Gln Ser Cys Gln Glu Leu Phe Arg
      35              40              45              50

cag caa ttc aga aaa ttt tgc tac cag gag aca cct      298
Gln Gln Phe Arg Lys Phe Cys Tyr Gln Glu Thr Pro
      55              60

<210> 3365
<211> 378
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 17..376

<400> 3365
atatcattgg tgagga atg gcc acc cac tgc cct ctt tac tgt gta gga gca      52
                                   Met Ala Thr His Cys Pro Leu Tyr Cys Val Gly Ala
                                   1              5              10

gat ctg atg atg aac aga hna ggt gag cac gtg tgg agt gag agc gag      100
Asp Leu Met Met Asn Arg Xaa Gly Glu His Val Trp Ser Glu Ser Glu
      15              20              25

gac tgc ctg cct ttc ttg cag cta gca crg att rca tct cct cst gcg      148
Asp Cys Leu Pro Phe Leu Gln Leu Ala Xaa Ile Xaa Ser Pro Xaa Ala
      30              35              40

gca aga vga cgc tcc acg aag tcc tgg aaa aag tct tca agt ctt tca      196
Ala Arg Xaa Arg Ser Thr Lys Ser Trp Lys Lys Ser Ser Ser Leu Ser
      45              50              55              60

gac ctt tac tgg ggc ttc cgg atg cag atg acg atg cgt ttg aag agt      244
Asp Leu Tyr Trp Gly Phe Arg Met Gln Met Thr Met Arg Leu Lys Ser
      65              70              75

aca gtg ctg acg tgg aag aag agg agc cag agg cgg rcc acc ccc aga      292
Thr Val Leu Thr Trp Lys Lys Arg Ser Gln Arg Arg Xaa Thr Pro Arg
      80              85              90

tgg ggg nng cya gca gta rat ctg ggg gct ccc ctn aga agg wga gtv      340
Trp Gly Xaa Xaa Ala Val Xaa Leu Gly Ala Pro Leu Arg Arg Xaa Val
      95              100              105

kag ccc cac agt aac cta dgt ggg gtc act gcc cct cc      378
Xaa Pro His Ser Asn Leu Xaa Gly Val Thr Ala Pro
      110              115              120

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<210> 3366
 <211> 427
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 232..426

<400> 3366
 aatcgcggtc gcgagccatg gaggaggagg catcgtcccc ggggctgggc tgcagcaagc 60
 cgcacctgga gaagctgacc ctgggcatca cgcgcatcct aggmytgtga rgwtgwtgag 120
 wtacmavacc tkgattaagg tamattaaaa tggcaaaaagc aagattatcc agaattctcc 180
 ccaggtgtga ctgaggtgac catcatagaa aagcctcctg ctgaacgtca t atg att 237
 Met Ile
 1
 tct tcc tgg gaa caa aag aat aac tgt gtg atg cct gaa gat gtg aag 285
 Ser Ser Trp Glu Gln Lys Asn Asn Cys Val Met Pro Glu Asp Val Lys
 5 10 15
 aac ttt tac ctg atg acc aat ggc ttc cac atg aca tgg agt gtg aag 333
 Asn Phe Tyr Leu Met Thr Asn Gly Phe His Met Thr Trp Ser Val Lys
 20 25 30
 ctg gat gag cam atc att cca ctg gga agc atg gca att aac agc atc 381
 Leu Asp Glu Xaa Ile Ile Pro Leu Gly Ser Met Ala Ile Asn Ser Ile
 35 40 45 50
 tca aaa ctg dct cag ctc acc cag tct tcc atg tat tca ctt cct a 427
 Ser Lys Leu Xaa Gln Leu Thr Gln Ser Ser Met Tyr Ser Leu Pro
 55 60 65

<210> 3367
 <211> 299
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 28..297

<400> 3367
 gagcgaggcg gggccgcccgg ggccgcc atg gag ccc gac tcg gtg att gag gac 54
 Met Glu Pro Asp Ser Val Ile Glu Asp
 1 5
 aag acc atc gag ctc atg ata agt aat gga aca tca tct gtg atc gtc 102
 Lys Thr Ile Glu Leu Met Ile Ser Asn Gly Thr Ser Ser Val Ile Val
 10 15 20 25
 tcc aga aag agg cca tca gaa gga aac tat caa aaa gam wnn gac ttg 150
 Ser Arg Lys Arg Pro Ser Glu Gly Asn Tyr Gln Lys Xaa Xaa Asp Leu
 30 35 40
 tgt att aaa rta ttc agc act ttg aga ggc caa ggc agc aga gcc ctt 198
 Cys Ile Lys Xaa Phe Ser Thr Leu Arg Gly Gln Gly Ser Arg Ala Leu
 45 50 55

gct aga agc cag tgg cat gct ctt gaa ctt ccc agc ctg cag aac tat	246
Ala Arg Ser Gln Trp His Ala Leu Glu Leu Pro Ser Leu Gln Asn Tyr	
60 65 70	
gag cta aaa ttc tcc act tta gca ata ctt aca gga tct ggg aca cac	294
Glu Leu Lys Phe Ser Thr Leu Ala Ile Leu Thr Gly Ser Gly Thr His	
75 80 85	
aga cc	299
Arg	
90	

<210> 3368
 <211> 205
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 10..204

<400> 3368	
cctccaaaa atg agc aag cct ggt tca cct gga tct gta att cct gct caa	51
Met Ser Lys Pro Gly Ser Pro Gly Ser Val Ile Pro Ala Gln	
1 5 10	
gca cac ggg aaa ata ttc aca aaa cca gat ccc caa tgg gac tcc aca	99
Ala His Gly Lys Ile Phe Thr Lys Pro Asp Pro Gln Trp Asp Ser Thr	
15 20 25 30	
gtt agt gca tcc gaa gct gaa aat ggt gtt cac cta aaa aca gag ctc	147
Val Ser Ala Ser Glu Ala Glu Asn Gly Val His Leu Lys Thr Glu Leu	
35 40 45	
caa caa aaa cag cta tca aat aac aac caa gca ctt tca aag aat cat	195
Gln Gln Lys Gln Leu Ser Asn Asn Asn Gln Ala Leu Ser Lys Asn His	
50 55 60	
cct cct cag a	205
Pro Pro Gln	
65	

<210> 3369
 <211> 354
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 26..352

<400> 3369	
attctggtct cagagcctga ggctg atg gcc tgt ggg gaa att tca ggg gag	52
Met Ala Cys Gly Glu Ile Ser Gly Glu	
1 5	
cac aga gag gaa gaa agg aga acg gaa acc cgt cca ggg gcc cca gcc	100
His Arg Glu Glu Glu Arg Arg Thr Glu Thr Arg Pro Gly Ala Pro Ala	
10 15 20 25	

ggc cct ttg caa aca gag gca ggg tca ggc gaa abn gag ggc cag gtc	148
Gly Pro Leu Gln Thr Glu Ala Gly Ser Gly Glu Xaa Glu Gly Gln Val	
30 35 40	
gca gat gaa ggc tgg agt ctg agc cct ctg gtc tca gcg gag agc agg	196
Ala Asp Glu Gly Trp Ser Leu Ser Pro Leu Val Ser Ala Glu Ser Arg	
45 50 55	
gga cat gtc ccc cca gga cgg gct cct gct tgc tcc cga ggg gcg cct	244
Gly His Val Pro Pro Gly Arg Ala Pro Ala Cys Ser Arg Gly Ala Pro	
60 65 70	
tgg cag ggc gga cat tgg aag ctg aat gcg gag gaa gca tcc gga agc	292
Trp Gln Gly Gly His Trp Lys Leu Asn Ala Glu Glu Ala Ser Gly Ser	
75 80 85	
ggc gct ctt ggc ctc agc cct cct gtc ctg gga tgg agt ttt gcc atg	340
Gly Ala Leu Gly Leu Ser Pro Pro Val Leu Gly Trp Ser Phe Ala Met	
90 95 100 105	
ttg cgc agg ctg gt	354
Leu Arg Arg Leu	

<210> 3370
 <211> 256
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 54..254

<400> 3370	
ctcatgcctc ctctgtccc cattgtactt cctgaaagag cagcccatcc ctg atg	56
Met	
1	
ggg cca cct cct cac atg gca gct gca ctc agc gcc agc tca gag cat	104
Gly Pro Pro Pro His Met Ala Ala Ala Leu Ser Ala Ser Ser Glu His	
5 10 15	
tcc agt gct cca gct gtt tgg aac tct ytc tgc tgt aac agc cct tca	152
Ser Ser Ala Pro Ala Val Trp Asn Ser Xaa Cys Cys Asn Ser Pro Ser	
20 25 30	
agg tct cct aat tgc cag agc ccc tgc ttt ccc ctc agt cct aac tcc	200
Arg Ser Pro Asn Cys Gln Ser Pro Cys Phe Pro Leu Ser Pro Asn Ser	
35 40 45	
ccc ttg agg ccc cct gct ctg gcc cag agc ttc ctc act cac tcc tct	248
Pro Leu Arg Pro Pro Ala Leu Ala Gln Ser Phe Leu Thr His Ser Ser	
50 55 60 65	
gct gcc aa	256
Ala Ala	

<210> 3371
 <211> 251
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS

<222> 90..251

<400> 3371

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aatagttccc atggttttctt ttgctcccag cggttgcgcg ggctggggttt ttggagcaaa    60
ggcaacggat actgctgagg ctcttgaga atg tcc cgt ttt cga ggc tgc agt    113
                               Met Ser Arg Phe Arg Gly Cys Ser
                               1           5
agc tcc ggt gtc cgg ttc trc agt gcc cga gag gga ggc ctc ggg ctc    161
Ser Ser Gly Val Arg Phe Xaa Ser Ala Arg Glu Gly Gly Leu Gly Leu
   10           15           20
cgg gcg ggg gaa tgt gtt gca gtt tgt ccn dga gcc cca agc cca gca    209
Arg Ala Gly Glu Cys Val Ala Val Cys Pro Xaa Ala Pro Ser Pro Ala
  25           30           35           40
aag ccg ccc gtt ccc cgc tgg ggc gca act ctc act gga act    251
Lys Pro Pro Val Pro Arg Trp Gly Ala Thr Leu Thr Gly Thr
           45           50
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<210> 3372

<211> 242

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 45..242

<400> 3372

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tagtacaggt tgagcatctc aaatttgga gttcaaagtc tgaa atg ctc cag atc    56
                               Met Leu Gln Ile
                               1
aga aac ttt ttg agc act gat atg atg ctc aaa gga aat rct cat tgg    104
Arg Asn Phe Leu Ser Thr Asp Met Met Leu Lys Gly Asn Xaa His Trp
  5           10           15           20
agc att ttg gga wtt yca kaa tct gtg gat ttg aga tgc tca acc agt    152
Ser Ile Leu Gly Xaa Xaa Xaa Ser Val Asp Leu Arg Cys Ser Thr Ser
           25           30           35
aag tat art aga gct att ccc aag atc cga aaa aat tct gaa atc aga    200
Lys Tyr Xaa Arg Ala Ile Pro Lys Ile Arg Lys Asn Ser Glu Ile Arg
           40           45           50
agc act tct ggt bcc agg cat ttt gga gaa ggg atg ctc aac    242
Ser Thr Ser Gly Xaa Arg His Phe Gly Glu Gly Met Leu Asn
           55           60           65
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<210> 3373

<211> 215

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 11..214

004220" 646E7566

<400> 3373
 atacactatt atg tgt caa tat att aat tat ata tta att aca ttt ata 49
 Met Cys Gln Tyr Ile Asn Tyr Ile Leu Ile Thr Phe Ile
 1 5 10
 gag gtt agg tat ata tgg cag atc ata tct gag cgt gaa tta cat tct 97
 Glu Val Arg Tyr Ile Trp Gln Ile Ile Ser Glu Arg Glu Leu His Ser
 15 20 25
 cca ata ttt kta ttt gtc atg att tat tgc agg gtt cac tta ttk gat 145
 Pro Ile Phe Xaa Phe Val Met Ile Tyr Cys Arg Val His Leu Xaa Asp
 30 35 40 45
 cta ccc caa ctt aag aca cat ttc caa gaa aat atc cat cac act aga 193
 Leu Pro Gln Leu Lys Thr His Phe Gln Glu Asn Ile His His Thr Arg
 50 55 60
 aag aaa gaa aga gga agg aag g 215
 Lys Lys Glu Arg Gly Arg Lys
 65

<210> 3374
 <211> 214
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 62..214

<400> 3374
 agaccccgcc ccccttaaga agagaagccg cggccctgc aggacggggg cctgtgtcgc 60
 t atg ggt tcc ccc gcc gcc ccg gag gwa gsg ctg ggc tac gtc cgc gag 109
 Met Gly Ser Pro Ala Ala Pro Glu Xaa Xaa Leu Gly Tyr Val Arg Glu
 1 5 10 15
 ttc act cgc vca mtc ctc cga cgt gct gkg caa cct caa acg agc ttc 157
 Phe Thr Arg Xaa Xaa Leu Arg Arg Ala Xaa Gln Pro Gln Thr Ser Xaa
 20 25 30
 gcc tgc scg gga tcc tca ctg asg tca cgc tgc tgm knt ggc ggg caa 205
 Ala Cys Xaa Gly Ser Ser Leu Xaa Ser Arg Cys Xaa Xaa Gly Gly Gln
 35 40 45
 ccc ctc aga 214
 Pro Leu Arg
 50

<210> 3375
 <211> 287
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 110..286

<400> 3375

caatggaaca gaacagagcc ctcagaaata acgccgctta tctacagcta tctgatcttt 60
gacaaacctg agaaaaacaa gcaatgggga aagattccct atttaataa atg gtg ctg 118
Met Val Leu

1
gga aac tgg tta gcc ata tgt aga aag ctg aaa ctg gat ccc ttc ctt 166
Gly Asn Trp Leu Ala Ile Cys Arg Lys Leu Lys Leu Asp Pro Phe Leu
5 10 15
aca cct tat asa aaa atc aat tca aga tgg att aaa gac tta aac gtt 214
Thr Pro Tyr Xaa Lys Ile Asn Ser Arg Trp Ile Lys Asp Leu Asn Val
20 25 30 35
aga cct aaa acc ata aaa rcc cta gaa gar aac cta ggc att acc att 262
Arg Pro Lys Thr Ile Lys Xaa Leu Glu Glu Asn Leu Gly Ile Thr Ile
40 45 50
cag gac ata ggc atg ggc aag gac t 287
Gln Asp Ile Gly Met Gly Lys Asp
55

<210> 3376
<211> 304
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 150..302

<400> 3376
cttgcttcca atttatwtgc tactacaaaa tgattaaaat gagtgacttg taaaaaaacc 60
aaataaatat gttgaaatta aatcaaagtt tgaacagatc ttgagaggta cctagtaatt 120
gaataggggt ggaataawac taatcacat atg tgc agg aaa cag cac ata gtw 173
Met Cys Arg Lys Gln His Ile Val
1 5
cag ttt ggg ttt ggg caa ggw rag agt agg agc caa ggc tgg aaa ggt 221
Gln Phe Gly Phe Gly Gln Gly Xaa Ser Arg Ser Gln Gly Trp Lys Gly
10 15 20
gag tta aag atg gmt tgt ggg cca ggc gtg gtg gct cgt gcc tgw ama 269
Glu Leu Lys Met Xaa Cys Gly Pro Gly Val Val Ala Arg Ala Xaa Xaa
25 30 35 40
tgc car cac ttt ggg agg cag agg cgg cca atc ac 304
Cys Gln His Phe Gly Arg Gln Arg Arg Pro Ile
45 50

<210> 3377
<211> 207
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 23..205

<400> 3377

ctatgggtcca caaaggcgga ag atg atg ttt atg gga ttt atc cgt ctg gga 52
Met Met Phe Met Gly Phe Ile Arg Leu Gly
1 5 10
gtg tgg tac aac ttc ttc cga gcc tgg aac gga ggc ttc tct gga aac 100
Val Trp Tyr Asn Phe Phe Arg Ala Trp Asn Gly Gly Phe Ser Gly Asn
15 20 25
ctg gaa gga gaa ggc ttc atc ctt ggg gga gtt ttc gwg gtg gga tca 148
Leu Glu Gly Glu Gly Phe Ile Leu Gly Gly Val Phe Xaa Val Gly Ser
30 35 40
gga aag cag ggc att ctt ctt gag cac cga gaa aaa gaa ttt gga gac 196
Gly Lys Gln Gly Ile Leu Leu Glu His Arg Glu Lys Glu Phe Gly Asp
45 50 55
aaa gta aac ct 207
Lys Val Asn
60

<210> 3378
<211> 226
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 38..226

<400> 3378
aggatctcag ggtgagtcgtg gtaadaagcc ttctgaa atg tta gac cag aga att 55
Met Leu Asp Gln Arg Ile
1 5
atc tgg aga ggg agg aaa tgc agg gca agt tcc tgc aaa gcc tca cac 103
Ile Trp Arg Gly Arg Lys Cys Arg Ala Ser Ser Cys Lys Ala Ser His
10 15 20
tca tgt tgg tct cam csg atg ttt atc agg gag aaa cag cct gta ctc 151
Ser Cys Trp Ser Xaa Xaa Met Phe Ile Arg Glu Lys Gln Pro Val Leu
25 30 35
cca ggg cag ccg ttt gaa cgg gca gag ccc act ttg ttc ctc gat tct 199
Pro Gly Gln Pro Phe Glu Arg Ala Glu Pro Thr Leu Phe Leu Asp Ser
40 45 50
gtt tct ttc cat gca atc cgc cct tcc 226
Val Ser Phe His Ala Ile Arg Pro Ser
55 60

<210> 3379
<211> 424
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 134..424

<400> 3379

atagcatgta ctttttttaa tgccgttgaa acagagttaa tttccttttag cacacaagtc 60
 ttrgagacaa aatnnaaaaa ggtctgcaac atgaaaagtc acaggcatca cawtcctcwt 120
 ttggccctc tcc atg ata tta tta tca gac aaa atc cag tct tct aaa 169
 Met Ile Leu Leu Ser Asp Lys Ile Gln Ser Ser Lys
 1 5 10
 aga gaa gtc caa tgt aat ttt act gaa aaa aat tat acc ttg att cca 217
 Arg Glu Val Gln Cys Asn Phe Thr Glu Lys Asn Tyr Thr Leu Ile Pro
 15 20 25
 gca gat atc aag aaa gat gtt act ata ctt gat ctc agt tat aac caa 265
 Ala Asp Ile Lys Lys Asp Val Thr Ile Leu Asp Leu Ser Tyr Asn Gln
 30 35 40
 att act ctt aat ggt aca gac aca aga gtt cta cag aca tac ttt tta 313
 Ile Thr Leu Asn Gly Thr Asp Thr Arg Val Leu Gln Thr Tyr Phe Leu
 45 50 55 60
 ctc ayw gag ctc tat ttg att gag aac aag gtt act atc tta cat aat 361
 Leu Xaa Glu Leu Tyr Leu Ile Glu Asn Lys Val Thr Ile Leu His Asn
 65 70 75
 aac ggt ttt ggt aac ctc tcc agt cta gaa att tta aat atc tgt aga 409
 Asn Gly Phe Gly Asn Leu Ser Ser Leu Glu Ile Leu Asn Ile Cys Arg
 80 85 90
 aac tcc atc tat gtt 424
 Asn Ser Ile Tyr Val
 95

<210> 3380
 <211> 393
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 198..392

<400> 3380
 atttttatca gtgcagtatt ggacaggata gagaaatttt cagtgcaggg tctggctaaa 60
 gcatgttttg ggtcagtgtc tcaacctctg gtctgggagt ccttgacct agaacattta 120
 ctttaattaac tggtgttggg acatttgagt attgccatca aagtcactaa tagccatggt 180
 tcttggattt ttggatt atg gat ccc ttt gaa aag cat ttg aaa gtt atg 230
 Met Asp Pro Phe Glu Lys His Leu Lys Val Met
 1 5 10
 tgc cat ctt ccc tca aag gca cat aaa cgg aac ttt atg tac agt ttc 278
 Cys His Leu Pro Ser Lys Ala His Lys Arg Asn Phe Met Tyr Ser Phe
 15 20 25
 agg gtg gta agg aac ccc tgc aat cta ttt atg gat cat agg tta ata 326
 Arg Val Val Arg Asn Pro Cys Asn Leu Phe Met Asp His Arg Leu Ile
 30 35 40
 att cct gct atg gga act gaa gat acc aag ata gag aag tct agt att 374
 Ile Pro Ala Met Gly Thr Glu Asp Thr Lys Ile Glu Lys Ser Ser Ile
 45 50 55
 tta gga atg tat aat aaa t 393
 Leu Gly Met Tyr Asn Lys
 60 65

<210> 3381
 <211> 368
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 195..368

<400> 3381
 atccccggggg ccagtcgcgg ccgggacatc gggcgctgcg gccggggacc cgctgctgag 60
 atagacagaa tatggcagag ctttatgagc cagagggacc agtagattgg aaggaacgat 120
 gtgtagctct ggagtcctaa ctcattgaaat ttagagttca agcaagcaag atacgagagc 180
 ttttagcata gaag atg caa cag ctt gag aga caa gtt att gat gct gaa 230
 Met Gln Gln Leu Glu Arg Gln Val Ile Asp Ala Glu
 1 5 10
 cgt caa gca gaa aaa gct ttt caa cag gta caa gtt atg gaa gat aaa 278
 Arg Gln Ala Glu Lys Ala Phe Gln Gln Val Gln Val Met Glu Asp Lys
 15 20 25
 tta aaa gca gct aat att caa acc agt gaa tca gag aca aga tta tat 326
 Leu Lys Ala Ala Asn Ile Gln Thr Ser Glu Ser Glu Thr Arg Leu Tyr
 30 35 40
 aat aag tgt caa gat ctg gag tcg cta ata cag gaa aaa gat 368
 Asn Lys Cys Gln Asp Leu Glu Ser Leu Ile Gln Glu Lys Asp
 45 50 55

<210> 3382
 <211> 400
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 8..400

<400> 3382
 caaaaaca atg cat ctg cag aga gat ggg gag gag cca ttt cct gct ttt 49
 Met His Leu Gln Arg Asp Gly Glu Glu Pro Phe Pro Ala Phe
 1 5 10
 aag tct tgg cag gag gac tct gag tct gga gaa gct cag ctg tct cca 97
 Lys Ser Trp Gln Glu Asp Ser Glu Ser Gly Glu Ala Gln Leu Ser Pro
 15 20 25 30
 caa gct gga aga atg aat cat cac ccc ttg gaa gag gac tgt cct cca 145
 Gln Ala Gly Arg Met Asn His His Pro Leu Glu Glu Asp Cys Pro Pro
 35 40 45
 gta tta tca cac cgc agt tta gat ttt ggt caa agc cag cgt ttc cta 193
 Val Leu Ser His Arg Ser Leu Asp Phe Gly Gln Ser Gln Arg Phe Leu
 50 55 60
 cat gat cca gaa aag ttg gat tcc tca tct aaa gca ctg tct ttt act 241
 His Asp Pro Glu Lys Leu Asp Ser Ser Ser Lys Ala Leu Ser Phe Thr
 65 70 75
 aga att cga aga tca tcc ttt agt tca aaa gat gaa aag aga gag gac 289

Arg	Ile	Arg	Arg	Ser	Ser	Phe	Ser	Ser	Lys	Asp	Glu	Lys	Arg	Glu	Asp		
80						85					90						
aga	aca	cct	tat	cag	ctg	gtc	aag	aaa	ctt	cag	aag	aaa	atc	aga	caa	337	
Arg	Thr	Pro	Tyr	Gln	Leu	Val	Lys	Lys	Leu	Gln	Lys	Lys	Ile	Arg	Gln		
95					100					105					110		
ttt	gag	gaa	cag	ttt	gaa	agg	gaa	aga	aat	agc	aag	scc	tcc	tac	agt	385	
Phe	Glu	Glu	Gln	Phe	Glu	Arg	Glu	Arg	Asn	Ser	Lys	Xaa	Ser	Tyr	Ser		
				115					120					125			
gat	att	gcc	gcc	aaa												400	
Asp	Ile	Ala	Ala	Lys													
				130													

<210> 3383
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 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 96..311

<400> 3383																	
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gaatgattgt	ctagcctcca	gcctcaactt	acttg	atg	ctt	gag	aga	ctc	aaa							113	
			Met	Leu	Glu	Arg	Leu	Lys									
			1				5										
gcc	ccg	tgg	tca	gct	gcc	ctg	caa	aga	aag	tat	ttt	gac	ctt	ggc	att	161	
Ala	Pro	Trp	Ser	Ala	Ala	Leu	Gln	Arg	Lys	Tyr	Phe	Asp	Leu	Gly	Ile		
			10				15					20					
tgg	aca	gct	ccc	atc	tct	ccc	atg	gcc	ctg	aca	atg	ctg	aat	ggg	ctc	209	
Trp	Thr	Ala	Pro	Ile	Ser	Pro	Met	Ala	Leu	Thr	Met	Leu	Asn	Gly	Leu		
			25				30					35					
ctg	att	aag	gac	tca	agc	cca	cct	atg	ctg	ctg	cac	cag	gtt	aac	aag	257	
Leu	Ile	Lys	Asp	Ser	Ser	Pro	Pro	Met	Leu	Leu	His	Gln	Val	Asn	Lys		
			40				45				50						
act	gcc	cag	tta	gat	acc	ttc	aac	tac	cag	agc	tgc	ttt	atg	caa	agt	305	
Thr	Ala	Gln	Leu	Asp	Thr	Phe	Asn	Tyr	Gln	Ser	Cys	Phe	Met	Gln	Ser		
55					60				65					70			
gtc	ttt	ga														313	
Val	Phe																

<210> 3384
 <211> 417
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 245..415

<400> 3384																	
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actgaaagaa ctagagaagc aagacaaaac cccaaagcta gaggaagaca agaaataact 120
 gaaaatctga gctgaactga aagaaaccga gacatgaaaa aaagaaattc aaaagatcta 180
 tgaattccgg gtaggtttct tgaaaatatt aataagaaag tctgctagca gactaataca 240
 gagg atg att gaa aga aac aca att aga aat gac aaa ggg aat gtt acc 289
 Met Ile Glu Arg Asn Thr Ile Arg Asn Asp Lys Gly Asn Val Thr
 1 5 10 15
 act gac ccc aca gaa ata gaa aca gcc atc aga aac tac tgc aaa cac 337
 Thr Asp Pro Thr Glu Ile Glu Thr Ala Ile Arg Asn Tyr Cys Lys His
 20 25 30
 ttc tat gca tac aaa cta gaa aac ttc aaa gag atg gat aaa ttc atg 385
 Phe Tyr Ala Tyr Lys Leu Glu Asn Phe Lys Glu Met Asp Lys Phe Met
 35 40 45
 gag aaa tac acc ctc cca caa ctg agc cat ga 417
 Glu Lys Tyr Thr Leu Pro Gln Leu Ser His
 50 55

 <210> 3385
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 <212> DNA
 <213> Homo sapiens

 <220>
 <221> CDS
 <222> 101..454

 <400> 3385
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 cagcaatcat gccctgggag ctaacgtaga gctttggata atg ctt ttg caa gtt 115
 Met Leu Leu Gln Val
 1 5
 gta cga gaa ggg aag ttc tcg ggg ttt ctt gac cct cct gca gcc tcc 163
 Val Arg Glu Gly Lys Phe Ser Gly Phe Leu Asp Pro Pro Ala Ala Ser
 10 15 20
 tct tgc ctc ggg ctg ccm aga tct tgg cgg ctg agg ctg gct tac ctt 211
 Ser Cys Leu Gly Leu Pro Arg Ser Trp Arg Leu Arg Leu Ala Tyr Leu
 25 30 35
 cga gcc gtt cct tca tgg gat ttg ctg ctc cct tca cca aca agc gaa 259
 Arg Ala Val Pro Ser Trp Asp Leu Leu Leu Pro Ser Pro Thr Ser Glu
 40 45 50
 agg ctt act cgg agc gta gaa tca tgg ggt aag cat tct ctg cct tgc 307
 Arg Leu Thr Arg Ser Val Glu Ser Trp Gly Lys His Ser Leu Pro Cys
 55 60 65
 atc ctt gca cct ccc ttt tcc ctc caa ata dbn ctg tcc agg caa gaa 355
 Ile Leu Ala Pro Pro Phe Ser Leu Gln Ile Xaa Leu Ser Arg Gln Glu
 70 75 80 85
 tgt cag ggt atc atc ggt ggg cma gat tca tcc cta gcc atc ccc ctc 403
 Cys Gln Gly Ile Ile Gly Gly Xaa Asp Ser Ser Leu Ala Ile Pro Leu
 90 95 100
 ccc agc tac aat act gat cct cag tcc tcc cct gcc act ctt ccg acc 451
 Pro Ser Tyr Asn Thr Asp Pro Gln Ser Ser Pro Ala Thr Leu Pro Thr
 105 110 115
 tta at 456
 Leu

<210> 3386
 <211> 445
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 55..444

<400> 3386
 ctcttttggtt acgctcgta gccggtcggc cgccgcctcc agccgtgtgc cgct atg 57
 Met
 1
 gga gtc ccg gcg ttc ttc cgc tgg ctc agc cgc aag tac ccg tcc atc 105
 Gly Val Pro Ala Phe Phe Arg Trp Leu Ser Arg Lys Tyr Pro Ser Ile
 5 10 15
 ata gtc aac tgc gtg gaa gag aag cca waa gaa tgc aat ggt gta aag 153
 Ile Val Asn Cys Val Glu Glu Lys Pro Xaa Glu Cys Asn Gly Val Lys
 20 25 30
 att cca gtt gat gcc agt aaa cct aat cca aat gat gtg gag ttt gat 201
 Ile Pro Val Asp Ala Ser Lys Pro Asn Pro Asn Asp Val Glu Phe Asp
 35 40 45
 aat ctg tat ttg gat atg aat gga atc atc cat ccc tgt act cat cct 249
 Asn Leu Tyr Leu Asp Met Asn Gly Ile Ile His Pro Cys Thr His Pro
 50 55 60 65
 gaa gac aaa cca gca cca aaa aat gaa gat gaa atg atg gtt gca att 297
 Glu Asp Lys Pro Ala Pro Lys Asn Glu Asp Glu Met Met Val Ala Ile
 70 75 80
 ttt gag tac att gac aga ctt ttc agt att gta aga cca aga aga ctt 345
 Phe Glu Tyr Ile Asp Arg Leu Phe Ser Ile Val Arg Pro Arg Arg Leu
 85 90 95
 ctc tac atg gca ata gat gga gtg gca cca cgt gct aaa atg aac cag 393
 Leu Tyr Met Ala Ile Asp Gly Val Ala Pro Arg Ala Lys Met Asn Gln
 100 105 110
 cag cgt tca agg agg ttc aag ggc atc aaa aga agg cat gga agc agc 441
 Gln Arg Ser Arg Arg Phe Lys Gly Ile Lys Arg Arg His Gly Ser Ser
 115 120 125
 agt c 445
 Ser
 130

<210> 3387
 <211> 180
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 12..179

<400> 3387

tcaaccagtg c atg ata tct ttc ccc atg gtg gtc ttc ctc tat ccc ttc 50
 Met Ile Ser Phe Pro Met Val Val Phe Leu Tyr Pro Phe
 1 5 10
 ctc aaa tgg tgg aga gac ccc tgc cgc cgt gag cta ccc acc ttc cac 98
 Leu Lys Trp Trp Arg Asp Pro Cys Arg Arg Glu Leu Pro Thr Phe His
 15 20 25
 tgg ttc ctc ctg gag ctg gcc atc ttc acg ctg atc gag gaa ggt cct 146
 Trp Phe Leu Leu Glu Leu Ala Ile Phe Thr Leu Ile Glu Glu Gly Pro
 30 35 40 45
 wgt tct act att yac acc ggc tcc ttc acc cgw c 180
 Xaa Ser Thr Ile Xaa Thr Gly Ser Phe Thr Arg
 50 55

<210> 3388
 <211> 211
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 53..211

<400> 3388
 acactcatgc ctgaagttga cgagaactat cctcctccag ttaaggagga gg atg ctg 58
 Met Leu
 1
 ctt ctg ttt aga cca aaa tct ccc tta tac agg gaa gct ccc tgt agt 106
 Leu Leu Phe Arg Pro Lys Ser Pro Leu Tyr Arg Glu Ala Pro Cys Ser
 5 10 15
 gca agc ctg aca agg gca ctc tca twc atg ctg ggg gct grg ggg aag 154
 Ala Ser Leu Thr Arg Ala Leu Ser Xaa Met Leu Gly Ala Xaa Gly Lys
 20 25 30
 ctt ctg gac tca atg tct cgg aca cct ctk gnd ccc awa caa gtc aaa 202
 Leu Leu Asp Ser Met Ser Arg Thr Pro Leu Xaa Pro Xaa Gln Val Lys
 35 40 45 50
 gga aga gca 211
 Gly Arg Ala

<210> 3389
 <211> 234
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 2..232

<400> 3389
 g atg gct ctg tct ggg ggg ctg cgg tgc tgc cgc cgg gta ctg tcc tgg 49
 Met Ala Leu Ser Gly Gly Leu Arg Cys Cys Arg Arg Val Leu Ser Trp
 1 5 10 15
 gtg cca gtg ctc gtt att gtc ctc gtc gtg ctc tgg tcc tac tat gcc 97

Val	Pro	Val	Leu	Val	Ile	Val	Leu	Val	Val	Leu	Trp	Ser	Tyr	Tyr	Ala		
			20					25					30				
tac	gtc	ttt	gaa	ctc	tgc	ctg	gtg	act	ggt	ttg	agc	cca	gca	gaa	aaa	145	
Tyr	Val	Phe	Glu	Leu	Cys	Leu	Val	Thr	Val	Leu	Ser	Pro	Ala	Glu	Lys		
		35					40				45						
ggt	att	tac	ctc	ata	ctc	tac	cat	gcc	atc	ttt	gtg	ttc	ttt	acc	tgg	193	
Val	Ile	Tyr	Leu	Ile	Leu	Tyr	His	Ala	Ile	Phe	Val	Phe	Phe	Thr	Trp		
		50				55				60							
acc	tac	tgg	aag	tct	atc	ttt	aca	ctc	cca	cag	cag	ccg	aa			234	
Thr	Tyr	Trp	Lys	Ser	Ile	Phe	Thr	Leu	Pro	Gln	Gln	Pro					
65					70					75							

<210> 3390
 <211> 367
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 157..366

<400> 3390																	
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gaaggcagtt	ggtaagaact	agattgcatg	tacaaagaca	ggtttactaa	gtgctgtaca	120											
gtggtcctga	ggttacagtt	gaattagaaa	aacgaa	atg	tac	tta	cag	gaa	ata								174
				Met	Tyr	Leu	Gln	Glu	Ile								
				1			5										
aga	aag	caa	acc	ttt	caa	atg	aga	gtg	atg	att	tct	tta	aaa	aaa	rtc	222	
Arg	Lys	Gln	Thr	Phe	Gln	Met	Arg	Val	Met	Ile	Ser	Leu	Lys	Lys	Xaa		
			10				15						20				
agt	ttt	ttt	ctc	tca	aat	aat	ggt	ctt	tat	ttc	acg	aaa	tcg	tca	atc	270	
Ser	Phe	Phe	Leu	Ser	Asn	Asn	Val	Leu	Tyr	Phe	Thr	Lys	Ser	Ser	Ile		
		25				30				35							
tta	agc	atg	agc	agg	gat	aaa	caa	ctc	cta	gaa	gga	act	caa	ttc	att	318	
Leu	Ser	Met	Ser	Arg	Asp	Lys	Gln	Leu	Leu	Glu	Gly	Thr	Gln	Phe	Ile		
		40				45				50							
ctt	cct	gga	ttt	tct	ctg	ttg	tta	aat	cac	aaa	aat	gat	agt	ccc	caa	a	367
Leu	Pro	Gly	Phe	Ser	Leu	Leu	Leu	Asn	His	Lys	Asn	Asp	Ser	Pro	Gln		
55					60					65					70		

<210> 3391
 <211> 382
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 138..380

<400> 3391																	
acattcagag	aaacttggtt	gctgtctttg	ctgtcaggaa	agaggaagac	tacctagaca	60											
tggtgctcca	gagcagaatt	tccagcagta	gattgaacct	tcggaggccg	agtcacagcc	120											

[illegible]

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<210> 3392
<211> 338
<212> DNA
<213> Homo sapiens
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<220>
<221> CDS
<222> 116..337
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<400>	3392	
tttgtacagg gtaggggcaa gtagcagaaa aatcaattaa ttcacataaa ggaacatttt		60
cattctaaat taatattgcc actgcaatta aatttatcta gtatttttaa catgt atg		118
	Met	
	1	
gat aac aca ctt tcc tgt gta cac ctt gga tac ctg gga ccg tta tat		166
Asp Asn Thr Leu Ser Cys Val His Leu Gly Tyr Leu Gly Pro Leu Tyr		
	5 10 15	
gtg atc aac tat cat ctt agt ttt tta gct tgg tta aca ctt gac ccc		214
Val Ile Asn Tyr His Leu Ser Phe Leu Ala Trp Leu Thr Leu Asp Pro		
	20 25 30	
tcc ccc cac ctc aaa atc agt aaa atg ctg tgg att ctg ctt ttt aaa		262
Ser Pro His Leu Lys Ile Ser Lys Met Leu Trp Ile Leu Leu Phe Lys		
	35 40 45	
aaa atc rgg cca aaa tct cag cat tct cca tgg ctc cca gtg ctt ctc		310
Lys Ile Xaa Pro Lys Ser Gln His Ser Pro Trp Leu Pro Val Leu Leu		
	50 55 60 65	
ggc agt ttt ttt ttt ttt ttt ttt t t		338
Gly Ser Phe Phe Phe Phe Phe Phe Phe		
	70	

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<210> 3393
<211> 261
<212> DNA
<213> Homo sapiens
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[illegible]

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<210> 3394
<211> 213
<212> DNA
<213> Homo sapiens
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<400> 3394
aacctgatgc cttaaggaaa aggttaagat gagagggggc ttccagagtc a atg aac
Met Asn
1
gtc acc ctt cag ccg acg gat acc ggg agc gct tgg gca aaa cag cag
Val Thr Leu Gln Pro Thr Asp Thr Gly Ser Ala Trp Ala Lys Gln Gln
5 10 15
aga aag aaa gac tgt ggt cgg gga agt gga atg ctt cga tgc agg cca
Arg Lys Lys Asp Cys Gly Arg Gly Ser Gly Met Leu Arg Cys Arg Pro
20 25 30
gag ttc aag gct ctg ggg ctg gcc tca caa gag gct tct tcc acg ggg
Glu Phe Lys Ala Leu Gly Leu Ala Ser Gln Glu Ala Ser Ser Thr Gly
35 40 45 50
ctt gac acc aga
Leu Asp Thr Arg
213

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2107

<213> Homo sapiens

<220>

<221> CDS

<222> 83..241

<400> 3395

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cgatatgcaa aacccattgg acgaccgaaa aataaattam agcaacgatt gttgtctgta      60
accagtgatg aaggatccat ga atg cat tca cag gaa ggg ggt cac ctg gta      112
                        Met His Ser Gln Glu Gly Gly His Leu Val
                        1         5         10
ggg gtc aaa aag act aaa gtc tgt acc rca cct tca tct ggt cat gct      160
Gly Val Lys Lys Thr Lys Val Cys Thr Xaa Pro Ser Ser Gly His Ala
                        15         20         25
gca tct ggg aag gac tca agc agc aga ttg gct gtt acw gac ccc act      208
Ala Ser Gly Lys Asp Ser Ser Ser Arg Leu Ala Val Thr Asp Pro Thr
                        30         35         40
cgg cct ggt gcc acc acc aaa atc acc aag ccc      241
Arg Pro Gly Ala Thr Thr Lys Ile Thr Lys Pro
                        45         50
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<210> 3396

<211> 291

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 41..289

<400> 3396

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ttcctcgggt cagactaccg gcggcgacga ccacgggagc atg gcg gav acc gac      55
                        Met Ala Xaa Thr Asp
                        1         5
ctg ttc atg gaa tgt gad rag gag gag ttg gag cca tgg cag ama atc      103
Leu Phe Met Glu Cys Xaa Xaa Glu Glu Leu Glu Pro Trp Gln Xaa Ile
                        10         15         20
agt gat gtc att gmg gac tct gta gtt gaa gat tat aat tca gwg gat      151
Ser Asp Val Ile Xaa Asp Ser Val Val Glu Asp Tyr Asn Ser Xaa Asp
                        25         30         35
aaa act acc aca gtt tct gtg agm cag cag cca gtc tcg gct cca gtg      199
Lys Thr Thr Thr Val Ser Val Xaa Gln Gln Pro Val Ser Ala Pro Val
                        40         45         50
ccc atc gct gcc cat gct tct gtt gct ggg cac ctc tct aca tcc acc      247
Pro Ile Ala Ala His Ala Ser Val Ala Gly His Leu Ser Thr Ser Thr
                        55         60         65
acc gtt agt agc agc ggg gca cag aac agc gac agt aca aag aa      291
Thr Val Ser Ser Ser Gly Ala Gln Asn Ser Asp Ser Thr Lys
                        70         75         80
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<210> 3397

<211> 376

<212> DNA
 <213> Homo sapiens
 <220>
 <221> CDS
 <222> 204..374

<400> 3397
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 tttatgtagt ttaggctgga aatggtttca cttgctcttt gactgtcagc aagactgaag 120
 atggccttttc ctggacagct agaaaacaca aaatcttgta ggtcattgsa cctatctcag 180
 ccataggtgc agtttgcttc tac atg atg cta aag gct gcg aat ggg atc ctg 233
 Met Met Leu Lys Ala Ala Asn Gly Ile Leu
 1 5 10
 atg gaa cta agg act cca atg tcg aac tct tct ttg ctg cat tcc ttt 281
 Met Glu Leu Arg Thr Pro Met Ser Asn Ser Ser Leu Leu His Ser Phe
 15 20 25
 ttc ttc act tac aag aaa ggc ctg aat gga gga ctt ttc tgt aac cag 329
 Phe Phe Thr Tyr Lys Lys Gly Leu Asn Gly Gly Leu Phe Cys Asn Gln
 30 35 40
 gaa cat ttt tta ggg gtc aaa gtg cta ata att aac tca acc agg tc 376
 Glu His Phe Leu Gly Val Lys Val Leu Ile Ile Asn Ser Thr Arg
 45 50 55

<210> 3398
 <211> 381
 <212> DNA
 <213> Homo sapiens
 <220>
 <221> CDS
 <222> 2..379

<400> 3398
 a atg ggg acc aag atg gcg gac ctt gat tcg cct ccg aag ctg tca ggg 49
 Met Gly Thr Lys Met Ala Asp Leu Asp Ser Pro Pro Lys Leu Ser Gly
 1 5 10 15
 gtg cag cag ccg tct gag ggg gtg gga ggt ggc cgc tgc tcc gaa atc 97
 Val Gln Gln Pro Ser Glu Gly Val Gly Gly Gly Arg Cys Ser Glu Ile
 20 25 30
 tcc gct gag ctc att cgc tcc ctg aca gag ctg cag gag ctg gag gct 145
 Ser Ala Glu Leu Ile Arg Ser Leu Thr Glu Leu Gln Glu Leu Glu Ala
 35 40 45
 gta tac gaa cgg ctc tgc ggc gag gag aaa gtg gtg gag aga gag ctg 193
 Val Tyr Glu Arg Leu Cys Gly Glu Glu Lys Val Val Glu Arg Glu Leu
 50 55 60
 gat gct ctt ttg gaa cag caa aac acc att gaa agt aag atg gtc act 241
 Asp Ala Leu Leu Glu Gln Gln Asn Thr Ile Glu Ser Lys Met Val Thr
 65 70 75 80
 ctc crs cga atg ggt cct aat ctg cag ctg akh gag gga gat gca aag 289
 Leu Xaa Arg Met Gly Pro Asn Leu Gln Leu Xaa Glu Gly Asp Ala Lys
 85 90 95

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cag ctg gct gga atg atc acc ttt acc tgc aac ctg gct gag aat gtg      337
Gln Leu Ala Gly Met Ile Thr Phe Thr Cys Asn Leu Ala Glu Asn Val
      100                      105                      110
tcc agc aaa gtt cgt cag ctt gac ctg gcc aag aaa cac tca ac      381
Ser Ser Lys Val Arg Gln Leu Asp Leu Ala Lys Lys His Ser
      115                      120                      125

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<210> 3399
 <211> 240
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 72..239

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<400> 3399
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aaatcacttt g atg cca cac aaa aag gaa aat tac aag gca gga cta gta      110
      Met Pro His Lys Lys Glu Asn Tyr Lys Ala Gly Leu Val
      1                      5                      10
ggg agt ttt tca cat ttg tta tgt gat gat tat gct ggc agc aca aag      158
Gly Ser Phe Ser His Leu Leu Cys Asp Asp Tyr Ala Gly Ser Thr Lys
      15                      20                      25
gtc aaa ctc agc tta act act tct agg tcg gtt att tcc tct gtt ata      206
Val Lys Leu Ser Leu Thr Thr Ser Arg Ser Val Ile Ser Ser Val Ile
      30                      35                      40                      45
aag ttg gca tta agt ttc aga ctt ggg ggt agg g      240
Lys Leu Ala Leu Ser Phe Arg Leu Gly Gly Arg
      50                      55

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<210> 3400
 <211> 182
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 17..181

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<400> 3400
atataagact attaaa atg gcc ata agg aac cat aca gaa ctt ttt gaa att      52
      Met Ala Ile Arg Asn His Thr Glu Leu Phe Glu Ile
      1                      5                      10
aaa atc tgg agg aat gga ttt aaa agc aga tct gag aaa gct gaa gag      100
Lys Ile Trp Arg Asn Gly Phe Lys Ser Arg Ser Glu Lys Ala Glu Glu
      15                      20                      25
aca att agt gaa ttg gaa aat ata tct gaa gaa att ttg cag aat gca      148
Thr Ile Ser Glu Leu Glu Asn Ile Ser Glu Glu Ile Leu Gln Asn Ala
      30                      35                      40
aca gag aga gaa aat aaa atg gag cac acc tcg a      182
Thr Glu Arg Glu Asn Lys Met Glu His Thr Ser

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45

50

55

<210> 3401
 <211> 423
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 254..421

<400> 3401
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 tcctcaactg gctaacttct agagagcaga aactgactga ttggaaaggt cattaaatat 120
 tcatatcctg aacatttctt aatcttgagg atatgaatca gtaactctta aaagcaaaat 180
 gttattttatc attaaatggt aacaatataa tcacatcttc ttgcattctt ggcaagtttc 240
 ctggtacaac aac atg aag cga caa aga cac ccc aga ttg cgc ccc cag 289
 Met Lys Arg Gln Arg His Pro Arg Leu Arg Pro Gln
 1 5 10
 tca gcc cag tct tct ttc cct csc tcc cct ggt cct tct cct gat gtg 337
 Ser Ala Gln Ser Ser Phe Pro Xaa Ser Pro Gly Pro Ser Pro Asp Val
 15 20 25
 caa ctg gca act ctg gct cag aga gtc aag gaa gtt ttg cvb yra tgt 385
 Gln Leu Ala Thr Leu Ala Gln Arg Val Lys Glu Val Leu Xaa Xaa Cys
 30 35 40
 gcc att ggg tgt cat cca gag aga cct ggc caa gac tt 423
 Ala Ile Gly Cys His Pro Glu Arg Pro Gly Gln Asp
 45 50 55

<210> 3402
 <211> 287
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 <213> Homo sapiens

<220>
 <221> CDS
 <222> 63..287

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 gg atg act ata ctt aac aaa gat gta ttg tat ctt gat aat gga cac 107
 Met Thr Ile Leu Asn Lys Asp Val Leu Tyr Leu Asp Asn Gly His
 1 5 10 15
 cct gaa tac act gac ttg att gct aca cac tgt ata tgt gta aaa aaa 155
 Pro Glu Tyr Thr Asp Leu Ile Ala Thr His Cys Ile Cys Val Lys Lys
 20 25 30
 ttc tca tgt acc aca tac act ttc aca aaa agc act ggc ttt cca ctt 203
 Phe Ser Cys Thr Thr Tyr Thr Phe Thr Lys Ser Thr Gly Phe Pro Leu
 35 40 45
 ccc ttt ccc agg act gat att tac atg aac tac aag gtg ggg ccc agt 251
 Pro Phe Pro Arg Thr Asp Ile Tyr Met Asn Tyr Lys Val Gly Pro Ser
 50 55 60

gcc ttt ctc tgg agt ttg aag aca cac cgc cac ata
 Ala Phe Leu Trp Ser Leu Lys Thr His Arg His Ile
 65 70 75

287

<210> 3403
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 <213> Homo sapiens

<220>
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 <222> 187..357

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 tctgttattt ggcttggaga tcaggtagt agtctcgagc atcacatgca aatgcagtac 120
 aattggaaca cttgagattt ctgcatcacc ccgtattcct ataacgagac tgatcattca 180
 tgggaa atg gtc aaa aga cat ctt ctg ggt agg gaa gat aat tta tca 228
 Met Val Lys Arg His Leu Leu Gly Arg Glu Asp Asn Leu Ser
 1 5 10
 ctg gac ata act aaa tta aag aga caa att ttt gaa gcc tct caa gct 276
 Leu Asp Ile Thr Lys Leu Lys Arg Gln Ile Phe Glu Ala Ser Gln Ala
 15 20 25 30
 cac tta tcc att gtg cct gga gct gag gcg tta gat cag gtg gca gaa 324
 His Leu Ser Ile Val Pro Gly Ala Glu Ala Leu Asp Gln Val Ala Glu
 35 40 45
 aat ctt tct gga tta aac ccc agg act tgg att a 358
 Asn Leu Ser Gly Leu Asn Pro Arg Thr Trp Ile
 50 55

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 <212> DNA
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<220>
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 aaactaagca aatctagtgg cagccatgtg gtatatacat tgctacttgt gagggatgga 120
 taa atg aaa aac att tct cct tta ttt gag gca ttt gtc aag cag aga 168
 Met Lys Asn Ile Ser Pro Leu Phe Glu Ala Phe Val Lys Gln Arg
 1 5 10 15
 tat gaa caa ata ggc aat gca aat cag agg ggt tgt agt agg gaa tgt 216
 Tyr Glu Gln Ile Gly Asn Ala Asn Gln Arg Gly Cys Ser Arg Glu Cys
 20 25 30
 gca tta ttc tgt gga aat cca caa aat gca tgg gca tac aaa cca aat 264
 Ala Leu Phe Cys Gly Asn Pro Gln Asn Ala Trp Ala Tyr Lys Pro Asn
 35 40 45
 tta aat agt cat aga agg aat cct gca gga a 295

Leu Asn Ser His Arg Arg Asn Pro Ala Gly
 50 55

<210> 3405
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 <212> DNA
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<220>
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 <222> 99..251

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 cccctcccca ccattcccag aaaaggagga mggggctg atg gam tyc tct ggg raa 116
 Met Xaa Xaa Ser Gly Xaa
 1 5
 ccc cct csc ctc cct gmg cmc cgt cat caa gaa gaa aat tcg aag aaa 164
 Pro Pro Xaa Leu Pro Xaa Xaa Arg His Gln Glu Glu Asn Ser Lys Lys
 10 15 20
 agg ttt agc agg gac aga gaa gcg acc tgt ccc gga aac ccc tta aag 212
 Arg Phe Ser Arg Asp Arg Glu Ala Thr Cys Pro Gly Asn Pro Leu Lys
 25 30 35
 cck gcg ggt aac atg ttt gct ccc tcc tcc ccc act ccg 251
 Pro Ala Gly Asn Met Phe Ala Pro Ser Ser Pro Thr Pro
 40 45 50

<210> 3406
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 <212> DNA
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 taatttct atg ctt agg gag tat acc aca gca aaa ttt aat agc ttg cca 110
 Met Leu Arg Glu Tyr Thr Thr Ala Lys Phe Asn Ser Leu Pro
 1 5 10
 tcc atg aag atc ata aaa aat tgc ttt tct aat tct ata att cac cag 158
 Ser Met Lys Ile Ile Lys Asn Cys Phe Ser Asn Ser Ile Ile His Gln
 15 20 25 30
 aac tgt tca ttt ttc ttt tta gga acc tat gga ttt ttg ttt cca agt 206
 Asn Cys Ser Phe Phe Phe Leu Gly Thr Tyr Gly Phe Leu Phe Pro Ser
 35 40 45
 tta cag aat ttg atg ctc gaa aac tgc ata agt tat aca aga tgg ctc a 255
 Leu Gln Asn Leu Met Leu Glu Asn Cys Ile Ser Tyr Thr Arg Trp Leu
 50 55 60

<210> 3407

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Tyr Ile Tyr Ala Arg Gly Ala Gln Asp Met Lys Cys Val Ser Ile Gln
55 60 65

tac ctg gaa gct gtg agg agg ct 390
Tyr Leu Glu Ala Val Arg Arg
70 75

<210> 3409
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<220>
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atg gat ctg cct ggg gtt tcc att gca gac gag ggg gag act ggc atg 106
Met Asp Leu Pro Gly Val Ser Ile Ala Asp Glu Gly Glu Thr Gly Met
1 5 10 15
ttc tcc ttg tgc acc atc cgg ggt cac cag tta tta gag gaa gta aca 154
Phe Ser Leu Cys Thr Ile Arg Gly His Gln Leu Leu Glu Glu Val Thr
20 25 30
caa ggg gat atg agt gca gca gac aca ttt ctg tcc gat ctg cca agg 202
Gln Gly Asp Met Ser Ala Ala Asp Thr Phe Leu Ser Asp Leu Pro Arg
35 40 45
gat gat atc tat gtg tca gat gtt gag gac gac ggt gat gac aca tct 250
Asp Asp Ile Tyr Val Ser Asp Val Glu Asp Asp Gly Asp Asp Thr Ser
50 55 60
ctg gat agt gac ctg gat cca gag gag ctg gca gga gtc agg gga cat 298
Leu Asp Ser Asp Leu Asp Pro Glu Glu Leu Ala Gly Val Arg Gly His
65 70 75 80
cag ggt cta agg gac caa aag cgt atg cga ctt act gaa gtg caa gat 346
Gln Gly Leu Arg Asp Gln Lys Arg Met Arg Leu Thr Glu Val Gln Asp
85 90 95
gat aaa gag gat ggg 361
Asp Lys Glu Asp Gly
100

<210> 3410
<211> 402
<212> DNA
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<220>
<221> CDS
<222> 104..400

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gggtccatt cgtcccttct ctttcttgcc aaagagacgg cct atg gat gac ttg 115

													Met	Asp	Asp	Leu	
													1				
atg	ctc	ttc	ttc	ttg	ggg	gct	ttg	tgc	aga	gaa	tct	ggg	gtg	ccc	tca		163
Met	Leu	Phe	Phe	Leu	Gly	Ala	Leu	Cys	Arg	Glu	Ser	Gly	Val	Pro	Ser		
5					10					15					20		
ctg	gga	aag	cag	gag	aga	atg	aga	gca	tat	gct	gct	gag	atg	ccc	cct		211
Leu	Gly	Lys	Gln	Glu	Arg	Met	Arg	Ala	Tyr	Ala	Ala	Glu	Met	Pro	Pro		
			25						30					35			
ctc	ctc	cca	agt	cct	tgt	cca	ccc	cct	tct	cat	ctt	ccc	aag	cca	gct		259
Leu	Leu	Pro	Ser	Pro	Cys	Pro	Pro	Pro	Ser	His	Leu	Pro	Lys	Pro	Ala		
			40					45					50				
tct	ccc	tgt	ccc	tat	ccc	ttg	nnc	ctg	ctg	acc	ttc	ccc	gtg	ggg	gtc		307
Ser	Pro	Cys	Pro	Tyr	Pro	Leu	Xaa	Leu	Leu	Thr	Phe	Pro	Val	Gly	Val		
		55					60					65					
ccc	cat	ctt	cca	ggg	acc	cgc	ctg	cag	tgc	caa	ggc	ctg	ggt	cat	tct		355
Pro	His	Leu	Pro	Gly	Thr	Arg	Leu	Gln	Cys	Gln	Gly	Leu	Gly	His	Ser		
	70					75					80						
ctc	ara	cgg	gca	gag	cgg	gga	gtg	ggt	ggt	ggg	gtg	tct	cct	ggg	at		402
Leu	Xaa	Arg	Ala	Glu	Arg	Gly	Val	Gly	Gly	Gly	Val	Ser	Pro	Gly			
85					90				95								

<210> 3411
 <211> 284
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 37..282

<400> 3411																	
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				Met	Lys	Thr	Gly	Glu	Leu								
				1				5									
gag	aaa	gaa	aca	gcc	cct	ttg	agg	aaa	gat	gca	gat	agt	tca	ata	tca		102
Glu	Lys	Glu	Thr	Ala	Pro	Leu	Arg	Lys	Asp	Ala	Asp	Ser	Ser	Ile	Ser		
			10					15					20				
gtc	tta	gag	atc	cat	agt	caa	aaa	gca	caa	ata	gag	gaa	ccc	gat	cct		150
Val	Leu	Glu	Ile	His	Ser	Gln	Lys	Ala	Gln	Ile	Glu	Glu	Pro	Asp	Pro		
		25					30					35					
cca	gaa	atg	gaa	act	tct	ctt	gat	tct	tct	gag	atg	gca	aaa	gat	ctc		198
Pro	Glu	Met	Glu	Thr	Ser	Leu	Asp	Ser	Ser	Glu	Met	Ala	Lys	Asp	Leu		
	40					45				50							
tct	tca	aaa	act	gct	tta	tct	tcc	acc	gag	tcg	tgt	acc	atg	aaa	ggt		246
Ser	Ser	Lys	Thr	Ala	Leu	Ser	Ser	Thr	Glu	Ser	Cys	Thr	Met	Lys	Gly		
	55				60				65					70			
gaa	gag	aag	tct	ccc	aaa	act	aag	aag	gat	aag	cgt	cc					284
Glu	Glu	Lys	Ser	Pro	Lys	Thr	Lys	Lys	Asp	Lys	Arg						
				75					80								

<210> 3412
 <211> 438
 <212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 87..437

<400> 3412

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catctgtgca gcagcttggc attaaa atg act gtc agg tat ggc aaa ttc ctc      113
                               Met Thr Val Arg Tyr Gly Lys Phe Leu
                               1           5
agt ctc tta aaa gat ggt gca gaa aat gat ctt acc tgg gtt tta aag      161
Ser Leu Leu Lys Asp Gly Ala Glu Asn Asp Leu Thr Trp Val Leu Lys
10           15           20           25
cat tgt gag aga ttc ctg aaa cag cag caa act tcc ata aaa tct tct      209
His Cys Glu Arg Phe Leu Lys Gln Gln Thr Ser Ile Lys Ser Ser
           30           35           40
ctt ctc tgc ctg caa ggg aat tat gct ggc cat gac tgg ttt gta tct      257
Leu Leu Cys Leu Gln Gly Asn Tyr Ala Gly His Asp Trp Phe Val Ser
           45           50           55
tct ctg ttc atg ata atg ttg gga gac aaa gaa aaa aca ttc caa ttt      305
Ser Leu Phe Met Ile Met Leu Gly Asp Lys Glu Lys Thr Phe Gln Phe
           60           65           70
ctt cat caa ttc tcc agg ctt ctg act tct gct ttt ctt tgg ttg cca      353
Leu His Gln Phe Ser Arg Leu Leu Thr Ser Ala Phe Leu Trp Leu Pro
           75           80           85
agg cta cat att tct gta aga ctt caa tct gtt ttt aaa gga ggg ttt      401
Arg Leu His Ile Ser Val Arg Leu Gln Ser Val Phe Lys Gly Gly Phe
           90           95           100           105
gam att tta aga aca tta tac tta cat tca mcg gga c      438
Xaa Ile Leu Arg Thr Leu Tyr Leu His Ser Xaa Gly
           110           115
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<210> 3413

<211> 354

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 199..354

<400> 3413

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agtctaactc tggctgggaa agccttgctg ttagaggctc tttcccagaa gttggacgaa      60
gaggctcagg cgttgctggt tcttgctctc caagtcaagt gggttactctg gtaatggatt      120
gcctctctcc gagctttcac cctggtgaga ctgtccagat ctagtctgta aamncagctt      180
agaagcactg ttgtaaaa atg act gaa gag ccc att aag gag atc ctg gga      231
                               Met Thr Glu Glu Pro Ile Lys Glu Ile Leu Gly
                               1           5           10
gcc cca aag gct cac atg gca gcg acg atg gag aag agc ccc aag agt      279
Ala Pro Lys Ala His Met Ala Ala Thr Met Glu Lys Ser Pro Lys Ser
           15           20           25
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gaa gtt gtg atc acc aca gtc cct ctg gtc agt gag att cag ttg atg 327
 Glu Val Val Ile Thr Thr Val Pro Leu Val Ser Glu Ile Gln Leu Met
 30 35 40

gct gct aca ggg ggt acg agc tct cct 354
 Ala Ala Thr Gly Gly Thr Ser Ser Pro
 45 50

<210> 3414
 <211> 419
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 133..417

<400> 3414
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 ctctttttct tctctcagga gattgggagt ctgaacttgg aagccaatgt gacagcagat 120
 agagccttgg cc atg gaa aag gga ctg gcc tct ctg aag agt gag atg agg 171
 Met Glu Lys Gly Leu Ala Ser Leu Lys Ser Glu Met Arg

 1 5 10
 gaa gtg gaa gga gag ctg gaa agg aag gag ctg gag ttt gac acg aat 219
 Glu Val Glu Gly Glu Leu Glu Arg Lys Glu Leu Glu Phe Asp Thr Asn
 15 20 25

atg gat gca gta cag atg gtg att aca gaa gcc cag aag gtt gat acc 267
 Met Asp Ala Val Gln Met Val Ile Thr Glu Ala Gln Lys Val Asp Thr
 30 35 40 45

aga gcc aag aac gct ggg gtt aca atc caa gac aca ctc aac aca tta 315
 Arg Ala Lys Asn Ala Gly Val Thr Ile Gln Asp Thr Leu Asn Thr Leu
 50 55 60

gac ggc ctc ctg cat ctg atg gga gcn sat vga gga gag gca ccn aca 363
 Asp Gly Leu Leu His Leu Met Gly Ala Xaa Xaa Gly Glu Ala Pro Thr
 65 70 75

gac cct gca ctt gat ggr cca gct ggs acc acc cag atc aat aaa ctg 411
 Asp Pro Ala Leu Asp Gly Pro Ala Gly Thr Thr Gln Ile Asn Lys Leu
 80 85 90

gct tat tt 419
 Ala Tyr
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<210> 3415
 <211> 222
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 4..222

<400> 3415
 cag atg ctg ttt ttt tgt ttt ttt aaa ttt tta tat ttt ttt gag aca 48

Met	Leu	Phe	Phe	Cys	Phe	Phe	Lys	Phe	Leu	Tyr	Phe	Phe	Glu	Thr	
1				5					10					15	
gag	tct	gct	ctg	ttg	ccc	agg	ctg	gag	tgc	agt	ggc	gcg	atc	ttg	gct
Glu	Ser	Ala	Leu	Leu	Pro	Arg	Leu	Glu	Cys	Ser	Gly	Ala	Ile	Leu	Ala
			20						25					30	
cac	tgc	agc	ctc	cat	ctc	ccg	ggw	tca	agc	gat	tct	cct	gcc	tcg	gcc
His	Cys	Ser	Leu	His	Leu	Pro	Gly	Ser	Ser	Asp	Ser	Pro	Ala	Ser	Ala
			35						40					45	
acc	cga	ata	gct	ggg	att	act	ggg	gtg	tgc	cac	cat	acc	cag	cta	aat
Thr	Arg	Ile	Ala	Gly	Ile	Thr	Gly	Val	Cys	His	His	Thr	Gln	Leu	Asn
			50						55					60	
ttt	ttt	tgt	att	ttt	agt	aga	sac	gga	gtt						
Phe	Phe	Cys	Ile	Phe	Ser	Arg	Xaa	Gly	Val						
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 <211> 353
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 77..352

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		Met	Ile	Ser	Ile	Thr	Glu	Trp	Gln	Lys	Ile	Gly	Val		
		1				5						10			
ggg	atc	acc	ggg	ttc	ggc	atc	ttc	ttc	atc	ctc	ttt	gga	aca	ctc	ctg
Gly	Ile	Thr	Gly	Phe	Gly	Ile	Phe	Phe	Ile	Leu	Phe	Gly	Thr	Leu	Leu
		15				20						25			
tac	ttt	gat	tcc	gtg	ctc	ctg	gcc	ttt	gga	aac	ctg	ctg	ttc	ctg	acg
Tyr	Phe	Asp	Ser	Val	Leu	Leu	Ala	Phe	Gly	Asn	Leu	Leu	Phe	Leu	Thr
		30				35					40				
ggc	ctg	tcc	ctc	atc	att	ggc	ctg	agg	aag	acc	ttt	tgg	ttc	ttc	ttc
Gly	Leu	Ser	Leu	Ile	Ile	Gly	Leu	Arg	Lys	Thr	Phe	Trp	Phe	Phe	Phe
					50					55					60
caa	cgg	cac	aaa	ctc	aag	gga	acc	agc	ttc	ctc	ctg	ggg	ggg	gtg	gtt
Gln	Arg	His	Lys	Leu	Lys	Gly	Thr	Ser	Phe	Leu	Leu	Gly	Gly	Val	Val
				65					70					75	
atc	gtg	ctc	cta	cgc	tgg	ccc	ctc	ctc	ggc	atg	ttc	ctg	gaa	cta	cgg
Ile	Val	Leu	Leu	Arg	Trp	Pro	Leu	Leu	Gly	Met	Phe	Leu	Glu	Leu	Arg
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<210> 3417
 <211> 319
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 22..318

<400> 3417

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                        1          5          10
acg gag caa gag ccg ctg gaa ggg aca gaa cag aca cta gat gcg gag      99
Thr Glu Gln Glu Pro Leu Glu Gly Thr Glu Gln Thr Leu Asp Ala Glu
                        15          20          25
gag gag cag gag gaa tcc gaa gaa gcg gcc tgt ggc agc aag aag cgg      147
Glu Glu Gln Glu Glu Ser Glu Glu Ala Ala Cys Gly Ser Lys Lys Arg
                        30          35          40
gta gtg cca ggt att gtg tac ctg ggc cat atc ccg ccg cgc ttc cgg      195
Val Val Pro Gly Ile Val Tyr Leu Gly His Ile Pro Pro Arg Phe Arg
                        45          50          55
ccc ctg cac gtc cgc aac ctt ctc agc gcc tat ggc gag gtc gga cgc      243
Pro Leu His Val Arg Asn Leu Ser Ala Tyr Gly Glu Val Gly Arg
                        60          65          70
gtc ttc ttt cag gct gag gac cgg ttc gtg aga cgc aag aag aag gca      291
Val Phe Phe Gln Ala Glu Asp Arg Phe Val Arg Arg Lys Lys Lys Ala
75          80          85          90
gca gca gct gcc gga ggg aaa aag cgg t      319
Ala Ala Ala Ala Gly Gly Lys Lys Arg
                        95

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<210> 3418

<211> 344

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 156..344

<400> 3418

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ggggacaaac ttcaacatca acaacctcaa attct atg gca gta tcc aat cct      173
                        Met Ala Val Ser Asn Pro
                        1          5
gcg tca agc ctg aat ccc ggg acc aga cct aat ccc agg aag agc acc      221
Ala Ser Ser Leu Asn Pro Gly Thr Arg Pro Asn Pro Arg Lys Ser Thr
                        10          15          20
aat ccc aga atg aac ccc aat cct ggg ata agc cca gat ctc aaa atg      269
Asn Pro Arg Met Asn Pro Asn Pro Gly Ile Ser Pro Asp Leu Lys Met
                        25          30          35
acc tcg agt ccc aag atg act cca aat tcc aag aca agt ctg aat aga      317
Thr Ser Ser Pro Lys Met Thr Pro Asn Ser Lys Thr Ser Leu Asn Arg
                        40          45          50
gca gtg acc cca aag agc cac aac gat      344
Ala Val Thr Pro Lys Ser His Asn Asp
55          60

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<210> 3419
 <211> 279
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> 10..279

<400> 3419
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 Met Phe Val Leu Trp Ala Phe Glu Asp Gly Trp Leu Ile Val
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 cta aac ttt gca aat ttt cac att ttt att ttt att ttc gtg aga cag 99
 Leu Asn Phe Ala Asn Phe His Ile Phe Ile Phe Ile Phe Val Arg Gln
 15 20 25 30
 agt ctt gct gtg ttg ccc agg ctg gag tgc agt ggt gtg atc tcg gtt 147
 Ser Leu Ala Val Leu Pro Arg Leu Glu Cys Ser Gly Val Ile Ser Val
 35 40 45
 cac tgc aac ctc ctc ctc ctg ggt tca agt gag ttt cag ctt gaa gca 195
 His Cys Asn Leu Leu Leu Leu Gly Ser Ser Glu Phe Gln Leu Glu Ala
 50 55 60
 gcc tca gcc tcc aga gta gct agt att aca ggc atg agc cac cat acc 243
 Ala Ser Ala Ser Arg Val Ala Ser Ile Thr Gly Met Ser His His Thr
 65 70 75
 cga cta att ttt gta ttt tta gta gag aca ggg cct 279
 Arg Leu Ile Phe Val Phe Leu Val Glu Thr Gly Pro
 80 85 90

<210> 3420
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 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 44..304

<400> 3420
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 Met Gly Glu His
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 gaa cag gtg aag ccc ttg gag acc agc tct tcc aaa gts aaa gcc aag 103
 Glu Gln Val Lys Pro Leu Glu Thr Ser Ser Ser Lys Val Lys Ala Lys
 5 10 15 20
 acc att gtg atg att ccc gac tcc cag aag ctc ctg cga tgt gaa ctt 151
 Thr Ile Val Met Ile Pro Asp Ser Gln Lys Leu Leu Arg Cys Glu Leu
 25 30 35
 gag tca ctc aag agc cag tta cag gcc cag acc aag gct ttc gag ttc 199
 Glu Ser Leu Lys Ser Gln Leu Gln Ala Gln Thr Lys Ala Phe Glu Phe
 40 45 50
 ctg aac cac tca gtg acc atg ttg gag aag gag agc tgc ttg cag caa 247

Leu	Asn	His	Ser	Val	Thr	Met	Leu	Glu	Lys	Glu	Ser	Cys	Leu	Gln	Gln	
	55						60					65				
atc	aag	att	cag	cag	ctt	gaa	gag	gtg	ctg	agc	ccc	aga	ggc	cgc	cag	295
Ile	Lys	Ile	Gln	Gln	Leu	Glu	Glu	Val	Leu	Ser	Pro	Arg	Gly	Arg	Gln	
	70					75					80					
gga	gag	aag	ga													306
Gly	Glu	Lys														
85																

<210> 3421
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 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 122..334

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tccaacctgt	cttctctctg	tctcctggca	gtctctcttg	cctcctagtt	tctaccta											120
c atg tcc	ctg gtg	gag gcc	atc agc	ctc tgg	aat gaa	ggg gtg	ctg gca									169
Met	Ser	Leu	Val	Glu	Ala	Ile	Ser	Leu	Trp	Asn	Glu	Gly	Val	Leu	Ala	
1			5						10				15			
gcg gac	aag aag	gac tgg	aag gga	gcc ctg	gat gcc	ttc agt	gcc gtc									217
Ala Asp	Lys Lys	Asp Trp	Lys Gly	Ala Leu	Asp Ala	Phe Ser	Ala Val									
	20			25		30										
cag gac	ccc cac	tcc cgg	att tgc	ttc aac	att ggc	tgc atg	tac act									265
Gln Asp	Pro His	Ser Arg	Ile Cys	Phe Asn	Ile Gly	Cys Met	Tyr Thr									
	35		40		45											
atc ctg	aag aac	atg act	gma gca	gag aag	gcc ttt	acc aga	agc att									313
Ile Leu	Lys Asn	Met Thr	Xaa Ala	Glu Lys	Ala Phe	Thr Arg	Ser Ile									
	50		55		60											
aac cgm	gac aag	cac ttg	gca gt													336
Asn Arg	Asp Lys	His Leu	Ala													
65		70														

<210> 3422
 <211> 358
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> 185..358

<400> 3422																
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aggggttcag	ctcagacgag	gtcgtggggc	caagagagga	gtttggtgac	agtcccaagt											120
ttgggctgcg	gagaatcgct	gtttctccac	gccactcac	aacctgcact	ggaagtgtct											180
gagg atg	aag gtg	ttc gtc	tgc tgc	gcc tcc	aca tcg	cac tcc	ggg gag									229
Met	Lys	Val	Phe	Val	Cys	Cys	Ala	Ser	Thr	Ser	His	Ser	Gly	Glu		

1	5	10	15	
aag ccg gtc ccc act ctc ccc cag ttc acc atg ggc ccc aat gtg aag				277
Lys Pro Val Pro Thr Leu Pro Gln Phe Thr Met Gly Pro Asn Val Lys				
20	25	30		
atc aac gtg ctg gaa gac ttt gag gga gag aac cct cag gtg ccc aag				325
Ile Asn Val Leu Glu Asp Phe Glu Gly Glu Asn Pro Gln Val Pro Lys				
35	40	45		
ctt gag aag agc atc agc ggg gac cag ccc cga				358
Leu Glu Lys Ser Ile Ser Gly Asp Gln Pro Arg				
50	55			

<210> 3423
 <211> 238
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 84..236

<400> 3423		
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atatttagtca gggatcctac tga atg ttt ttg tgc aag gaa gtg aaa tgg tca	113	
Met Phe Leu Cys Lys Glu Val Lys Trp Ser		
1	5	10
aat tta tgg gct gtg aag att aat ctg ctg act ata gca tat act atc		161
Asn Leu Trp Ala Val Lys Ile Asn Leu Leu Thr Ile Ala Tyr Thr Ile		
15	20	25
aag cta gat tgg ggg atc tac tat tat ata agt atg aaa tat aag ctg		209
Lys Leu Asp Trp Gly Ile Tyr Tyr Tyr Ile Ser Met Lys Tyr Lys Leu		
30	35	40
aac agg agc agg gtg aga aac agt gct tc		238
Asn Arg Ser Arg Val Arg Asn Ser Ala		
45	50	

<210> 3424
 <211> 335
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 2..334

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a atg tta ata aga gct aat gga acc cat cac aag ata tta cca atg ttc	49		
Met Leu Ile Arg Ala Asn Gly Thr His His Lys Ile Leu Pro Met Phe			
1	5	10	15
cct ctt tac aga gag ccc aca aag cca ggc ctt gag cca agt gta tgc		97	
Pro Leu Tyr Arg Glu Pro Thr Lys Pro Gly Leu Glu Pro Ser Val Cys			
20	25	30	
cag gca cct ctc tct gca ttt tca gct cca tct cac aga gga gta act			145

agtggcaccg caattccggc tgctgcgggg aagtttagtt ggcccagggg cgccgtgtca 60
 ccgaaagaca cttggattgc gacattcgga cccagtgcga acgttttc atg tat ctt 117
 Met Tyr Leu
 1
 aaa tcc ttc aag gag cgg att gca agt tgc ttc ttc tcg agg caa cct 165
 Lys Ser Phe Lys Glu Arg Ile Ala Ser Cys Phe Phe Ser Arg Gln Pro
 5 10 15
 ctc cac cca gcg cca agg agt ccc tcc agg cca ccg atc agt gag caa 213
 Leu His Pro Ala Pro Arg Ser Pro Ser Arg Pro Pro Ile Ser Glu Gln
 20 25 30 35
 aca agt ctc caa aat ttc ctt tgg gac tca agt tta ccc acc gcg aat 261
 Thr Ser Leu Gln Asn Phe Leu Trp Asp Ser Ser Leu Pro Thr Ala Asn
 40 45 50
 tct ctt ttc act tcc ttt cta tgg ttc aaa cca aca gca cac 303
 Ser Leu Phe Thr Ser Phe Leu Trp Phe Lys Pro Thr Ala His
 55 60 65

<210> 3427
 <211> 296
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 124..294

<400> 3427
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 tctgaggaat atagctctta ggcttcagc ctctaccatg caggagagaa cacagaagga 120
 ctg atg tat gtt ggt gga tcc atg tat gtg tcc agc aca gcg gcc tgc 168
 Met Tyr Val Gly Gly Ser Met Tyr Val Ser Ser Thr Ala Ala Cys
 1 5 10 15
 tgg act ctg aga act ggg aaa gat cag agc aag cct tgc ctc tta tct 216
 Trp Thr Leu Arg Thr Gly Lys Asp Gln Ser Lys Pro Cys Leu Leu Ser
 20 25 30
 tcg gga aac cag aat atg ttt ggg gtg gta gga gcc aca cag act ctt 264
 Ser Gly Asn Gln Asn Met Phe Gly Val Val Gly Ala Thr Gln Thr Leu
 35 40 45
 ctg agc ccc ctc act cac ttc ctt ccc cct gt 296
 Leu Ser Pro Leu Thr His Phe Leu Pro Pro
 50 55

<210> 3428
 <211> 344
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 87..344

<400> 3428

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gctcttttgt tctcttttcc ttagcctctt cggatgatctt tggctctgaag ggctatgtgg      60
ctgagcggaa ggggtgagagg gaggag atg cag gat gcc cac gtc atc ctg aac      113
                               Met Gln Asp Ala His Val Ile Leu Asn
                               1                               5

gac atc acc gag gag tgt agg ccc cca tcg tcc ctc att act cgg gtt      161
Asp Ile Thr Glu Glu Cys Arg Pro Pro Ser Ser Leu Ile Thr Arg Val
10                               15                               20                               25

tca tat ttt gct gtk ttt gat gga cat gga gga att cga gcc tca aaa      209
Ser Tyr Phe Ala Val Phe Asp Gly His Gly Gly Ile Arg Ala Ser Lys
                               30                               35                               40

ttt gct gca cag aat ttg cat caa aac tta atc aga aaa ttk sct aaa      257
Phe Ala Ala Gln Asn Leu His Gln Asn Leu Ile Arg Lys Xaa Xaa Lys
                               45                               50                               55

ggg gat gta atc agt gta gag raa acc gtg aag aga tgc ctt ttg gac      305
Gly Asp Val Ile Ser Val Glu Xaa Thr Val Lys Arg Cys Leu Leu Asp
                               60                               65                               70

act ttc aag cat act gat gaa gag tcc tta aac aag ctg      344
Thr Phe Lys His Thr Asp Glu Glu Ser Leu Asn Lys Leu
                               75                               80                               85

<210> 3429
<211> 341
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 45..341

<400> 3429
gcacgcagcc ttccgcacgc ctgatccagt ggttctgggm ggtg atg gag tcc ttc      56
                               Met Glu Ser Phe
                               1

tcc aac aca gag cgc tct ctt ttc ctt cgc ttc gtc tgg ggc cgg acg      104
Ser Asn Thr Glu Arg Ser Leu Phe Leu Arg Phe Val Trp Gly Arg Thr
5                               10                               15                               20

agg ctg ccc agg acc atc gcc gac ttc cgg ggc cga gac ttc gtc atc      152
Arg Leu Pro Arg Thr Ile Ala Asp Phe Arg Gly Arg Asp Phe Val Ile
                               25                               30                               35

cag gtg ttg gat aaa tac aac cct cca gac cac ttc ctc cct gag tcc      200
Gln Val Leu Asp Lys Tyr Asn Pro Pro Asp His Phe Leu Pro Glu Ser
                               40                               45                               50

tac acc tgt ttc ttc ttg ctg aag ctg ccc agg tat tcc tgc aag cag      248
Tyr Thr Cys Phe Phe Leu Leu Lys Leu Pro Arg Tyr Ser Cys Lys Gln
                               55                               60                               65

gtg ctg gag gag aag ctc aag tac gcc atc cac ttc tgc aag tcc ata      296
Val Leu Glu Glu Lys Leu Lys Tyr Ala Ile His Phe Cys Lys Ser Ile
                               70                               75                               80

gac aca gat gac tac gct cgc atc gca ctt aca gga gag cag cct      341
Asp Thr Asp Asp Tyr Ala Arg Ile Ala Leu Thr Gly Glu Gln Pro
85                               90                               95

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<210> 3430

<211> 200
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 8..199

<400> 3430
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 Met Lys Cys Ile Ser Leu Tyr Leu Glu Asp Glu Ala Gln Thr
 1 5 10
 ccc aca cct ctg tct ccc cca ggg ctc ggg atg tct cca gca gcc cgg 97
 Pro Thr Pro Leu Ser Pro Pro Gly Leu Gly Met Ser Pro Ala Ala Arg
 15 20 25 30
 cca cgc agc ttc cca ggt ggg ctc ggg gag gtg gga gca ggg acc atc 145
 Pro Arg Ser Phe Pro Gly Gly Leu Gly Glu Val Gly Ala Gly Thr Ile
 35 40 45
 tct gtc ccc tcc acc ctc act cca tcc acc tcg gag acc acc cta tcc 193
 Ser Val Pro Ser Thr Leu Thr Pro Ser Thr Ser Glu Thr Thr Leu Ser
 50 55 60
 cct act a 200
 Pro Thr

<210> 3431
 <211> 230
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 78..230

<400> 3431
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 ctgaaaaatt gtttgga atg cca gaa ata aga aag ttg ttc tcc aga gct 110
 Met Pro Glu Ile Arg Lys Leu Phe Ser Arg Ala
 1 5 10
 gga aac cca tct ttc gtt tgt agt gtc act gtt gtg gct cca agc tca 158
 Gly Asn Pro Ser Phe Val Cys Ser Val Thr Val Val Ala Pro Ser Ser
 15 20 25
 gtg ata gga aag gac ggt ggt tac aca cca gcc ttc aga acc caa ggc 206
 Val Ile Gly Lys Asp Gly Gly Tyr Thr Pro Ala Phe Arg Thr Gln Gly
 30 35 40
 ccc cag tat tgt tgt cag ctg cct 230
 Pro Gln Tyr Cys Cys Gln Leu Pro
 45 50

<210> 3432
 <211> 411
 <212> DNA
 <213> Homo sapiens

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<210> 3433
<211> 242
<212> DNA
<213> Homo sapiens
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<400> 3433
ctcccaacga cgcagcccggttctgcagcc ggtgaagaaa cgcggctggs scaagggcaa      60
gaagcggaag aagattctgc cgr atg ggs ccc aag gca ccg gtc acg ggc tac      113
                Met Gly Pro Lys Ala Pro Val Thr Gly Tyr
                1                5                10

gtg cgc ttc ctg aac gag cgg cgc grg cag atc cgc acg cgc cac ccg      161
Val Arg Phe Leu Asn Glu Arg Arg Xaa Gln Ile Arg Thr Arg His Pro
                15                20                25

gat ctg ccc ttt ccc gag atc acc aag atg ctg ggc gcc gag tgg agc      209

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Asp Leu Pro Phe Pro Glu Ile Thr Lys Met Leu Gly Ala Glu Trp Ser
 30 35 40
 aag ctg cag cca acg gaa aag cag cgg tac caa
 Lys Leu Gln Pro Thr Glu Lys Gln Arg Tyr Gln
 45 50

242

<210> 3434
 <211> 292
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 116..292

<400> 3434
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 aagtggctga ccabgtcttc ctgggccatc tgggtccccga dgtcagcctg gtgtc atg 118
 Met
 1
 ggc ttc ccc ggt cct aaa gga rat gat gtg agt tcc ttc atk rat ttc 166
 Gly Phe Pro Gly Pro Lys Gly Xaa Asp Val Ser Ser Phe Xaa Xaa Phe
 5 10 15
 tts rat aaa tat ttg act gga agg ctt tta ttt tcc ata tgg agt aaa 214
 Xaa Xaa Lys Tyr Leu Thr Gly Arg Leu Leu Phe Ser Ile Trp Ser Lys
 20 25 30
 gaa atg gtc aaa act cag tct cct ctt caa agc atg gag gag tat atg 262
 Glu Met Val Lys Thr Gln Ser Pro Leu Gln Ser Met Glu Glu Tyr Met
 35 40 45
 arr atc aaa ttg cat gta gga agg gag ctc 292
 Xaa Ile Lys Leu His Val Gly Arg Glu Leu
 50 55

<210> 3435
 <211> 338
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 58..336

<400> 3435
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 atg aac rra tat gca agt cca ttc aac tgw caa ttg ard tat ttg gak 105
 Met Asn Xaa Tyr Ala Ser Pro Phe Asn Xaa Gln Leu Xaa Tyr Leu Xaa
 1 5 10 15
 ttg agc agr ttc gag tgt gtr cat aga gat gga aga gta att aca ctg 153
 Leu Ser Arg Phe Glu Cys Val His Arg Asp Gly Arg Val Ile Thr Leu
 20 25 30
 tct tat cag gag cag gag cta cag gat ttt ctt ctg tct cag atg tca 201
 Ser Tyr Gln Glu Gln Glu Leu Gln Asp Phe Leu Leu Ser Gln Met Ser

35	40	45	
cag cac cag gta cat gca gtt cag caa ctc gcc aag gtt atg ggc tgg			249
Gln His Gln Val His Ala Val Gln Gln Leu Ala Lys Val Met Gly Trp			
50	55	60	
caa gta ctg agc ttc agt aat cat gtg gga ctt gga cct ata gag agc			297
Gln Val Leu Ser Phe Ser Asn His Val Gly Leu Gly Pro Ile Glu Ser			
65	70	75	80
abt ggt aat gca tct gcc atc acg gtg gcy ccc caa gtg gt			338
Xaa Gly Asn Ala Ser Ala Ile Thr Val Ala Pro Gln Val			
85	90		

<210> 3436
 <211> 302
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 37..300

<400> 3436	
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Met Ser Leu Ala Val Phe	
1	5
ctt cct tct gtt ttt tgg aat agt ttg agt agg att tgg gta tta gtt	102
Leu Pro Ser Val Phe Trp Asn Ser Leu Ser Arg Ile Trp Val Leu Val	
10	15
ctc ttt aaa tgt ttg gta gaa ttt agc agt aaa gcc atg ggg tcc tgg	150
Leu Phe Lys Cys Leu Val Glu Phe Ser Ser Lys Ala Met Gly Ser Trp	
25	30
act ttt tct tta ctg ggt gta tta gtc tgt ttt cac act gct gat aaa	198
Thr Phe Ser Leu Leu Gly Val Leu Val Cys Phe His Thr Ala Asp Lys	
40	45
gac ata ccc cag act gag act ggg caa ttt aca aaa gaa aga ggt tta	246
Asp Ile Pro Gln Thr Glu Thr Gly Gln Phe Thr Lys Glu Arg Gly Leu	
55	60
att gga ctt aac agt tcc aca tgg ctg ggg aaa ctc aca ata atg gtg	294
Ile Gly Leu Asn Ser Ser Thr Trp Leu Gly Lys Leu Thr Ile Met Val	
75	80
gaa ggc aa	302
Glu Gly	

<210> 3437
 <211> 403
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 223..402

<400> 3437

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 ggaatgtcag aagactgaga acattgttcc ttcttcatac tgctgctctg ttgccagaga 120
 atcccaattt acactcaaag cttctttgat taagtgctag gagataaatt tgcattttct 180
 caaggaaaag gctaaaagtg gtagcaggtg gcatttaccg tc atg gag agc agg 234

Met Glu Ser Arg

1

gat cat aac aac ccc cag gag gga ccc acg tcc tcc agc ggt aga agg 282
 Asp His Asn Asn Pro Gln Glu Gly Pro Thr Ser Ser Ser Gly Arg Arg
 5 10 15 20

gct gca gtg gaa gac aat cmg ttg ctg att aaa gct gtt caa aac gaa 330
 Ala Ala Val Glu Asp Asn Xaa Leu Leu Ile Lys Ala Val Gln Asn Glu
 25 30 35

gat gtt gac ctg gtc cag caa ttg ctg gaa ggt gga gcc aat gtt aat 378
 Asp Val Asp Leu Val Gln Gln Leu Leu Glu Gly Gly Ala Asn Val Asn
 40 45 50

ttc cag gaa gag aag ggg gct ggg a 403
 Phe Gln Glu Glu Lys Gly Ala Gly
 55 60

<210> 3438

<211> 243

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 68..241

<400> 3438

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 tttcacc atg cct gga tca ctt cct ttg aat gca gaa gct tgc tgg cca 109
 Met Pro Gly Ser Leu Pro Leu Asn Ala Glu Ala Cys Trp Pro
 1 5 10

aaa gat gtg gga att gtt gcc ctt gag atc tat ttt cct tct caa tat 157
 Lys Asp Val Gly Ile Val Ala Leu Glu Ile Tyr Phe Pro Ser Gln Tyr
 15 20 25 30

gtt gat caa gca gag ttg gaa aaa tat gat ggt gta gat gct gga aag 205
 Val Asp Gln Ala Glu Leu Glu Lys Tyr Asp Gly Val Asp Ala Gly Lys
 35 40 45

tat acc att ggc ttg ggc cag gcc aag atg ggc ttc tg 243
 Tyr Thr Ile Gly Leu Gly Gln Ala Lys Met Gly Phe
 50 55

<210> 3439

<211> 223

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 8..223

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<222> 29..265

<400> 3441

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aggctccccct ttcggcctct cgttcttt atg cga ctt gaa tct ccc gac gaa      52
                        Met Arg Leu Glu Ser Pro Asp Glu
                        1           5

aat ttt gcg gta gtt cag gaa cat gcc att cat cac atc gat ggc ccg      100
Asn Phe Ala Val Val Gln Glu His Ala Ile His His Ile Asp Gly Pro
    10           15           20

ctc cgc aga ttc ctg ctt ttg gaa gtg cac gaa ccc gta gcc ctt ggg      148
Leu Arg Arg Phe Leu Leu Leu Glu Val His Glu Pro Val Ala Leu Gly
    25           30           35           40

ccc ctt ttc gtc aca ggc cac ttt gca gga gag gat gtt gcc gaa cgc      196
Pro Leu Phe Val Thr Gly His Phe Ala Gly Glu Asp Val Ala Glu Arg
                45           50           55

cga gaa gat gtt gta cag cgc ctt gtt gtc gat ggt ctt gcc cag gtt      244
Arg Glu Asp Val Val Gln Arg Leu Val Val Asp Gly Leu Ala Gln Val
                60           65           70

ctt gat gaa gac gtt gcc cac cc      267
Leu Asp Glu Asp Val Ala His
    75

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<210> 3442

<211> 235

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 72..233

<400> 3442

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acataataaga t atg ctt atc ttt ctt tct ttc ttt ctt ttt gat atg gag      110
                        Met Leu Ile Phe Leu Ser Phe Phe Leu Phe Asp Met Glu
                        1           5           10

tct cgc tct ctt gcc cag gct gga ctg cag tgg cac aat ctc ggc tca      158
Ser Arg Ser Leu Ala Gln Ala Gly Leu Gln Trp His Asn Leu Gly Ser
    15           20           25

ctg caa cct ttg cct cct gga ttc aag cga ttc tcc tgc ctc agc ctc      206
Leu Gln Pro Leu Pro Pro Gly Phe Lys Arg Phe Ser Cys Leu Ser Leu
    30           35           40           45

cca agt agc tgg gac tac agg cgc gca cc      235
Pro Ser Ser Trp Asp Tyr Arg Arg Ala
    50

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<210> 3443

<211> 166

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 4..165

tct agc ctc cag gcg ctg tgc tct ggc ctg ccc ctg cgg ccc ctc cca	105
Ser Ser Leu Gln Ala Leu Cys Ser Gly Leu Pro Leu Arg Pro Leu Pro	
5 10 15	
gag aac cgg gga cgc cag gct ggg gtg ccc cat gcc cct gtc agg acc	153
Glu Asn Arg Gly Arg Gln Ala Gly Val Pro His Ala Pro Val Arg Thr	
20 25 30	
ccc agc ctc agc cct gtg gag aaa cag ctg gcg ctg agg aac gcc ctg	201
Pro Ser Leu Ser Pro Val Glu Lys Gln Leu Ala Leu Arg Asn Ala Leu	
35 40 45	
cgc tac ttc ccc ccg ga	218
Arg Tyr Phe Pro Pro	
50	

<210> 3446
 <211> 373
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 86..373

<400> 3446	
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cgaatctggg ccaaatagaa agaac atg ttc ttc aag tat aca tgg aat aac	112
Met Phe Phe Lys Tyr Thr Trp Asn Asn	
1 5	
ttt ttg cat aca caa gtg gaa att tgt att gca ctg att ctt gca agt	160
Phe Leu His Thr Gln Val Glu Ile Cys Ile Ala Leu Ile Leu Ala Ser	
10 15 20 25	
cct ttt gaa aac aca gaa aat gcc aca att acc gat caa gac tcc act	208
Pro Phe Glu Asn Thr Glu Asn Ala Thr Ile Thr Asp Gln Asp Ser Thr	
30 35 40	
ggt gat aat ttg tta tta aaa cat ctt ttc caa aaa tgt caa tta ata	256
Gly Asp Asn Leu Leu Leu Lys His Leu Phe Gln Lys Cys Gln Leu Ile	
45 50 55	
gaa cga ata ctt gaa gcc tgg gaa atg aat gag aag aaa cag gct gag	304
Glu Arg Ile Leu Glu Ala Trp Glu Met Asn Glu Lys Lys Gln Ala Glu	
60 65 70	
gga gga aga cgg cat ggt tac atg gga cac cta acg agg ata gct aac	352
Gly Gly Arg Arg His Gly Tyr Met Gly His Leu Thr Arg Ile Ala Asn	
75 80 85	
tgt atc gtg cac aca ctg act	373
Cys Ile Val His Thr Leu Thr	
90 95	

<210> 3447
 <211> 323
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS

<222> 147..323

<400> 3447

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aaccactgct caaggaaata aaagaggata caaacaaatg gaagaacatt ccatgctcat 120
gggtaggaag aatcaatatc gtgaaa atg gcc ata ctg ccc aag gta att tac 173

Met Ala Ile Leu Pro Lys Val Ile Tyr

aga ttc aat gcc atc ccc atc aag cta cca atg cct ttc ttc aca gaa 221
Arg Phe Asn Ala Ile Pro Ile Lys Leu Pro Met Pro Phe Phe Thr Glu
10 15 20 25

ttg gaa aaa act act tta aag ttc ata tgg aac caa aaa aga gcc cgc 269
Leu Glu Lys Thr Thr Leu Lys Phe Ile Trp Asn Gln Lys Arg Ala Arg
30 35 40

atc gcc aar wca atc cta agc caa aag gac aaa gct gga ggc atc aca 317
Ile Ala Lys Xaa Ile Leu Ser Gln Lys Asp Lys Ala Gly Gly Ile Thr
45 50 55

cta cca 323
Leu Pro

<210> 3448

<211> 230

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 51..230

<400> 3448

tttggggcac tttcccaata ctaaaggact ctccaaaagt ccccatcttg atg cct 56
Met Pro

gtg cct att cca gct gcg gcg gat gca gga gat gct aca caa aat aca 104
Val Pro Ile Pro Ala Ala Ala Asp Ala Gly Asp Ala Thr Gln Asn Thr
5 10 15

aaa aca gat gaa gga gaa cta tta act ggc ttt cag ccc tgg ata ttt 152
Lys Thr Asp Glu Gly Glu Leu Thr Gly Phe Gln Pro Trp Ile Phe
20 25 30

aaa tct cct cct ctt ctt cct gtc cat gcc ggc ccc tcc cag cac cag 200
Lys Ser Pro Pro Leu Leu Pro Val His Ala Gly Pro Ser Gln His Gln
35 40 45 50

ctc tgc tca ggc ccc ttc agc tac cgc cac 230
Leu Cys Ser Gly Pro Phe Ser Tyr Arg His
55 60

<210> 3449

<211> 270

<212> DNA

<213> Homo sapiens

<220>

[illegible]

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<210> 3450
<211> 214
<212> DNA
<213> Homo sapiens
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<220>
<221> CDS
<222> 33..212
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[illegible]

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<210> 3451
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<212> DNA
<213> Homo sapiens
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2137

<221> CDS
<222> 35..187

<400> 3451
cccaagtttt accattctct atttgtgccc taca atg gct cca ccc ttt gaa ata 55
Met Ala Pro Pro Phe Glu Ile
1 5
acg cct ggt cta aat gtt act ttt tct agt ggg cct tcc ttg att atc 103
Thr Pro Gly Leu Asn Val Thr Phe Ser Ser Gly Pro Ser Leu Ile Ile
10 15 20
cat ccc act gtg att cct ttt cct gcc cat agc ctc tcc gac aag cct 151
His Pro Thr Val Ile Pro Phe Pro Ala His Ser Leu Ser Asp Lys Pro
25 30 35
tgc att ctc att cat atg acc ttg ttt gcc aat gcc t 188
Cys Ile Leu Ile His Met Thr Leu Phe Ala Asn Ala
40 45 50

<210> 3452
<211> 420
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 7..420

<400> 3452
taagtg atg aag ctg aaa tta tac cta tgt ata tta ggt ccc tgg ggc 48
Met Lys Leu Lys Leu Tyr Leu Cys Ile Leu Gly Pro Trp Gly
1 5 10
tgc aak rkc aaa gta cca cta att ggg ttt ctt aaa aga ata aan hta 96
Cys Xaa Xaa Lys Val Pro Leu Ile Gly Phe Leu Lys Arg Ile Xaa Xaa
15 20 25 30
tat nwt ctc aca gtt ctg aaa cct agd agt ctg ara tca ann tca gca 144
Tyr Xaa Leu Thr Val Leu Lys Pro Xaa Ser Leu Xaa Ser Xaa Ser Ala
35 40 45
ggg ttg gtt cct tct gag gac tct aaa aaa gaa tct gtt tca tgc ctc 192
Gly Leu Val Pro Ser Glu Asp Ser Lys Lys Glu Ser Val Ser Cys Leu
50 55 60
tct cct agg ttc tgg tgg tgg ctg gga agc ctg akt gtt act tgg ctt 240
Ser Pro Arg Phe Trp Trp Trp Leu Gly Ser Leu Xaa Val Thr Trp Leu
65 70 75
ata cat gca tca ctc cag tct ctg tct cct ttt tct cat gcc att ttc 288
Ile His Ala Ser Leu Gln Ser Leu Ser Pro Phe Ser His Ala Ile Phe
80 85 90
tca tgt gtc tct gtg ttt tcc ttt gct tat aag gat acc agt cat att 336
Ser Cys Val Ser Val Phe Ser Phe Ala Tyr Lys Asp Thr Ser His Ile
95 100 105 110
gaa tta ggg cct gct cta ata acc tca tct caa tta cct ctg caa gga 384
Glu Leu Gly Pro Ala Leu Ile Thr Ser Ser Gln Leu Pro Leu Gln Gly
115 120 125
acc aat ttc caa ata atg tca cac tca cat gta gca 420

Thr Asn Phe Gln Ile Met Ser His Ser His Val Ala
 130 135

<210> 3453
 <211> 341
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 121..339

<400> 3453
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 attgggggtgc agtagttcgs tccccasrag ggacccccca garaatccgg cagctgakag 120
 atg ang ggg att gcc ccg gaa gag gga ggc gtg gac gcg aag gac acg 168
 Met Xaa Gly Ile Ala Pro Glu Glu Gly Gly Val Asp Ala Lys Asp Thr
 1 5 10 15
 tct gcc aca tcc cag tca gtt aat gga tca mcc caa gcg gaa caa cct 216
 Ser Ala Thr Ser Gln Ser Val Asn Gly Ser Xaa Gln Ala Glu Gln Pro
 20 25 30
 tca ttg gaa tct aca agc aaa gaa gcc ttc ttt agc aga gtg gav aca 264
 Ser Leu Glu Ser Thr Ser Lys Glu Ala Phe Phe Ser Arg Val Xaa Thr
 35 40 45
 ttt tct tct ttg aaa tgg gca ggt aag ccc ttt gag ctg tct cca ctc 312
 Phe Ser Ser Leu Lys Trp Ala Gly Lys Pro Phe Glu Leu Ser Pro Leu
 50 55 60
 gtc tgt gca aaa tat ggc tgg gtc aca gt 341
 Val Cys Ala Lys Tyr Gly Trp Val Thr
 65 70

<210> 3454
 <211> 389
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 136..387

<400> 3454
 aaaaacakca ggtaatgata acaacagtct ccttcacttt catagkaatt tgatgaaatc 60
 gtccaagtgc ttccataact gaagattaag tttcctaatt ctctgcacct taaattcaag 120
 gaaacaaatc ttgta atg ctg cag caa ttt aac gca cta gcc caa ctc cgt 171
 Met Leu Gln Gln Phe Asn Ala Leu Ala Gln Leu Arg
 1 5 10
 cgt att gac cag ttg aca att gat cct caa gga aat cca gtt gtc aat 219
 Arg Ile Asp Gln Leu Thr Ile Asp Pro Gln Gly Asn Pro Val Val Asn
 15 20 25
 ttt aca ctc tgg aaa tac tat gta ctg ttt agg cta agc cat ttc agt 267
 Phe Thr Leu Trp Lys Tyr Tyr Val Leu Phe Arg Leu Ser His Phe Ser
 30 35 40

ggg acc cag gat cca ggg aac atg gga acc ggc gtc cca gcc tcg gag	1	287
Gly Thr Gln Asp Pro Gly Asn Met Gly Thr Gly Val Pro Ala Ser Glu		
5 10 15		
cag ata agc tgt gcc aaa gag gat cca caa gtt tat tgc cct gaa gag		335
Gln Ile Ser Cys Ala Lys Glu Asp Pro Gln Val Tyr Cys Pro Glu Glu		
20 25 30		
act ggc ggc acc aag gat gtg cag gtt aca gac tgt aag agt ccc gaa		383
Thr Gly Gly Thr Lys Asp Val Gln Val Thr Asp Cys Lys Ser Pro Glu		
35 40 45		
gac agc cg		391
Asp Ser		
50		

<210> 3457
 <211> 359
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 62..358

<400> 3457	
aagacctaata actatarraa ccctagaaga aaacctaggc aataccattc aggacatagg	60
c atg ggc aaa gac ttc att act aaa aca cca aaa gca atg gta aca aaa	109
Met Gly Lys Asp Phe Ile Thr Lys Thr Pro Lys Ala Met Val Thr Lys	
1 5 10 15	
acc aaa att gac aaa tgg gaw cta aaa tgg aam cwa aag agc ttc tgc	157
Thr Lys Ile Asp Lys Trp Xaa Leu Lys Trp Xaa Xaa Lys Ser Phe Cys	
20 25 30	
aca gca aga gaa act atc atc aga gtg aac aga caa cct aca gaa tgg	205
Thr Ala Arg Glu Thr Ile Ile Arg Val Asn Arg Gln Pro Thr Glu Trp	
35 40 45	
gag aaa att ttt gca atc cat cca tat gac aaa gga cta ata tcc aga	253
Glu Lys Ile Phe Ala Ile His Pro Tyr Asp Lys Gly Leu Ile Ser Arg	
50 55 60	
atc tac aag gaa ctt aaa caa att tac aag aaa aaa caa ccc tat cga	301
Ile Tyr Lys Glu Leu Lys Gln Ile Tyr Lys Lys Lys Gln Pro Tyr Arg	
65 70 75 80	
aaa gag ggc aaa gga tat gaa cag aca ttt ctc aaa aga aga cat twa	349
Lys Glu Gly Lys Gly Tyr Glu Gln Thr Phe Leu Lys Arg Arg His Xaa	
85 90 95	
tgc aac caa c	359
Cys Asn Gln	

<210> 3458
 <211> 377
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS

<222> 130..375

<400> 3458

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tagaaacttt atattgggaa taaagggtttc cccttggttat aattaacacc aactagtgat      60
gtctcctcct ccctccccc tgtgcttccc ctgtctgaac aactactcga tttaagaagg      120
ggacttagg atg agg aag gat gtg gtt tcc ttc cca ctt ggc aag cac tcc      171
      Met Arg Lys Asp Val Val Ser Phe Pro Leu Gly Lys His Ser
      1          5          10
gtg tca gaa tgg aag act tgt gtc tgg gcc tgg cac ggt tcc gtc agg      219
Val Ser Glu Trp Lys Thr Cys Val Trp Ala Trp His Gly Ser Val Arg
15          20          25          30
ccc tct tac cag ccc agt cgt gtc tgt gac cag agc acg tgg gag gtg      267
Pro Ser Tyr Gln Pro Ser Arg Val Cys Asp Gln Ser Thr Trp Glu Val
      35          40          45
cac atc cgt gta gaa aaa cct ccc act ggc tgc cag ctc tgg att ttt      315
His Ile Arg Val Glu Lys Pro Pro Thr Gly Cys Gln Leu Trp Ile Phe
      50          55          60
gaa ata att cct aat gaa tgc agt ctt gcc cag gcc aaa cct ctt aca      363
Glu Ile Ile Pro Asn Glu Cys Ser Leu Ala Gln Ala Lys Pro Leu Thr
      65          70          75
gga atg atg acc ac      377
Gly Met Met Thr
      80
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<210> 3459

<211> 188

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 27..188

<400> 3459

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agccagaggk wcgagctagc ccgacg atg gcc cag ggg aca ttg atc cgt gtg      53
      Met Ala Gln Gly Thr Leu Ile Arg Val
      1          5
acc cca gag cag ccc acc cat gcc gtg tgt gtg ctg ggc acc ttg act      101
Thr Pro Glu Gln Pro Thr His Ala Val Cys Val Leu Gly Thr Leu Thr
10          15          20          25
cag ctt gac atc tgc agc tct gcc cct gag gac tgm acg tcc ttc aag      149
Gln Leu Asp Ile Cys Ser Ser Ala Pro Glu Asp Xaa Thr Ser Phe Lys
      30          35          40
cat caa cgc ctc ccc agg ggt ggt cgt gga tat tgc cca      188
His Gln Arg Leu Pro Arg Gly Gly Arg Gly Tyr Cys Pro
      45          50
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<210> 3460

<211> 221

<212> DNA

<213> Homo sapiens

<220>
 <221> CDS
 <222> 65..220

<400> 3460
 gcggttctag gggagcgtgc gggcgccggg gtccggcggc gagaggccac cttctggcct 60
 tgcg atg aat cct cgg ttt ccc ctt ctc aga tgg ggt tnt cgt gag ggt 109
 Met Asn Pro Arg Phe Pro Leu Leu Arg Trp Gly Xaa Arg Glu Gly
 1 5 10 15
 aca acg tcg gca tta gac att cca ggt gac gcc cgt acg cgg tgg gcg 157
 Thr Thr Ser Ala Leu Asp Ile Pro Gly Asp Ala Arg Thr Arg Trp Ala
 20 25 30
 gtt cgg gcc gga gct ctg gaa cgc tgg ccc tgg agg cgt cga ccc ctc 205
 Val Arg Ala Gly Ala Leu Glu Arg Trp Pro Trp Arg Arg Arg Pro Leu
 35 40 45
 gtt act gat gca ggg c 221
 Val Thr Asp Ala Gly
 50

<210> 3461
 <211> 300
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 126..299

<400> 3461
 atttggttttg attttaacaa ccaaaaatag aaataaaatt agaactgcgt tttaagttct 60
 aatttgcat tattaatttg tccaaaagca agaactcttg gaaatccttg aaaatataag 120
 ctgga atg ttt tac tta gcc atg caa gtc att tat gta tac atc cag cca 170
 Met Phe Tyr Leu Ala Met Gln Val Ile Tyr Val Tyr Ile Gln Pro
 1 5 10 15
 gct gga aat ctg aga agt aaa gag gta gga ctg gaa bka agg aga aag 218
 Ala Gly Asn Leu Arg Ser Lys Glu Val Gly Leu Glu Xaa Arg Arg Lys
 20 25 30
 ctt gag tct tta agg cta gag ccc agc tgt gct gcy kcc atc ttc tca 266
 Leu Glu Ser Leu Arg Leu Glu Pro Ser Cys Ala Ala Xaa Ile Phe Ser
 35 40 45
 gga atg gca gtg cgt att ttc tgg ctg aaa agt a 300
 Gly Met Ala Val Arg Ile Phe Trp Leu Lys Ser
 50 55

<210> 3462
 <211> 412
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 91..411

<400> 3462
 cccaatttgt ctgatgaaaa cagcgtggat gaagtggaga ttagtgtgag ccttgccaaa 60
 gatgagcctg acacaaatct cgtggcctta atg aag gaa gaa ggg gtg aaa ctt 114
 Met Lys Glu Glu Gly Val Lys Leu
 1 5
 cta aga gaa gca atg gga att tac atc agc acc ctc aaa aca gag ttc 162
 Leu Arg Glu Ala Met Gly Ile Tyr Ile Ser Thr Leu Lys Thr Glu Phe
 10 15 20
 acc cag ggc atg atc tta cct aca atg aat gga gag tca gta gac cca 210
 Thr Gln Gly Met Ile Leu Pro Thr Met Asn Gly Glu Ser Val Asp Pro
 25 30 35 40
 gtg ggg cag cca gca ctg aaa act gwg gag cgc aag gct aag cct gct 258
 Val Gly Gln Pro Ala Leu Lys Thr Xaa Glu Arg Lys Ala Lys Pro Ala
 45 50 55
 cct tca aaa acc cag gcc aga cct gtt gga gtc aaa atc ccc act tgt 306
 Pro Ser Lys Thr Gln Ala Arg Pro Val Gly Val Lys Ile Pro Thr Cys
 60 65 70
 aag atc act ctt aag gaa acc ttc ctg acg tca cca gag gag ctc tat 354
 Lys Ile Thr Leu Lys Glu Thr Phe Leu Thr Ser Pro Glu Glu Leu Tyr
 75 80 85
 aga gtg ttt acc acc caa gga gct ggt gca ggg ctt tas cca tgc tcc 402
 Arg Val Phe Thr Thr Gln Gly Ala Gly Ala Gly Leu Xaa Pro Cys Ser
 90 95 100
 tgc aac att a 412
 Cys Asn Ile
 105

<210> 3463
 <211> 339
 <212> DNA
 <213> Homo sapiens
 <220>
 <221> CDS
 <222> 153..338

<400> 3463
 cagttctctt ttgctgcaac caccatctc aaactracta tcaatcattt atttagctca 60
 taattcttca gatcagcctg gaagtctttt ggtcttgggt gactttgctg gttgatgatg 120
 ggtctgggctg ggtcccaggg gcctctattc ac atg acc tct cat ccc cca gca 173
 Met Thr Ser His Pro Pro Ala
 1 5
 gct atg ctg cac ttt atc aca ggg tgg cag ggt ttc aaa gag cag cga 221
 Ala Met Leu His Phe Ile Thr Gly Trp Gln Gly Phe Lys Glu Gln Arg
 10 15 20
 tgg ggg caa gcc cca atg cac gag cat ctt tca agc ctt tgc ttg tat 269
 Trp Gly Gln Ala Pro Met His Glu His Leu Ser Ser Leu Cys Leu Tyr
 25 30 35
 cac ctt tgc tca ctt ccc atg gac caa agc aag tca cac agc gga stt 317
 His Leu Cys Ser Leu Pro Met Asp Gln Ser Lys Ser His Ser Gly Xaa
 40 45 50 55

caa gtc aat gag aag gca cgc a
 Gln Val Asn Glu Lys Ala Arg
 60

339

<210> 3464
 <211> 302
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 52..300

<400> 3464

aaaagctgtg	tgaggaggag	gaggaagtga	gaggaggagg	ccccgggcac	c	atg gcc	57
						Met Ala	
						1	
cag gcc	ctg ggg	gag gac	ctg gtg	cag cct	ccc gag	ctg cag	gmt gac
Gln Ala	Leu Gly	Glu Asp	Leu Val	Gln Pro	Pro Glu	Leu Gln	Xaa Asp
	5		10			15	
tcc agc	tcc ttg	ggg tcc	gac tca	gag ctc	agc ggg	cct ggc	cca tat
Ser Ser	Ser Leu	Gly Ser	Asp Ser	Glu Leu	Ser Gly	Pro Gly	Pro Tyr
	20		25			30	
cgc cag	gcc gac	cgc tat	gga ttc	att ggg	ggc agc	tca gca	gag cca
Arg Gln	Ala Asp	Arg Tyr	Gly Phe	Ile Gly	Gly Ser	Ser Ala	Glu Pro
	35		40			45	50
ggg ccg	ggc cac	cca cct	gca gac	ctc atc	cgc caa	cgg gag	atg aag
Gly Pro	Gly His	Pro Pro	Ala Asp	Leu Ile	Arg Gln	Arg Glu	Met Lys
	55			60		65	
tgg gtg	gag atg	acc tcg	cac tgg	gag aaa	acc atg	tcc cgg	cgg tac
Trp Val	Glu Met	Thr Ser	His Trp	Glu Lys	Thr Met	Ser Arg	Arg Tyr
	70			75		80	
aag aa							302
Lys							

<210> 3465
 <211> 352
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 8..352

<400> 3465

atctggm	atg cct	gat ctc	tcc ctt	tct ttc	atg aac	cct agg	ctt ctg	49
	Met Pro	Asp Leu	Ser Leu	Ser Phe	Met Asn	Pro Arg	Leu Leu	
	1		5			10		
gat gat	gtc agc	ttt cac	ccc tgc	atc cgg	ttc aag	cgt tgg	gaa tct	97
Asp Asp	Val Ser	Phe His	Pro Cys	Ile Arg	Phe Lys	Arg Trp	Glu Ser	
	15		20		25		30	
gaa aga	gtt ttg	tca ttt	att cct	cca gat	gga aat	ttc cga	ctc ata	145

Glu	Arg	Val	Leu	Ser	Phe	Ile	Pro	Pro	Asp	Gly	Asn	Phe	Arg	Leu	Ile	
				35					40					45		
tca	tac	cgt	gtc	agc	tca	caa	aat	cta	gtg	gca	ata	cca	gtg	tat	gtg	193
Ser	Tyr	Arg	Val	Ser	Ser	Gln	Asn	Leu	Val	Ala	Ile	Pro	Val	Tyr	Val	
			50					55					60			
aaa	cat	agt	atc	agc	ttt	aag	gag	aac	agt	tct	tgc	ggc	aga	ttt	gat	241
Lys	His	Ser	Ile	Ser	Phe	Lys	Glu	Asn	Ser	Ser	Cys	Gly	Arg	Phe	Asp	
		65					70					75				
ata	aca	att	gga	cca	aag	cag	aat	atg	ggg	aaa	act	att	gaa	ggm	att	289
Ile	Thr	Ile	Gly	Pro	Lys	Gln	Asn	Met	Gly	Lys	Thr	Ile	Glu	Gly	Ile	
	80					85					90					
aca	gtg	aca	gtt	cac	atg	cca	aaa	gtt	gtg	ctg	aac	ctg	mac	ctg	aca	337
Thr	Val	Thr	Val	His	Met	Pro	Lys	Val	Val	Leu	Asn	Leu	Xaa	Leu	Thr	
95					100					105					110	
ccc	aca	caa	agc	agc												352
Pro	Thr	Gln	Ser	Ser												
					115											

<210> 3466
 <211> 407
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 193..405

<400>	3466															
cattgttttag	tcctgaaact	aaaacctatt	ttataaatag	tagggttaat	tcctcgaaac											60
aatttcttta	ttaataaatg	tcctgtgggt	ttagaaatat	caggtaaata	tttgaataca											120
gaatgatgat	tgcaattact	gttacaagcg	tgaacacaa	acttcagatc	aatctagag											180
ttgcttcatt	ta atg cat	gct agc aac	agc ctt aac	ttt gga ttc	agt tat											231
	Met His Ala	Ser Asn Ser	Leu Asn Phe	Gly Phe Ser	Tyr											
	1		5		10											
ttg aaa cac	ttt tcc ggc	atc ttt ccc	ttt cta atg	ttg tgg ggt	gga											279
Leu Lys His	Phe Ser Gly	Ile Phe Pro	Phe Leu Met	Leu Trp Gly	Gly											
	15		20		25											
aac cgg atg	gca aat cac	tgt gag ccg	gat acc tca	gca cag tcc	acc											327
Asn Arg Met	Ala Asn His	Cys Glu Pro	Asp Thr Ser	Ala Gln Ser	Thr											
30		35		40												
ttg tgt gtg	act tca caa	atg ggg gac	ttc aca aat	ggg gta act	gaa											375
Leu Cys Val	Thr Ser Gln	Met Gly Asp	Phe Thr Asn	Gly Val Thr	Glu											
	50		55		60											
tgt tat tac	ttt caa att	ttg aca cgg	agc gt													407
Cys Tyr Tyr	Phe Gln Ile	Leu Thr Arg	Ser													
	65		70													

<210> 3467
 <211> 321
 <212> DNA
 <213> Homo sapiens

<220>

<221> CDS
<222> 61..321

<400> 3467
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 atg aaa gga ttt ctt agc gga cat gct gag aat tta ctt cga ggt gtg 108
 Met Lys Gly Phe Leu Ser Gly His Ala Glu Asn Leu Leu Arg Gly Val
 1 5 10 15
 tac gaa aca tgt act acg atg acg atg agc ctt ctg aag tgg gtt cgg 156
 Tyr Glu Thr Cys Thr Thr Met Thr Met Ser Leu Leu Lys Trp Val Arg
 20 25 30
 cag act cct wca cct agc cgt cca tcc gat tcc gat gta tct ctg gag 204
 Gln Thr Pro Xaa Pro Ser Arg Pro Ser Asp Ser Asp Val Ser Leu Glu
 35 40 45
 gag gac cgg gag gca gtg cgc aga gaa gcg gas gnc agg ccc agg cac 252
 Glu Asp Arg Glu Ala Val Arg Arg Glu Ala Xaa Xaa Arg Pro Arg His
 50 55 60
 agt tgg aaa aag crn aga caa agc ccg ttg cat ttg cgg ttc gga caa 300
 Ser Trp Lys Lys Xaa Arg Gln Ser Pro Leu His Leu Arg Phe Gly Gln
 65 70 75 80
 atg tca gct aca gtg cgg ccc 321
 Met Ser Ala Thr Val Arg Pro
 85

<210> 3468
 <211> 338
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 66..338

<400> 3468
 aagaggagag agacacattc agcagccaaa ggactcgggtg gaaagagcag aacaccatag 60
 acaat atg tgc ctc ttg gga ccc aag gtg ctg ctg ttt ctt gct gca ttc 110
 Met Ser Leu Leu Gly Pro Lys Val Leu Leu Phe Leu Ala Ala Phe
 1 5 10 15
 atc atc acc tct gac tgg ata ccc ctg ggg gtc aat agt caa cga gga 158
 Ile Ile Thr Ser Asp Trp Ile Pro Leu Gly Val Asn Ser Gln Arg Gly
 20 25 30
 gac gat gtg act caa gcg act cca gaa aca ttc aca gaa gat cct aat 206
 Asp Asp Val Thr Gln Ala Thr Pro Glu Thr Phe Thr Glu Asp Pro Asn
 35 40 45
 ctg gtg aat gat ccc gct aca gat gaa aca gtt ttg gct gtt ttg gct 254
 Leu Val Asn Asp Pro Ala Thr Asp Glu Thr Val Leu Ala Val Leu Ala
 50 55 60
 gat att gca cct tcc aca gat gac ttg gag tgc tgg gat gag aaa ttt 302
 Asp Ile Ala Pro Ser Thr Asp Asp Leu Glu Cys Trp Asp Glu Lys Phe
 65 70 75
 acc tgc aca agg ctc tac tct gtg cat cgg ccg gta 338
 Thr Cys Thr Arg Leu Tyr Ser Val His Arg Pro Val

80

85

90

<210> 3469
 <211> 314
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 131..313

<400> 3469
 tttgaagaag ataaataagg tgacattttt aagggtcaaa gaaaatgtca aaaactagaa 60
 tgatgtcttt acatagggtt taaaaacttt ccaaattaac agggaaaata attctttacc 120
 ttgaaaataa atg ttt gct agt gaa agc aaa tac aat ctt ttt act aaa 169
 Met Phe Ala Ser Glu Ser Lys Tyr Asn Leu Phe Thr Lys
 1 5 10
 tgt ttt att aaa ttt ttt tta ctt gta gac aca ggg tcc tac tgt att 217
 Cys Phe Ile Lys Phe Phe Leu Leu Val Asp Thr Gly Ser Tyr Cys Ile
 15 20 25
 acc cag gct ggt ctt gaa tgc ctg gcc tca agc aat cct cct acc tca 265
 Thr Gln Ala Gly Leu Glu Cys Leu Ala Ser Ser Asn Pro Pro Thr Ser
 30 35 40 45
 gtc ttc caa agt gct ggg act aca gac atg agc cat cac act ggg tct c 314
 Val Phe Gln Ser Ala Gly Thr Thr Asp Met Ser His His Thr Gly Ser
 50 55 60

<210> 3470
 <211> 339
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 <213> Homo sapiens

<220>
 <221> CDS
 <222> 34..339

<400> 3470
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 Met Gly Gln Phe Thr Ala Ala
 1 5
 atg gtt ggg aga att tcc tgt ctg gga gtc tgg raa act gcc aag agt 102
 Met Val Gly Arg Ile Ser Cys Leu Gly Val Trp Xaa Thr Ala Lys Ser
 10 15 20
 gga aag ctg cag cca gcc agc gag gcc tct gtt gtc act ggc cca aac 150
 Gly Lys Leu Gln Pro Ala Ser Glu Ala Ser Val Val Thr Gly Pro Asn
 25 30 35
 aac aac aaa aac aac cgc aac aac aac aac aac aac aaa aca tgc cac 198
 Asn Asn Lys Asn Asn Arg Asn Asn Asn Asn Asn Asn Lys Thr Cys His
 40 45 50 55
 gtg tgc act ggc ata tac aaa cac gcc cac aga acc aaa cca agc gga 246
 Val Cys Thr Gly Ile Tyr Lys His Ala His Arg Thr Lys Pro Ser Gly
 60 65 70

caa ggc ttc aag gag agc ttc tgg gcg gct cat ccc cgc ggc gag gca	294
Gln Gly Phe Lys Glu Ser Phe Trp Ala Ala His Pro Arg Gly Glu Ala	
75 80 85	
tat ccc ttg gca tgg tgc cac tgc agc cca gct ccc agc ccc ccc	339
Tyr Pro Leu Ala Trp Cys His Cys Ser Pro Ala Pro Ser Pro Pro	
90 95 100	

<210> 3471
 <211> 196
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 43..195

<400> 3471	
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Met Phe Met Ala	
1	
tac ttc agc ttc aac ctc cct ggg ctc aag cat ttc tca tac ctc aga	102
Tyr Phe Ser Phe Asn Leu Pro Gly Leu Lys His Phe Ser Tyr Leu Arg	
5 10 15 20	
tcc cca agt agc tgg gac tac agg cac aca cca tca cac ccg gct aat	150
Ser Pro Ser Ser Trp Asp Tyr Arg His Thr Pro Ser His Pro Ala Asn	
25 30 35	
ttt tgt ata ttt tgt aga gtc aga gtt tca cca ttt tcc cca ggc t	196
Phe Cys Ile Phe Cys Arg Val Arg Val Ser Pro Phe Ser Pro Gly	
40 45 50	

<210> 3472
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 <212> DNA
 <213> Homo sapiens

<220>
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 <222> 160..393

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gctcattccc gcagctcccc cagctccccg gctggccccc gggctctgggt gctgggtggaa	120
ctgagccaag accattgccc ccgcctaggt tgggaggct atg tgt gac tgg aag	174
Met Cys Asp Trp Lys	
1 5	
gac gtc ctg tcg ggt ggc gag aag cag aga atc ggc atg gcc cgc atg	222
Asp Val Leu Ser Gly Gly Glu Lys Gln Arg Ile Gly Met Ala Arg Met	
10 15 20	
ttc tac cac agg ccc aag tac gcc ctc ctg gat gaa tgc acc agc gcc	270
Phe Tyr His Arg Pro Lys Tyr Ala Leu Leu Asp Glu Cys Thr Ser Ala	
25 30 35	
gtg agc atc gac gtg gaa ggc aag atc ttc cag ghg gcc aan wgn cgc	318

Val	Ser	Ile	Asp	Val	Glu	Gly	Lys	Ile	Phe	Gln	Xaa	Ala	Xaa	Xaa	Arg	
	40						45					50				
ggg	cat	tgc	ctg	ctc	tcc	atc	acc	cam	cgg	scc	tsc	ctg	tgg	aaa	tac	366
Gly	His	Cys	Leu	Leu	Ser	Ile	Thr	Xaa	Arg	Xaa	Xaa	Leu	Trp	Lys	Tyr	
	55					60					65					
aca	cac	act	tgc	tac	agt	tcg	atg	ggg	a							394
Thr	His	Thr	Cys	Tyr	Ser	Ser	Met	Gly								
70					75											

<210> 3473
 <211> 300
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 128..298

<400> 3473																
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gtcccagcta	ctcgggaggc	tgaggcagga	gratggcttc	aaccagaggag	gcggakcttg											120
cagtgag	atg	aga	tcg	cgc	cac	tgc	act	cca	gtc	tgg	gcg	aca	gag	caa		169
	Met	Arg	Ser	Arg	His	Cys	Thr	Pro	Val	Trp	Ala	Thr	Glu	Gln		
	1				5					10						
gac	tct	gtc	tca	aaa	aaa	gaa	ata	gac	gta	cac	tct	ggg	aca	wga	cag	217
Asp	Ser	Val	Ser	Lys	Lys	Glu	Ile	Asp	Val	His	Ser	Gly	Thr	Xaa	Gln	
15					20					25				30		
aaa	aag	tat	cct	cac	act	tgc	tgg	gta	ata	gta	act	gtg	cta	ttc	cta	265
Lys	Lys	Tyr	Pro	His	Thr	Cys	Trp	Val	Ile	Val	Thr	Val	Leu	Phe	Leu	
				35					40				45			
tca	aga	aac	cct	aag	gtt	tct	agg	ctt	gtt	ctg	ga					300
Ser	Arg	Asn	Pro	Lys	Val	Ser	Arg	Leu	Val	Leu						
			50					55								

<210> 3474
 <211> 212
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 12..212

<400> 3474																
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	Met	Leu	Leu	Leu	Asn	Glu	Asn	Leu	Lys	Ala	Glu	Ile	Gln			
	1				5					10						
aag	aat	gaa	gct	caa	ggc	agc	tgt	atc	ttg	ttt	ctg	ttt	tgc	ttt	gag	98
Lys	Asn	Glu	Ala	Gln	Gly	Ser	Cys	Ile	Leu	Phe	Leu	Phe	Cys	Phe	Glu	
15					20					25						
agt	cag	aat	atg	cga	tca	aaa	tct	atc	ttc	ccc	ttc	ctt	atc	ctt	cat	146
Ser	Gln	Asn	Met	Arg	Ser	Lys	Ser	Ile	Phe	Pro	Phe	Leu	Ile	Leu	His	

30		35		40		45	
ttt ttt ccc cag cag ata aga aaa aaa ata gtg gtg ctt ctt tta gga							194
Phe Phe Pro Gln Gln Ile Arg Lys Lys Ile Val Val Leu Leu Leu Gly							
	50		55		60		
ctt aat tct cag aag gca							212
Leu Asn Ser Gln Lys Ala							
	65						

<210> 3475
 <211> 351
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 46..351

<400> 3475	
caattaaacc acacagaaaa tgatgtgact catcttcaaa aggaa atg agc aat tgt	57
	Met Ser Asn Cys
	1
aga gca ggt gaa aac gct ggc atg ggt agg ttc act aag gtg ggt gag	105
Arg Ala Gly Glu Asn Ala Gly Met Gly Arg Phe Thr Lys Val Gly Glu	
5 10 15 20	
caa gaa agg aca gtg gac acc ctg ccg tcc ccc cag cac ccc gtg gct	153
Gln Glu Arg Thr Val Asp Thr Leu Pro Ser Pro Gln His Pro Val Ala	
25 30 35	
cat tgc tgc agt cag ctg gag gag agg tgg cag agg ttg cag agc cag	201
His Cys Cys Ser Gln Leu Glu Glu Arg Trp Gln Arg Leu Gln Ser Gln	
40 45 50	
gtc atc tcg gag ctg gat gct tgt aag gaa tgc acg cag ggg gtc cag	249
Val Ile Ser Glu Leu Asp Ala Cys Lys Glu Cys Thr Gln Gly Val Gln	
55 60 65	
agg gag gtc tcc atg gtg gag ggc agg gtg tct mrt atg gag aaa act	297
Arg Glu Val Ser Met Val Glu Gly Arg Val Ser Xaa Met Glu Lys Thr	
70 75 80	
tgc agc aag ctg gac tct atc tca gga aat ctt cag agg atc aag gaa	345
Cys Ser Lys Leu Asp Ser Ile Ser Gly Asn Leu Gln Arg Ile Lys Glu	
85 90 95 100	
ggg ctc	351
Gly Leu	

<210> 3476
 <211> 260
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 64..258

<400> 3476

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ttatggaaga tactctctat actttgctgc ccctgtacct ttgctcatag tattcttata 60
ttg atg cct ttc ttc ctc atg att ccc atc att gtc cyw aam aat ttt 108
    Met Pro Phe Phe Leu Met Ile Pro Ile Ile Val Xaa Xaa Asn Phe
        1             5             10             15
ttt ktt aat tkt ttt tat tat act tta agt tct agg gta cat gtg cac 156
Phe Xaa Asn Xaa Phe Tyr Tyr Thr Leu Ser Ser Arg Val His Val His
        20             25             30
aac atg cag gtt tgt tac ata tgt gta cat gtg cca tgt tgg tgt gct 204
Asn Met Gln Val Cys Tyr Ile Cys Val His Val Pro Cys Trp Cys Ala
        35             40             45
gca ccc att aac ttg tca ttt aca tta ggt ata tct cct aat gct atc 252
Ala Pro Ile Asn Leu Ser Phe Thr Leu Gly Ile Ser Pro Asn Ala Ile
        50             55             60
cca tcc cc 260
Pro Ser
    65

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<210> 3477
 <211> 184
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 18..182

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<400> 3477
tagctgggat tgcaggc atg tgc cac cac gcc cgg cta att ttt gta ttt 50
    Met Cys His His Ala Arg Leu Ile Phe Val Phe
        1             5             10
tta gta gag atg gga ttt ctc cat gtt ggt cag act tgt ctc gga ctc 98
Leu Val Glu Met Gly Phe Leu His Val Gly Gln Thr Cys Leu Gly Leu
        15             20             25
cca acc tct ggt gat ctg ccc gcc tcg gct tcc caa agt gct ggg att 146
Pro Thr Ser Gly Asp Leu Pro Ala Ser Ala Ser Gln Ser Ala Gly Ile
        30             35             40
acg ggc atg agc cac cgt gcg tgt cct ttt ttt ttt tt 184
Thr Gly Met Ser His Arg Ala Cys Pro Phe Phe Phe
        45             50             55

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<210> 3478
 <211> 277
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 113..277

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<400> 3478
tttttgtttc ttggcgccat ttaggtgtaa gaacggtaat gtcctgaatg acgatccttt 60
tcatttacca aacggttcta atgctgccaa cccccaatga acataaagga gc atg aag 118

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Met Lys
1
tgc ctc gtt tgt atc aat aca tta tgg aga ata aat aga ata cag ttc 166
Cys Leu Val Cys Ile Asn Thr Leu Trp Arg Ile Asn Arg Ile Gln Phe
5 10 15
ttt aga gaa aga tac ttt cag att cat gtg atc ctt agg gca tta aat 214
Phe Arg Glu Arg Tyr Phe Gln Ile His Val Ile Leu Arg Ala Leu Asn
20 25 30
acg atg cac tcc att gtt ttt ttg tta ttc tgt ttc aaa gaa aat gac 262
Thr Met His Ser Ile Val Phe Leu Leu Phe Cys Phe Lys Glu Asn Asp
35 40 45 50
tgt ctt gac cca gtt 277
Cys Leu Asp Pro Val
55

<210> 3479
<211> 404
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 142..402

<400> 3479
tcgtattggc acagttctct atgtaagcaa tttagagagg aagcaaagg gaaaagtttg 60
agttagctgt tctctgtcct agaatttccc tgcattaatc ttgtccttga aaatatatat 120
aatactggtc ccttaaactc c atg agg ctt tgt ctc att atg tat tgt tct 171
Met Arg Leu Cys Leu Ile Met Tyr Cys Ser
1 5 10
ttt ggt acc ctt tcc cac tta act tac ctt ttg ctc cta agt cct ata 219
Phe Gly Thr Leu Ser His Leu Thr Tyr Leu Leu Leu Leu Ser Pro Ile
15 20 25
aaa tac ccc ttg gat ctg gat ttt tta tac ccg att ttc tcc act gtg 267
Lys Tyr Pro Leu Asp Leu Asp Phe Leu Tyr Pro Ile Phe Ser Thr Val
30 35 40
tat aaa agg tat att gtg act gta aat ttt tgt ata tca tgt tct gag 315
Tyr Lys Arg Tyr Ile Val Thr Val Asn Phe Cys Ile Ser Cys Ser Glu
45 50 55
agc ttc tta ctt tct gat ctc ata gca cta ttc ctg atc aga gaa ctc 363
Ser Phe Leu Leu Ser Asp Leu Ile Ala Leu Phe Leu Ile Arg Glu Leu
60 65 70
cag ttg ctt caa cac aca gta tca gta gtg cag cca ccc ac 404
Gln Leu Leu Gln His Thr Val Ser Val Val Gln Pro Pro
75 80 85

<210> 3480
<211> 285
<212> DNA
<213> Homo sapiens

<220>
<221> CDS

<222> 116..283

<400> 3480

aagaagcctg tgtgagagca gctcggcgct ccggcacagc agagagcgct gggagccgga 60
ggggagcgca gcrnggtttt ggccagtggc cgtgcagtcc aaggggctgg atggc atg 118
Met

1
syk gam ccc aag ctc agc tca gcg tcc gga ccc aat aac agt ttt acc 166
Xaa Xaa Pro Lys Leu Ser Ser Ala Ser Gly Pro Asn Asn Ser Phe Thr
5 10 15

aag gga gca gct ttc tat cct ggc cac act gag gtg yat agc gta atg 214
Lys Gly Ala Ala Phe Tyr Pro Gly His Thr Glu Val Xaa Ser Val Met
20 25 30

tcc atg ttg ttc tac act ctg atc aca gct ttt ctg atc ggc ata cag 262
Ser Met Leu Phe Tyr Thr Leu Ile Thr Ala Phe Leu Ile Gly Ile Gln
35 40 45

gcg gaa cca cac tca gag agc ga 285
Ala Glu Pro His Ser Glu Ser
50 55

<210> 3481

<211> 276

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 3..275

<400> 3481

ag atg aca cca ctg cac tcc tgc ctg ggc gac aga gcg aga ccc ggt 47
Met Thr Pro Leu His Ser Cys Leu Gly Asp Arg Ala Arg Pro Gly
1 5 10 15

ctc aaa aat aaa ata aaa ata ttt tta aaa aat gga aat ggt cta atg 95
Leu Lys Asn Lys Ile Lys Ile Phe Leu Lys Asn Gly Asn Gly Leu Met
20 25 30

ttt gca cgt tac ctg cag gta ttt tct agc ttt gct cat gag gtg tgg 143
Phe Ala Arg Tyr Leu Gln Val Phe Ser Ser Phe Ala His Glu Val Trp
35 40 45

atg ctt gtg acg ttc ctt gtg tgt gtt tta ttc att ttt tta agt ttt 191
Met Leu Val Thr Phe Leu Val Cys Val Leu Phe Ile Phe Leu Ser Phe
50 55 60

tca ctt tcg aga cag ggt ttc tgt atg ttg ccc agg ctg gtc tca ggc 239
Ser Leu Ser Arg Gln Gly Phe Cys Met Leu Pro Arg Leu Val Ser Gly
65 70 75

tcc tgg cct caa gtg atc ctc cca cct ggc ccc ctt t 276
Ser Trp Pro Gln Val Ile Leu Pro Pro Gly Pro Leu
80 85 90

<210> 3482

<211> 276

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 118..276

<400> 3482

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aaccctggag aacctgcccc ggaaccaaga gccgcagcca gctcaagcct ctcgagtggg      60
gcctttccag cccctgcaac agatccsggg atctgtagtt gggcggaggg gctcgtt      117
atg gga aag ggg tgc gtg cgc gtt tgt gct aaa aca aga aag gca aga      165
Met Gly Lys Gly Cys Val Arg Val Cys Ala Lys Thr Arg Lys Ala Arg
1           5           10           15
atc tcc gag aac aaa act ctg gtc ctc gcc tgg ccg ggg acc gca gaa      213
Ile Ser Glu Asn Lys Thr Leu Val Leu Ala Trp Pro Gly Thr Ala Glu
          20          25          30
gac agt ggg cgg cag cgc caa ggc ggg tca ggg gcc ggt cca gcc aag      261
Asp Ser Gly Arg Gln Arg Gln Gly Ser Gly Ala Gly Pro Ala Lys
          35          40          45
ttt gct ccg gct gct      276
Phe Ala Pro Ala Ala
50

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<210> 3483

<211> 296

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 143..295

<400> 3483

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ccaagtttat ctaatagatg tgctatgaag agaacagaat gatgggactt taaaaaaatt      60
tttacagtta tttttatatt gtagaatgag ctgaaagcca gtggtggcga aatcaaaatt      120
cataaaatgg agcaaaagga ga atg tgc ccc cag gtc ctg agg tct gca tca      172
                Met Cys Pro Gln Val Leu Arg Ser Ala Ser
                1           5           10
ccc atc agg aag ggg aaa aga ttt ctg caa atg aga ata gcc tgg cag      220
Pro Ile Arg Lys Gly Lys Arg Phe Leu Gln Met Arg Ile Ala Trp Gln
          15          20          25
tcc gtt cha ccc ctg ccg aag atg act ccc gtg act cag gtt aag agt      268
Ser Val Xaa Pro Leu Pro Lys Met Thr Pro Val Thr Gln Val Lys Ser
          30          35          40
gag gtt caa cag cct gtc cat ccc aag c      296
Glu Val Gln Gln Pro Val His Pro Lys
          45          50

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<210> 3484

<211> 241

<212> DNA

<213> Homo sapiens

[illegible]

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<220>  
<221> CDS  
<222> 118..309
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<210> 3486
<211> 365
<212> DNA
<213> Homo sapiens
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<221> CDS
<222> 92..364

<400> 3486

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aactatgatg tacttagaag atagggagga atcaaagga atttcaaaca gattccaggc      60
aaatggtaaa attactcatc cataaaggta a atg tta agg aaa caa agt gag      112
                               Met Leu Arg Lys Gln Ser Glu
                               1           5
att ttt tta aaa aga gac agg gtc tca ctg aag tgc aat ggc tca atc      160
Ile Phe Leu Lys Arg Asp Arg Val Ser Leu Lys Cys Asn Gly Ser Ile
           10           15           20
aca gct cac aac ttt cta ggc tca ggt gat cct ccc tcc tcg gcc atc      208
Thr Ala His Asn Phe Leu Gly Ser Gly Asp Pro Pro Ser Ser Ala Ile
           25           30           35
cag gta gct ggg act aca ggt gtg cgc cac tat gcc tgg cta att ttt      256
Gln Val Ala Gly Thr Thr Gly Val Arg His Tyr Ala Trp Leu Ile Phe
           40           45           50           55
tat ttt ttt ttt tca aga gag ggg gtt tcs cct tkt tgc cca ggc tgg      304
Tyr Phe Phe Phe Ser Arg Glu Gly Val Ser Pro Xaa Cys Pro Gly Trp
           60           65           70
tct cga act ctt ggg ctc aag mag tcc acc kgm htt ggc ctc cca aag      352
Ser Arg Thr Leu Gly Leu Lys Xaa Ser Thr Xaa Xaa Gly Leu Pro Lys
           75           80           85
kgt tgg gag tta c      365
Xaa Trp Glu Leu
           90

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<210> 3487
<211> 415
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 178..414

<400> 3487

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caaatcaag aaaatccaac atagatggtc aaaatattca taggtgactg agagtatcca      60
aatgggccag gtgactgaga atacgcaaac aggccagaat aatatctgtg ttaaatttga      120
ccctctatatt tattaacata tctgtcatga cctttctctg tacctgctgt agtactc      177
atg tat aga ctc agt ctt ata gca ggc cct ggg tcc tat cct gtg cta      225
Met Tyr Arg Leu Ser Leu Ile Ala Gly Pro Gly Ser Tyr Pro Val Leu
1           5           10           15
aga tgg gga gtt tgg gac atc cct agt tca tta gtt caa gtg act tac      273
Arg Trp Gly Val Trp Asp Ile Pro Ser Ser Leu Val Gln Val Thr Tyr
           20           25           30
cat cag ccc aac ctc act aca aat ttg gat ctg cct ttg ttc ttc agt      321
His Gln Pro Asn Leu Thr Thr Asn Leu Asp Leu Pro Leu Phe Phe Ser
           35           40           45
tgt agt atc tcg gct acc cat tct tgt gtc aag cct cca tct gta att      369
Cys Ser Ile Ser Ala Thr His Ser Cys Val Lys Pro Pro Ser Val Ile
           50           55           60

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att ggt atc tct tct ttc ctg agc ttt cct tat caa act ttg gta t 415
 Ile Gly Ile Ser Ser Phe Leu Ser Phe Pro Tyr Gln Thr Leu Val
 65 70 75

<210> 3488
 <211> 238
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 7..237

<400> 3488
 acatgc atg gtc tcg ggg aag aag ctt cct ctg gcc tgg cgc agg ccg 48
 Met Val Ser Gly Lys Lys Leu Pro Leu Ala Trp Arg Arg Pro
 1 5 10
 ttc cat ctg cct ccc agg tct gcg tcc cta acc cct tcc cca gst ttg 96
 Phe His Leu Pro Pro Arg Ser Ala Ser Leu Thr Pro Ser Pro Xaa Leu
 15 20 25 30
 ght gtt tta ccc cga aac agg aag gaa cag ggg tcc tgt aga aca ggg 144
 Xaa Val Leu Pro Arg Asn Arg Lys Glu Gln Gly Ser Cys Arg Thr Gly
 35 40 45
 gtc ctg ggg aag gtg tcc agg gca ggg tcc tgg gaa ggg tgt ccc kwc 192
 Val Leu Gly Lys Val Ser Arg Ala Gly Ser Trp Glu Gly Cys Pro Xaa
 50 55 60
 tgc ttc ctc tcc agc tgt ggc tcc atc tgh cca gct tgc ctg cct c 238
 Cys Phe Leu Ser Ser Cys Gly Ser Ile Xaa Pro Ala Cys Leu Pro
 65 70 75

<210> 3489
 <211> 282
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 6..281

<400> 3489
 ttcag atg act ctc ccg aaa act tac acc ata gct aat caa ttt cct ctt 50
 Met Thr Leu Pro Lys Thr Tyr Thr Ile Ala Asn Gln Phe Pro Leu
 1 5 10 15
 aat aag ctc act gaa ctt ctc cga cat gac atg gca gcc gct ggc ttc 98
 Asn Lys Leu Thr Glu Leu Leu Arg His Asp Met Ala Ala Ala Gly Phe
 20 25 30
 act gaa gca ctt acc ttt gcc ctg tgc tcc caa gaa gat att gct gat 146
 Thr Glu Ala Leu Thr Phe Ala Leu Cys Ser Gln Glu Asp Ile Ala Asp
 35 40 45
 aaa cta ggt gtg gat atc tct gca aca aag gca gtc cac ata agt aat 194
 Lys Leu Gly Val Asp Ile Ser Ala Thr Lys Ala Val His Ile Ser Asn
 50 55 60

cct aaa aca gct gaa ttt cag gtg gca cgc act acc ctt ctt cct ggc	242
Pro Lys Thr Ala Glu Phe Gln Val Ala Arg Thr Thr Leu Leu Pro Gly	
65 70 75	
ctc ctg aag acv kna gca gca aat cgt aag atg ccc cct t	282
Leu Leu Lys Thr Xaa Ala Ala Asn Arg Lys Met Pro Pro	
80 85 90	

<210> 3490
 <211> 320
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 113..319

<400> 3490	
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tgtaggagag agaccgtgtg ccgtggggct ggtggcctgc tcagggacag cc atg ggg	118
	Met Gly
	1
acc tgg cag ctc aaa aca gat ggc agc aga aca aaa gaa act ttt gct	166
Thr Trp Gln Leu Lys Thr Asp Gly Ser Arg Thr Lys Glu Thr Phe Ala	
5 10 15	
ttg gaa gca cag cca aac tcc cca ggg cat cgt cat aga tgg cac cta	214
Leu Glu Ala Gln Pro Asn Ser Pro Gly His Arg His Arg Trp His Leu	
20 25 30	
gag cat ggg ctg cct cag tca ggg gga cgt gcc tgt gtt gtc cag aga	262
Glu His Gly Leu Pro Gln Ser Gly Gly Arg Ala Cys Val Val Gln Arg	
35 40 45 50	
gcc cag cca ggg acg aaa aag gag atg agg ccc ctt tcc tcc atg tcc	310
Ala Gln Pro Gly Thr Lys Lys Glu Met Arg Pro Leu Ser Ser Met Ser	
55 60 65	
cca tgc cca c	320
Pro Cys Pro	

<210> 3491
 <211> 377
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 179..376

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ccgttctctg ggctccgtgg ggctggagcc agctcagcat gtgggtgcctg tggcaaaa	178
atg ctg cag tgg acc ctg cgt gtc ctg ggc atg ggt gga atc aga gac	226
Met Leu Gln Trp Thr Leu Arg Val Leu Gly Met Gly Gly Ile Arg Asp	
1 5 10 15	

ttg ctg tcc aag tca gaa tct cag ctt ttc tcc ttt ctc ctc tac cct	274
Leu Leu Ser Lys Ser Glu Ser Gln Leu Phe Ser Phe Leu Leu Tyr Pro	
20 25 30	
cct ctc agg tac ctg tgt gac aag gtc gtc cct ggg aac agg gtt acc	322
Pro Leu Arg Tyr Leu Cys Asp Lys Val Val Pro Gly Asn Arg Val Thr	
35 40 45	
atc atg ggc atc tac tcc atc aag aag ttt ggc ctg acc abc agc agg	370
Ile Met Gly Ile Tyr Ser Ile Lys Lys Phe Gly Leu Thr Xaa Ser Arg	
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Gly Leu	
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 <213> Homo sapiens

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 <221> CDS
 <222> 117..428

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taattctcca aaatactaca gtgatctctg agaagaacaa attagaatca gattat atg	119
Met	
1	
gcc gca tct tca caa ctc cgt ctt aca gag caa cat ttc att gaa ttg	167
Ala Ala Ser Ser Gln Leu Arg Leu Thr Glu Gln His Phe Ile Glu Leu	
5 10 15	
gat gaa aat aga cag aga tta ttg cag aaa tgc aag gaa ctt atg aaa	215
Asp Glu Asn Arg Gln Arg Leu Leu Gln Lys Cys Lys Glu Leu Met Lys	
20 25 30	
aga gct agg caa gta tgt aac ctg ggt gca gag cag act ctt cct caa	263
Arg Ala Arg Gln Val Cys Asn Leu Gly Ala Glu Gln Thr Leu Pro Gln	
35 40 45	
gaa tac cak aca gtt ttc caa gac ctt cca aac aca ttg gat gaa att	311
Glu Tyr Xaa Thr Val Phe Gln Asp Leu Pro Asn Thr Leu Asp Glu Ile	
50 55 60 65	
gat gct tta tta act gaa gaa aga tca aga gct tcc tgc ttc acg gga	359
Asp Ala Leu Leu Thr Glu Glu Arg Ser Arg Ala Ser Cys Phe Thr Gly	
70 75 80	
ctg aat cct aca att gtt cag gaa tat aca aaa aga gaa gaa gaa ata	407
Leu Asn Pro Thr Ile Val Gln Glu Tyr Thr Lys Arg Glu Glu Glu Ile	
85 90 95	
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Glu Gln Leu Thr Glu Glu His	
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 Met Leu Ile Ser Asp Arg Leu Gly Tyr His Arg Asp Val Pro Asp
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 aca agg aat gca gca tgt aaa gaa aag ttc tac cca cct gac ctg cca 97
 Thr Arg Asn Ala Ala Cys Lys Glu Lys Phe Tyr Pro Pro Asp Leu Pro
 20 25 30
 gct gct agt gtt gtt atc tgt ttc tat aat gaa gcg ttt tct gcc ttg 145
 Ala Ala Ser Val Val Ile Cys Phe Tyr Asn Glu Ala Phe Ser Ala Leu
 35 40 45
 ctt cgg aca gtg cac agt gtc ata gac cgc acg cca gca cac ctg ctt 193
 Leu Arg Thr Val His Ser Val Ile Asp Arg Thr Pro Ala His Leu Leu
 50 55 60
 cat gag atc atc ctt gtg gat gat gat agt gac ttt gat gat ttg aaa 241
 His Glu Ile Ile Leu Val Asp Asp Asp Ser Asp Phe Asp Asp Leu Lys
 65 70 75
 gga gaa cta gat gaa tat gtc caa aaa tac ctc cct gga aaa att aaa 289
 Gly Glu Leu Asp Glu Tyr Val Gln Lys Tyr Leu Pro Gly Lys Ile Lys
 80 85 90 95
 gtc ata aga aat aca aag cgt gag ggg ttg att cga ggg aga atg att 337
 Val Ile Arg Asn Thr Lys Arg Glu Gly Leu Ile Arg Gly Arg Met Ile
 100 105 110
 ggc gcg gcc cac gcg aca gga gaa gtc ctt gtg tt 372
 Gly Ala Ala His Ala Thr Gly Glu Val Leu Val
 115 120

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<220>
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 <222> 56..304

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 Gln Val Ala Asp Val Pro Glu Lys Pro Arg Val Pro Ala Phe Ala Cys
 5 10 15
 cag gtg gcc ggc tgc tgc cag gtg ttc gat gcc ctg gac gac tac gag 154
 Gln Val Ala Gly Cys Cys Gln Val Phe Asp Ala Leu Asp Asp Tyr Glu
 20 25 30
 cac cac tac cac acg ctg cac gga aat gtt tgc tcc ttt tgc aag cgg 202
 His His Tyr His Thr Leu His Gly Asn Val Cys Ser Phe Cys Lys Arg

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Ala Phe Pro Ser Gly His Leu Leu Asp Ala His Ile Leu Glu Trp His			
50	55	60	65
gat tcg ctc ttc cag atc ctg tct gak agg cak gac atg tat mar tgc			298
Asp Ser Leu Phe Gln Ile Leu Ser Xaa Arg Xaa Asp Met Tyr Xaa Cys			
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Leu Val			

<210> 3495
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<220>
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Met Asp Ala Thr Ile Ala Pro His Arg Ile Pro Pro Glu Met	
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ccc cag tac ggg gag gag aac cac atc ttc gag ttg atg cag gta tta	156
Pro Gln Tyr Gly Glu Glu Asn His Ile Phe Glu Leu Met Gln Val Leu	
15 20 25 30	
acc acc tgg gtg tct gcc ctg cac cca cag awc atg ctg gag caa stc	204
Thr Thr Trp Val Ser Ala Leu His Pro Gln Xaa Met Leu Glu Gln Xaa	
35 40 45	
ctg atc cac cag ycc gam gat ccs atc ccc ttc atg atc cag cac ttg	252
Leu Ile His Gln Xaa Xaa Asp Pro Ile Pro Phe Met Ile Gln His Leu	
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cat aga gac tcc	264
His Arg Asp Ser	
65	

<210> 3496
 <211> 320
 <212> DNA
 <213> Homo sapiens

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 <222> 124..318

<400> 3496	
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ctt atg agt acc caa gam gga ctg tct atg cat gca cac cca caa gcc	168
Met Ser Thr Gln Xaa Gly Leu Ser Met His Ala His Pro Gln Ala	
1 5 10 15	

tat aca cca ttt ata tac cta cac gca cgc aag aga cgc gga gag ata	216
Tyr Thr Pro Phe Ile Tyr Leu His Ala Arg Lys Arg Arg Gly Glu Ile	
20 25 30	
ggc gat gca gac tcg cga ttc aat gat cga tat gct cat aar agt gct	264
Gly Asp Ala Asp Ser Arg Phe Asn Asp Arg Tyr Ala His Lys Ser Ala	
35 40 45	
caa tta tmt ttt ctg tat ttt gta tgc tgt att ttc caa gac gta tat	312
Gln Leu Xaa Phe Leu Tyr Phe Val Cys Cys Ile Phe Gln Asp Val Tyr	
50 55 60	
tat ktn ny	320
Tyr Xaa	
65	

<210> 3497
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 <212> DNA
 <213> Homo sapiens

<220>
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 <222> 7..183

<400> 3497	
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Met Ser Met Thr Pro Glu Gln Leu Gln Ala Trp Arg Trp Glu	
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aga gaa att gat gag aga aat cgc cca ctt tct gat gag gaa tta gat	96
Arg Glu Ile Asp Glu Arg Asn Arg Pro Leu Ser Asp Glu Glu Leu Asp	
15 20 25 30	
gct atg ttc cca gaa gga tat aag gta ctt cct cct cca gct ggt tat	144
Ala Met Phe Pro Glu Gly Tyr Lys Val Leu Pro Pro Pro Ala Gly Tyr	
35 40 45	
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Val Pro Ile Arg Thr Pro Ala Arg Lys Leu Thr Ala Thr	
50 55	

<210> 3498
 <211> 293
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 30..293

<400> 3498	
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Met Thr Ala Gly Glu Trp Xaa Xaa	
1 5	
gtt tta tcc aag tat gaa gat cag att act att ttc act gac tac cta	101
Val Leu Ser Lys Tyr Glu Asp Gln Ile Thr Ile Phe Thr Asp Tyr Leu	
10 15 20	

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<221> CDS  
<222> 85..285
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<210> 3500
<211> 257
<212> DNA
<213> Homo sapiens
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<220>  
<221> CDS  
<222> 71..256
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2164

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Ser	Val	Ser	Pro	Ala	Pro	Gly	Lys	Trp	Pro	Leu	Ala	Glu	Gln	Val	Ser	
15						20					25					
tgc	ccg	gga	cgc	tct	tcc	cca	gtg	ccc	gcc	tgc	ggg	act	cca	gct	cct	205
Cys	Pro	Gly	Arg	Ser	Ser	Pro	Val	Pro	Ala	Cys	Gly	Thr	Pro	Ala	Pro	
30						35				40					45	
tgt	tcc	ggc	tcc	tgc	tgc	act	agc	tcc	tgg	cga	ctg	agg	ctt	ctc	ccg	253
Cys	Ser	Gly	Ser	Cys	Cys	Thr	Ser	Ser	Trp	Arg	Leu	Arg	Leu	Leu	Pro	
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aca	c															257
Thr																

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cacctgtcct	aggggagtct	gtcctgcaag	ataacagctt	tgacctgaat	aatggtagtg	180										
acgctgaaca	ggaagaa	atg	gaa	act	caa	tct	tca	gac	ttc	cca	cca	tcc	230			
		Met	Glu	Thr	Gln	Ser	Ser	Asp	Phe	Pro	Pro	Ser				
		1				5						10				
ctg	acc	cag	cca	gct	cct	gat	cag	tca	tcc	act	att	cag	cta	cat	cca	278
Leu	Thr	Gln	Pro	Ala	Pro	Asp	Gln	Ser	Ser	Thr	Ile	Gln	Leu	His	Pro	
		15					20					25				
gca	acc	tca	cca	gca	gtc	tcg	cca	aca	acc	tcc	cca	gca	gtc	tcc	cta	326
Ala	Thr	Ser	Pro	Ala	Val	Ser	Pro	Thr	Thr	Ser	Pro	Ala	Val	Ser	Leu	
		30					35					40				
gtg	gtt	tct	cca	gca	gcc	tcc	cca	gct	g							354
Val	Val	Ser	Pro	Ala	Ala	Ser	Pro	Ala								
		45					50									

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 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 100..432

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aggcagcagt	atcaagataa	agaggmagtt	gtcttatgg	atg	aat	act	gtt	ggg	114

	Met	Asn	Thr	Val	Gly	
	1			5		
ccc tac cat aat cgt caa gaa aca tat aag tac ttt tca ctt cca ttc						162
Pro Tyr His Asn Arg Gln Glu Thr Tyr Lys Tyr Phe Ser Leu Pro Phe						
	10			15	20	
tgt gtg ggg tca aaa aaa agt atc agt cat tac cat gaa act ctg gga						210
Cys Val Gly Ser Lys Lys Ser Ile Ser His Tyr His Glu Thr Leu Gly						
	25			30	35	
gaa gca ctt caa ggg gtt gaa ttg gaa ttt agt ggt ctg gat att aaa						258
Glu Ala Leu Gln Gly Val Glu Leu Glu Phe Ser Gly Leu Asp Ile Lys						
	40			45	50	
ttt aaa gat gat gtg atg cca gcc act tac tgt gaa att gat tta gat						306
Phe Lys Asp Asp Val Met Pro Ala Thr Tyr Cys Glu Ile Asp Leu Asp						
	55			60	65	
aaa gaa aag aga gat gca ttt gta tat gcc ata aaa aat cat tac tgg						354
Lys Glu Lys Arg Asp Ala Phe Val Tyr Ala Ile Lys Asn His Tyr Trp						
	70			75	80	85
tac cag atg tac ata gat gat tta cca ata tgg ggt att gtt ggt gag						402
Tyr Gln Met Tyr Ile Asp Asp Leu Pro Ile Trp Gly Ile Val Gly Glu						
	90			95	100	
gct gat gaa aat gga gaa gat tac tat ctt t						433
Ala Asp Glu Asn Gly Glu Asp Tyr Tyr Leu						
	105			110		

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 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 100..393

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gctgtcttaa ctctgtgct tggcggacag acaggcgag atg gcg gcg gag gtg	114
	Met Ala Ala Glu Val
	1 5
ttg ccg att gcg agg tgg cag tat tgt ggg gcg ccc gac ggg agc cag	162
Leu Pro Ile Ala Arg Trp Gln Tyr Cys Gly Ala Pro Asp Gly Ser Gln	
	10 15 20
aga gct gta ctg gtc cag ttc tcc aac ggg aag cta cag agt cca ggc	210
Arg Ala Val Leu Val Gln Phe Ser Asn Gly Lys Leu Gln Ser Pro Gly	
	25 30 35
aac atg cgc ttt acc ttg tat gag aac aaa gat tcc acc aac ccc agg	258
Asn Met Arg Phe Thr Leu Tyr Glu Asn Lys Asp Ser Thr Asn Pro Arg	
	40 45 50
aag agg aat caa cgg atc ctg gca gct gaa aca gat agg ctc tcc tat	306
Lys Arg Asn Gln Arg Ile Leu Ala Ala Glu Thr Asp Arg Leu Ser Tyr	
	55 60 65
gtg gga aac aat ttt ggg act gga gcc ctc aaa tgc aac act ttg tgc	354
Val Gly Asn Asn Phe Gly Thr Gly Ala Leu Lys Cys Asn Thr Leu Cys	
	70 75 80 85

agg cac ttt gtg gga att ttg aac aag acc tct ggc ctt a 394
 Arg His Phe Val Gly Ile Leu Asn Lys Thr Ser Gly Leu
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<210> 3504
 <211> 358
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> 164..358

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 aatgaaaata catatgggta aaggtgataa cacctatttt cccctttga aaggtgatag 120
 gttgcagtga tgtaatatgc aaatgtgagg cagaaatggt gat atg gtg ttt ctt 175
 Met Val Phe Leu
 1
 cat tac ctc cca gaa caa ctg tgt ctg agc atg ctg ggc agc tgg aga 223
 His Tyr Leu Pro Glu Gln Leu Cys Leu Ser Met Leu Gly Ser Trp Arg
 5 10 15 20
 ggt cac cct gga cag tta acc acg ctc ttt att tcc aaa tcc atg atc 271
 Gly His Pro Gly Gln Leu Thr Thr Leu Phe Ile Ser Lys Ser Met Ile
 25 30 35
 aaa tgg cag gwg gca aaa tcc atc cgt tgt cag tgc agg aag gac cca 319
 Lys Trp Gln Xaa Ala Lys Ser Ile Arg Cys Gln Cys Arg Lys Asp Pro
 40 45 50
 ctc aat ggg gtt cct ctc tgc att tgg gcg tct tcg gta 358
 Leu Asn Gly Val Pro Leu Cys Ile Trp Ala Ser Ser Val
 55 60 65

<210> 3505
 <211> 299
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 55..297

<400> 3505
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 Met
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 His Leu Leu Asp Leu Glu Ser Met Gly Lys Ser Ser Asp Gly Lys Ser
 5 10 15
 tat gtt att acg ggg agc tgg aat cca aaa tcc cca cat ttt caa gtt 153
 Tyr Val Ile Thr Gly Ser Trp Asn Pro Lys Ser Pro His Phe Gln Val
 20 25 30
 gta aat gaa gaa act cct aaa gat aaa gtc ctg ttt atg acc aca gct 201

Val	Asn	Glu	Glu	Thr	Pro	Lys	Asp	Lys	Val	Leu	Phe	Met	Thr	Thr	Ala	
35						40					45					
gta	gat	ttg	gta	ata	aca	gaa	gta	cag	gag	cct	gtt	cga	ttt	ctc	ctg	249
Val	Asp	Leu	Val	Ile	Thr	Glu	Val	Gln	Glu	Pro	Val	Arg	Phe	Leu	Leu	
50					55					60					65	
gag	aca	aaa	gtc	cgc	gtt	tgc	tca	cct	aat	gaa	aga	tta	ttc	tgg	ccc	297
Glu	Thr	Lys	Val	Arg	Val	Cys	Ser	Pro	Asn	Glu	Arg	Leu	Phe	Trp	Pro	
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a atg	gat cca	tta ata	gcc aat	aat tca	ggg gta	aac aaa	cgg cag	atc								169	
Met	Asp	Pro	Leu	Ile	Ala	Asn	Asn	Ser	Gly	Val	Asn	Lys	Arg	Gln	Ile		
1			5						10					15			
aca	gac	ctc	gtt	gac	cag	agt	ata	caa	atc	aat	gca	cat	tgt	ttt	gtg	217	
Thr	Asp	Leu	Val	Asp	Gln	Ser	Ile	Gln	Ile	Asn	Ala	His	Cys	Phe	Val		
			20					25					30				
gta	aca	gca	gat	aat	cgc	tat	att	ctt	atc	tgt	gga	ttc	tgg	gat	aag	265	
Val	Thr	Ala	Asp	Asn	Arg	Tyr	Ile	Leu	Ile	Cys	Gly	Phe	Trp	Asp	Lys		
		35					40					45					
agc	ttc	aga	gtt	tat	tct	aca	gaa	aca	ggg	aaa	ttg	act	cag	att	gta	313	
Ser	Phe	Arg	Val	Tyr	Ser	Thr	Glu	Thr	Gly	Lys	Leu	Thr	Gln	Ile	Val		
	50					55					60						
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Phe	Gly	His	Trp	Asp	Val	Val	Thr	Cys	Leu	Ala	Arg	Ser	Glu	Ser	Tyr		
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<220>
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 <222> 118..309

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atg	atc	cag	gct	ctg	gct	gga	ttc	ttt	acc	tac	ttt	gta	atc	ctg	gct	165	
Met	Ile	Gln	Ala	Leu	Ala	Gly	Phe	Phe	Thr	Tyr	Phe	Val	Ile	Leu	Ala		

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Glu Asn Gly Phe Arg Pro Val Asp Leu Leu Gly Ile Arg Leu His Trp				
	20	25	30	
gaa gat aaa tac ttg aat gac ctg gag gac agc tac gga cag cag tgg				261
Glu Asp Lys Tyr Leu Asn Asp Leu Glu Asp Ser Tyr Gly Gln Gln Trp				
	35	40	45	
acc tat gag caa cga aaa gtt gtg gag ttc aca tgc caa acg gcc tca				309
Thr Tyr Glu Gln Arg Lys Val Val Glu Phe Thr Cys Gln Thr Ala Ser				
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<210> 3508
 <211> 231
 <212> DNA
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<220>
 <221> CDS
 <222> 75..230

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cctttctgcc acag atg acg gaa aca ttt aaa gtt atg gat tgt gtc tct	110
Met Thr Glu Thr Phe Lys Val Met Asp Cys Val Ser	
	1 5 10
gca tcc tct tcc ctt cac acc agc caa tgt gtt ttt cat ttc tct tgg	158
Ala Ser Ser Ser Leu His Thr Ser Gln Cys Val Phe His Phe Ser Trp	
	15 20 25
ctg gct caa ttt ccc aca tgt tct ccc aag ctc ttc ctc tcc act ccc	206
Leu Ala Gln Phe Pro Thr Cys Ser Pro Lys Leu Phe Leu Ser Thr Pro	
	30 35 40
cag ggc ttc cca cca caa acc gca c	231
Gln Gly Phe Pro Pro Gln Thr Ala	
45	50

<210> 3509
 <211> 311
 <212> DNA
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<220>
 <221> CDS
 <222> 115..309

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Met	
	1
ggc tca gcc aag agc gtc cca gtc aca cca gcg cgg cct ccg ccg cac	165
Gly Ser Ala Lys Ser Val Pro Val Thr Pro Ala Arg Pro Pro Pro His	
	5 10 15

aac aag cat ctg gct cga gtg gcg gac ccc cgt tca cct agt gct ggc	213
Asn Lys His Leu Ala Arg Val Ala Asp Pro Arg Ser Pro Ser Ala Gly	
20 25 30	
atc ctg cgc act ccc atc cag gtg gag agc tct cca cag cca ggc cta	261
Ile Leu Arg Thr Pro Ile Gln Val Glu Ser Ser Pro Gln Pro Gly Leu	
35 40 45	
cca gca ggg gag caa ctg gag ggt ctt aaa cat gcc cag gac tca gat	309
Pro Ala Gly Glu Gln Leu Glu Gly Leu Lys His Ala Gln Asp Ser Asp	
50 55 60 65	
cc	311

<210> 3510
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 <212> DNA
 <213> Homo sapiens

<220>
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 <222> 180..383

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aagagaaaat tatattttgt accaatttat ataaagttca tctagctcag cttttggag	179
atg tcc ctg ggg cta gag atg aaa tat cgt ttt cct gtc cac aga cag	227
Met Ser Leu Gly Leu Glu Met Lys Tyr Arg Phe Pro Val His Arg Gln	
1 5 10 15	
cgg tct gca gtt cac ccc atg aac tca tac agg tca gaa tta aac ccc	275
Arg Ser Ala Val His Pro Met Asn Ser Tyr Arg Ser Glu Leu Asn Pro	
20 25 30	
gag ctt tgt tta tgg agg gtg aga tat att tcc aag tat ttc ttt ctc	323
Glu Leu Cys Leu Trp Arg Val Arg Tyr Ile Ser Lys Tyr Phe Phe Leu	
35 40 45	
ttt tca cat ttt cca cat cat tac cat cat cat tgt cgt cat cat cat	371
Phe Ser His Phe Pro His His Tyr His His His Cys Arg His His His	
50 55 60	
tgt cat cat cca at	385
Cys His His Pro	
65	

<210> 3511
 <211> 174
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 5..172

<400> 3511	
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Met Pro Tyr Lys Glu Ala Ser His Cys Val Cys Ser Phe Leu Ala	

1	5	10	15	
ttt aac ctt cct cca cgt aag gac aca gtg aac aag gtg cca tct tgg				97
Phe Asn Leu Pro Pro Arg Lys Asp Thr Val Asn Lys Val Pro Ser Trp				
	20	25	30	
aaa caa aca gca gcc ttc acc aga cac cag acc ttc tgg cac ctt gac				145
Lys Gln Thr Ala Ala Phe Thr Arg His Gln Thr Phe Trp His Leu Asp				
	35	40	45	
ctt gcg ctt tcc agc ctc cag aac cgt gt				174
Leu Ala Leu Ser Ser Leu Gln Asn Arg				
	50	55		

<210> 3512
 <211> 368
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 112..366

<400> 3512	
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gacctggggga atcacgctgg tgctcttctt gcacgatacc gagctgcggc a atg gga	117
	Met Gly
	1
gga gca ggg gga gct gct cct gcc cct caw mtt cct gct cct ggt gct	165
Gly Ala Gly Gly Ala Ala Pro Ala Pro Xaa Xaa Pro Ala Pro Gly Ala	
	5
ggg ctc cct gct gct cta cct cgc tgt gtc act cat gga ccc tgg ctg	213
Gly Leu Pro Ala Ala Leu Pro Arg Cys Val Thr His Gly Pro Trp Leu	
	20
aat gtg cag ccc cag cct cag gag gag ctc aaa gag gag cag aca gcc	261
Asn Val Gln Pro Gln Pro Gln Glu Glu Leu Lys Glu Glu Gln Thr Ala	
	35
atg gtt cct cca gcc atc cct ctt cgg cgc tgc aga tac tgc ctg gtg	309
Met Val Pro Pro Ala Ile Pro Leu Arg Arg Cys Arg Tyr Cys Leu Val	
	55
ctg cag ccc ctg agg gct cgg cac tgc cgt gag tgc cgc cgt tgc gtc	357
Leu Gln Pro Leu Arg Ala Arg His Cys Arg Glu Cys Arg Arg Cys Val	
	70
cgc cgc tac ga	368
Arg Arg Tyr	
	85

<210> 3513
 <211> 388
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 121..387

<400> 3513

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cccctaaccc tgaggctgcc gcgcggcggt cactgcgccg gggtagtggg cccagtggt      60
gcgctctctg gccgttcctt acactttgct tcaggctcca gtgcaggggc gtagtgggat    120
atg gcc aac tcg ggc tgc aag gac gtc acg ggt cca gat gag gag agt      168
Met Ala Asn Ser Gly Cys Lys Asp Val Thr Gly Pro Asp Glu Glu Ser
1          5          10          15
ttt ctg tac ttt gcb tac ggc agc aac ctg ctg aca gag agg atc cac      216
Phe Leu Tyr Phe Ala Tyr Gly Ser Asn Leu Leu Thr Glu Arg Ile His
          20          25          30
ctc cga aac ccc tcg gcg gcg ttc ttc tgt gtg gcc cgc ctg cag gat      264
Leu Arg Asn Pro Ser Ala Ala Phe Phe Cys Val Ala Arg Leu Gln Asp
          35          40          45
ttt vag ctt gac ttt ggc aat tcc caa ggc aaa aca agt caa act tgg      312
Phe Xaa Leu Asp Phe Gly Asn Ser Gln Gly Lys Thr Ser Gln Thr Trp
          50          55          60
cat gga ggg ata gcc acc att ttt caa agt cct ggc gat gaa gtg tgg      360
His Gly Gly Ile Ala Thr Ile Phe Gln Ser Pro Gly Asp Glu Val Trp
65          70          75          80
gga gta gta tgg aaa atg aac aaa agc a      388
Gly Val Val Trp Lys Met Asn Lys Ser
          85

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<210> 3514

<211> 295

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 16..294

<400> 3514

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gtgacggact gttct atg act gca aag atg gaa acg acc ttc tat gac gat      51
          Met Thr Ala Lys Met Glu Thr Thr Phe Tyr Asp Asp
          1          5          10
gcc ctc aac gcc tcg ttc ctc ccg tcc gag agc ggm cct tat ggc tac      99
Ala Leu Asn Ala Ser Phe Leu Pro Ser Glu Ser Gly Pro Tyr Gly Tyr
          15          20          25
agt aac ccc aag atc ctg aaa cag agc atg acc ctg aac ctg gcc gac      147
Ser Asn Pro Lys Ile Leu Lys Gln Ser Met Thr Leu Asn Leu Ala Asp
          30          35          40
cca gtg ggg agc ctg aag ccg cac ctc cgc gcc aag aac tcg gac ctc      195
Pro Val Gly Ser Leu Lys Pro His Leu Arg Ala Lys Asn Ser Asp Leu
45          50          55          60
ctc acc tcg ccc gac gtg ggg ctg ctc aag ctg gcg tcg ccc gag ctg      243
Leu Thr Ser Pro Asp Val Gly Leu Leu Lys Leu Ala Ser Pro Glu Leu
          65          70          75
gag cgc ctg ata atc cag tcc agc aac ggg cac atc acc acc acg ccg      291
Glu Arg Leu Ile Ile Gln Ser Ser Asn Gly His Ile Thr Thr Thr Pro
          80          85          90
acc c      295
Thr

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SECRET

SECRET

[illegible]

SECRET

SECRET

[illegible]

<213> Homo sapiens

<220>

<221> CDS

<222> 32..328

<400> 3520

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cattctagcg ggaaatatta ttcacagttt a atg aag tct gat cta gtg gaa      52
                               Met Lys Ser Asp Leu Val Glu
                               1           5
tat ttc act ttg gaa atg ctt cac ttg gga aac aat cgt att gaa gty      100
Tyr Phe Thr Leu Glu Met Leu His Leu Gly Asn Asn Arg Ile Glu Val
          10           15           20
ctt gaa gaa gga tcg ttt atg aac cta acg aga tta caa aaa ctc tat      148
Leu Glu Glu Gly Ser Phe Met Asn Leu Thr Arg Leu Gln Lys Leu Tyr
          25           30           35
cta aat ggt aac cac ctg acc aaa tta agt aaa ggc atc gtc ctt ggt      196
Leu Asn Gly Asn His Leu Thr Lys Leu Ser Lys Gly Ile Val Leu Gly
          40           45           50           55
ctc cat aat ctt gaa tac tta tat ctt gaa tac aat gcc att awk gaa      244
Leu His Asn Leu Glu Tyr Leu Tyr Leu Glu Tyr Asn Ala Ile Xaa Glu
          60           65           70
ata ctg cca gga acc ttt aat cca atg cct aaa ctt aaa gtc ctg tat      292
Ile Leu Pro Gly Thr Phe Asn Pro Met Pro Lys Leu Lys Val Leu Tyr
          75           80           85
tta aat aac aac ctc ctc caa gtt tta cca cca cta      328
Leu Asn Asn Asn Leu Leu Gln Val Leu Pro Pro Leu
          90           95

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<210> 3521

<211> 245

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 34..243

<400> 3521

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tcagataaaa ctggaacact gacgaagaat gaa atg act gtt act cac ata ttt      54
                               Met Thr Val Thr His Ile Phe
                               1           5
act tca gat ggt ctg cat gct gag gtt act gga gtt ggc tat aat caa      102
Thr Ser Asp Gly Leu His Ala Glu Val Thr Gly Val Gly Tyr Asn Gln
          10           15           20
ttt ggg gaa gtg att gtt gat ggt gat gtt gtt cat gga ttc tat aac      150
Phe Gly Glu Val Ile Val Asp Gly Asp Val Val His Gly Phe Tyr Asn
          25           30           35
cca gct gtt agc aga att gtt gag gcg ggc tgt gtg tgc aat gat gct      198
Pro Ala Val Ser Arg Ile Val Glu Ala Gly Cys Val Cys Asn Asp Ala
          40           45           50           55
gta att aga aac aat act cta atg ggg aag cca aca gaa ggg gcc tt      245

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Val Ile Arg Asn Asn Thr Leu Met Gly Lys Pro Thr Glu Gly Ala
60 65 70

<210> 3522
<211> 307
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 72..305

<400> 3522
gtgtgggggc cgcagcgctd agggagccgg tgccatctgt gggggctttg ggccakgggt 60
ctccggacag c atg agc ktg ggc ttc atc ggc gct ggc cag ctg gct ttt 110
Met Ser Xaa Gly Phe Ile Gly Ala Gly Gln Leu Ala Phe
1 5 10
gcc ctg gcc aag ggc ttc aca kca gca ggc gtc ttg gct gcc cac aag 158
Ala Leu Ala Lys Gly Phe Thr Xaa Ala Gly Val Leu Ala Ala His Lys
15 20 25
ata atg gct agc tcc cca gac atg gac ctg gcc aca gtt tct gct ctc 206
Ile Met Ala Ser Ser Pro Asp Met Asp Leu Ala Thr Val Ser Ala Leu
30 35 40 45
agg wrd atg ggg gtg aar wwg aca ccc cac aac aag gag acg gtg cag 254
Arg Xaa Met Gly Val Lys Xaa Thr Pro His Asn Lys Glu Thr Val Gln
50 55 60
cac agt gat gtg ctc ttc ctg gst gtg aag cca cac atc atc ccc tkc 302
His Ser Asp Val Leu Phe Leu Xaa Val Lys Pro His Ile Ile Pro Xaa
65 70 75
atc ct 307
Ile

<210> 3523
<211> 203
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 5..202

<400> 3523
cgac atg cac cgc aaa ttc gtg gtg cat ctg ttc gcc gag gag tgg ggc 49
Met His Arg Lys Phe Val Val His Leu Phe Ala Glu Glu Trp Gly
1 5 10 15
cag tac gtg gac ttg ccc aag ggc ttc gcg gtg agc gag cgc tgc aag 97
Gln Tyr Val Asp Leu Pro Lys Gly Phe Ala Val Ser Glu Arg Cys Lys
20 25 30
gtg cgc ctc gtg ccg ctg cag atc cag ctc act acc ctg gga aat ctt 145
Val Arg Leu Val Pro Leu Gln Ile Gln Leu Thr Thr Leu Gly Asn Leu
35 40 45
aca cct tca agc act gtg ttt ttc tgc tgt gat atg cag gaa agg ttc 193

Thr Pro Ser Ser Thr Val Phe Phe Cys Cys Asp Met Gln Glu Arg Phe
 50 55 60
 aga cca gac c
 Arg Pro Asp
 65

203

<210> 3524
 <211> 361
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 36..359

<400> 3524
 acttttagag tttacttcaa ccacgtggag cttcc atg gcg gcc tct cag gtc 53
 Met Ala Ala Ser Gln Val
 1 5
 ctg ggg gag aag att aac atc ctg tgc gga gag act gtc aaa gct ggg 101
 Leu Gly Glu Lys Ile Asn Ile Leu Ser Gly Glu Thr Val Lys Ala Gly
 10 15 20
 gac agg gac ccg ctg ggg aac gac tgt ccc gag caa gat agg ctc ccc 149
 Asp Arg Asp Pro Leu Gly Asn Asp Cys Pro Glu Gln Asp Arg Leu Pro
 25 30 35
 cag cgc tcc tgg agg cag aag tgt gcc tcc tac gtt ttg gcc ctg agg 197
 Gln Arg Ser Trp Arg Gln Lys Cys Ala Ser Tyr Val Leu Ala Leu Arg
 40 45 50
 ccc tgg agc ttc agt gcc tca ctc aca ccg gtg gcc ctg ggc agt gcc 245
 Pro Trp Ser Phe Ser Ala Ser Leu Thr Pro Val Ala Leu Gly Ser Ala
 55 60 65 70
 ctt gcc tac aga tcc cac ggt gtc ctg gat ccc agg ctc ttg gtg ggt 293
 Leu Ala Tyr Arg Ser His Gly Val Leu Asp Pro Arg Leu Leu Val Gly
 75 80 85
 tgt gcc gtg gct gtc ctg gct gtg cac gtg gcc ggt aat ttg gtc aac 341
 Cys Ala Val Ala Val Leu Ala Val His Val Ala Gly Asn Leu Val Asn
 90 95 100
 act tac tat gac ttt tch aa 361
 Thr Tyr Tyr Asp Phe Ser
 105

<210> 3525
 <211> 386
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 76..384

<400> 3525
 gtaattagga ggaaggctcg ctgggaatac ggatatagcc tccgggtgag gagttgtgac 60

tggtgttttag gtgtc atg gag aaa ctc cag ctg ggc cca gag att ctg cag	111
Met Glu Lys Leu Gln Leu Gly Pro Glu Ile Leu Gln	
1 5 10	
cgg gaa aat cca agg ctt att tat gcc agg ctg agt gga ttt ggc cag	159
Arg Glu Asn Pro Arg Leu Ile Tyr Ala Arg Leu Ser Gly Phe Gly Gln	
15 20 25	
tca gga agc ttc tgc cgg tta gct ggc cac gat atc aac tat ttg gct	207
Ser Gly Ser Phe Cys Arg Leu Ala Gly His Asp Ile Asn Tyr Leu Ala	
30 35 40	
ttg tca ggt gtt ctc tca aaa att ggc aga agt ggt gag aat ccg tat	255
Leu Ser Gly Val Leu Ser Lys Ile Gly Arg Ser Gly Glu Asn Pro Tyr	
45 50 55 60	
gcc ccg ctg aat ctc ctg gct gac ttt gct ggt ggt ggc ctt atg tgt	303
Ala Pro Leu Asn Leu Leu Ala Asp Phe Ala Gly Gly Gly Leu Met Cys	
65 70 75	
gca ctg ggc att ata atg gct ctt ttt gac cgc aca cgc act ggc aag	351
Ala Leu Gly Ile Ile Met Ala Leu Phe Asp Arg Thr Arg Thr Gly Lys	
80 85 90	
ggt cag gtc att gat gca aat atg gtg gaa ggc at	386
Gly Gln Val Ile Asp Ala Asn Met Val Glu Gly	
95 100	

<210> 3526
 <211> 451
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> CDS
 <222> 38..451

<400> 3526	
actccccgcgc gtactcgggcc gcctgagcga tactaaa atg tct gat gat gct ggt	55
Met Ser Asp Asp Ala Gly	
1 5	
gac acc tta gcc act gga gac aaa gca gaa gtt act gag atg cct aat	103
Asp Thr Leu Ala Thr Gly Asp Lys Ala Glu Val Thr Glu Met Pro Asn	
10 15 20	
agt gat tct tta cct gag gat gca gaa gtg cat tgt gat tca gct gca	151
Ser Asp Ser Leu Pro Glu Asp Ala Glu Val His Cys Asp Ser Ala Ala	
25 30 35	
gtt tca cat gag cca aca cca gct gac ccc aga ggg gag ggg cat gaa	199
Val Ser His Glu Pro Thr Pro Ala Asp Pro Arg Gly Glu Gly His Glu	
40 45 50	
aat gca gct gtg cag ggt gca ggg gct gcc gcc att ggg ccc cct gtg	247
Asn Ala Ala Val Gln Gly Ala Gly Ala Ala Ala Ile Gly Pro Pro Val	
55 60 65 70	
cag cct cag gat gcc aac gcc ctg gag ccc cct ctc aat gga gac gtg	295
Gln Pro Gln Asp Ala Asn Ala Leu Glu Pro Pro Leu Asn Gly Asp Val	
75 80 85	
act gag gat aca ctt gct gaa tgt att gat tcc gtc agc ctt gag gca	343
Thr Glu Asp Thr Leu Ala Glu Cys Ile Asp Ser Val Ser Leu Glu Ala	
90 95 100	

004220 6657560

gaa ccc aga tcc gaa ata ccc ctg caa gaa cag aat tat ctg gct gtg	391
Glu Pro Arg Ser Glu Ile Pro Leu Gln Glu Gln Asn Tyr Leu Ala Val	
105 110 115	
gat tcc cct cca agt gga gga gga tgg gca ggc tgg gga tcc tgg ggc	439
Asp Ser Pro Pro Ser Gly Gly Gly Trp Ala Gly Trp Gly Ser Trp Gly	
120 125 130	
aaa tct ctg ctc	451
Lys Ser Leu Leu	
135	

<210> 3527
 <211> 399
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 237..398

<400> 3527	
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ctcctgcagc ctctgcaccc atgagcctag cttaggggtca gtaacttgtg gtttagcaaa	120
aaacagactt aactttataa tgttagcaaa aggattaagt tttaaataata tcagaatcga	180
gatgggaaag aaacctaaca aagtgctaataaaaaataga attgggtaaaa aatatt atg	239
Met	
1	
ttt cat gaa aga agc cag aca caa aca gct ata tat tgt atg att gca	287
Phe His Glu Arg Ser Gln Thr Gln Thr Ala Ile Tyr Cys Met Ile Ala	
5 10 15	
twd ata aga aat gtt cag aat aga cac atc tat ata gag aaa agg cag	335
Xaa Ile Arg Asn Val Gln Asn Arg His Ile Tyr Ile Glu Lys Arg Gln	
20 25 30	
att agt ggt tgt agg agg ctg gga gag ggn gaa tgg gaa gtg act act	383
Ile Ser Gly Cys Arg Arg Leu Gly Glu Gly Glu Trp Glu Val Thr Thr	
35 40 45	
aac agg tac agg aag a	399
Asn Arg Tyr Arg Lys	
50	

<210> 3528
 <211> 308
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 113..307

<400> 3528	
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cctttctgat cataataggt aacttagggg ggggccctga gatggcatca gg atg ggg	118
Met Gly	

tttccgcattc attggtttgc aagtactggc gtgacctttg ttttagacttc cagttttgga 120
 agcagctgga tcttagtagt cgtcagcagg tcaactgatga attgttgga aaaattgcat 180
 caagaagtca gaataataatt gaaatcaaca tttctgattg tcgcagt atg tct gat 236
 Met Ser Asp

aat ggc gta tgt gtt tta gca ttt aaa tgt cct gga ctt ctt agg tat 284
 Asn Gly Val Cys Val Leu Ala Phe Lys Cys Pro Gly Leu Leu Arg Tyr

5 10 15
 aca gcc tac agg tgt aaa cag ctt tct gac acc tct att att gcg gtt 332
 Thr Ala Tyr Arg Cys Lys Gln Leu Ser Asp Thr Ser Ile Ile Ala Val
 20 25 30 35

gcc tct cac tgt cct tta ctt cag aaa gtg cat gta ggc aac cag grc 380
 Ala Ser His Cys Pro Leu Leu Gln Lys Val His Val Gly Asn Gln Xaa
 40 45 50

aaa ctc act gat gaa ggr ctc aag cag ctg ggt t 414
 Lys Leu Thr Asp Glu Gly Leu Lys Gln Leu Gly
 55 60

<210> 3533
 <211> 225
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 63..224

<400> 3533
 gggacgtggg aaaatgacta cgcgtcactc gtgatgtcgc gcatccgata ggcccttttc 60
 ag atg gca aaa ggc ctg agg gtg aat ctg ggc gag ctg gtt gag tcc 107
 Met Ala Lys Gly Leu Arg Val Asn Leu Gly Glu Leu Val Glu Ser

1 5 10 15
 atg cgt ttg tgc ttc ctc tca gtc cac ttt cgc tta cga tgg ggc gac 155
 Met Arg Leu Cys Phe Leu Ser Val His Phe Arg Leu Arg Trp Gly Asp
 20 25 30

tct tgt cca tcg tca cct cac cgg gaa act ttt cct gcc ggg cca gtt 203
 Ser Cys Pro Ser Ser Pro His Arg Glu Thr Phe Pro Ala Gly Pro Val
 35 40 45

aat ggt ccc ctg tac cac ccc c 225
 Asn Gly Pro Leu Tyr His Pro
 50

<210> 3534
 <211> 473
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 142..471

<400> 3534

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accgatgctg gaaggggttc tttggscctg agtgaagaga gacccagagg gaacactgag      60
gtgcctgccc aaccactctg tcccgggttc cttcagcagg accagccatg ctggtcgttc      120
agatkscttt cytcctttcc c atg gcc cac ttc atc ctc ttt gtc ttt acg      171
                        Met Ala His Phe Ile Leu Phe Val Phe Thr
                        1         5         10
gtt tcc act ata ttt cac gtt cag cag cgg cta gcg aag att caa gcc      219
Val Ser Thr Ile Phe His Val Gln Gln Arg Leu Ala Lys Ile Gln Ala
                        15         20         25
atg tgg gag tta ccg gtg cag ata cca gtg cta gcc tca aca tca aag      267
Met Trp Glu Leu Pro Val Gln Ile Pro Val Leu Ala Ser Thr Ser Lys
                        30         35         40
gca ctg gga ccc agc cag ctc agg ggg atg tgg acg atc aat gcg ata      315
Ala Leu Gly Pro Ser Gln Leu Arg Gly Met Trp Thr Ile Asn Ala Ile
                        45         50         55
ggc cgc ctg ggg aac cag gtg ggc gag tac gcc aca ctg tat gcc ctg      363
Gly Arg Leu Gly Asn Gln Val Gly Glu Tyr Ala Thr Leu Tyr Ala Leu
                        60         65         70
gcc aag atg aac ggg cgg ccc gcc ttc atc chn nsc cag atg cac agc      411
Ala Lys Met Asn Gly Arg Pro Ala Phe Ile Xaa Xaa Gln Met His Ser
                        75         80         85         90
nnn btg gcc ccc atc ttc aga atc acc ctg ccg gtg ctg cac agc gcc      459
Xaa Xaa Ala Pro Ile Phe Arg Ile Thr Leu Pro Val Leu His Ser Ala
                        95         100         105
aca gcc agc agg at
Thr Ala Ser Arg
                        110

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<210> 3535
 <211> 385
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 74..385

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<400> 3535
aaatgatcat attgaacagt tcctgggtac atgtgcaaga cgtgcagggt tgttacatag      60
gtaaacgtgt gct atg atg gtt tgc ttc acc tat caa ccc att gtc tct      109
                        Met Met Val Cys Phe Thr Tyr Gln Pro Ile Val Ser
                        1         5         10
gga atc ggt ggt ttc ytg gkc chc ast gac ttc aag aat gaa gcc gca      157
Gly Ile Gly Gly Phe Leu Xaa Xaa Xaa Asp Phe Lys Asn Glu Ala Ala
                        15         20         25
gac cct gcc gga ata caa ctt aca agg gaa atg aag gac ctc ttc aag      205
Asp Pro Ala Gly Ile Gln Leu Thr Arg Glu Met Lys Asp Leu Phe Lys
                        30         35         40
gag aac tac aaa aca ctg ctc aag gaa ata aga gag gac aca agc aaa      253
Glu Asn Tyr Lys Thr Leu Leu Lys Glu Ile Arg Glu Asp Thr Ser Lys
                        45         50         55         60
tgg aaa aat att cca tgc tca tgg ata gga aga atc att atc atg aaa      301
Trp Lys Asn Ile Pro Cys Ser Trp Ile Gly Arg Ile Ile Ile Met Lys
                        65         70         75

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atg gcc ata ctg ccc aaa gta atn kat aga ttc aat gct atc cca atc 349
 Met Ala Ile Leu Pro Lys Val Xaa Xaa Arg Phe Asn Ala Ile Pro Ile
 80 85 90
 aag cta cca ttt act ttc ttc aca gaa ttg gra aaa 385
 Lys Leu Pro Phe Thr Phe Phe Thr Glu Leu Xaa Lys
 95 100

<210> 3536
 <211> 316
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 93..314

<400> 3536
 tggaagggttt catacgggaa gtgacatggt aagatctgga tcttaaagaa cttgggggttc 60
 ccgaagaagc tcggtgcat caacaggaaa gg atg aga ctt tgg att cca gaa 113
 Met Arg Leu Trp Ile Pro Glu
 1 5
 gaa cac tgc ygg ggg tty ccc ccc gag tct gcc act tgc tgt aac ctc 161
 Glu His Cys Xaa Gly Phe Pro Pro Glu Ser Ala Thr Cys Cys Asn Leu
 10 15 20
 aga gga tcc aga acg gca gct ggt ymt tgc tgg act gtt cct gtc cat 209
 Arg Gly Ser Arg Thr Ala Ala Gly Xaa Cys Trp Thr Val Pro Val His
 25 30 35
 gtg cct ggt cat ggt gct ggg gaa cct gct cat cat ccg gcc atg agc 257
 Val Pro Gly His Gly Ala Gly Glu Pro Ala His His Pro Ala Met Ser
 40 45 50 55
 cct gac tcc cac ctc cac acc tcc atg tac ttc ttc ctc tcc aac ctg 305
 Pro Asp Ser His Leu His Thr Ser Met Tyr Phe Phe Leu Ser Asn Leu
 60 65 70
 tcc ttg cct ct 316
 Ser Leu Pro

<210> 3537
 <211> 347
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 119..346

<400> 3537
 atgggccgga ggagagcccc ggccgggtggg tcgctggrac gggcccttat gcgccatcag 60
 actcagcgga scgaagrecca tcgtcacact grctcctggt tgcacacaag tgartca 118
 atg atg gsy atk rat tgg ggt cgn ktt aat ctt cag tca gtg act gaa 166
 Met Met Xaa Xaa Xaa Trp Gly Arg Xaa Asn Leu Gln Ser Val Thr Glu
 1 5 10 15
 cag agc tcc ctt gat gac ttc ctt gct act gca gaa ctt gca gga aca 214

Gln	Ser	Ser	Leu	Asp	Asp	Phe	Leu	Ala	Thr	Ala	Glu	Leu	Ala	Gly	Thr	
			20					25					30			
gag	ttt	gta	gct	gaa	aaa	ctt	aat	att	aag	ttt	gtg	cct	hnt	gag	gct	262
Glu	Phe	Val	Ala	Glu	Lys	Leu	Asn	Ile	Lys	Phe	Val	Pro	Xaa	Glu	Ala	
		35					40				45					
aga	act	gga	cta	ctg	tct	ttc	gag	gag	agc	cag	aga	att	aag	aag	ctc	310
Arg	Thr	Gly	Leu	Leu	Ser	Phe	Glu	Glu	Ser	Gln	Arg	Ile	Lys	Lys	Leu	
	50					55				60						
cat	gaa	gaa	aac	aaa	cag	ttc	ttg	tgt	ata	ccg	agg	a				347
His	Glu	Glu	Asn	Lys	Gln	Phe	Leu	Cys	Ile	Pro	Arg					
65				70					75							

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 <211> 332
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> 161..331

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ggtcggaggg	ctgcggggccc	gaagcctctg	tccctcctgt	tcttgtccgg	cgctgcttag											120	
cccccccgcg	tagtcatcat	ggratctgat	tttaaaccga	atg gat tat	ctg cag											175	
				Met Asp Tyr	Leu Gln												
				1	5												
gtg gga gta	aca tct cag	aag act atg	aag cta att	cct gcc tca	aga											223	
Val Gly Val	Thr Ser Gln	Lys Thr Met	Lys Leu Ile	Pro Ala Ser	Arg												
	10		15		20												
cac aga gct	aca caa aag	gtg gtt att	gga gat cat	gat ggg gta	gtt											271	
His Arg Ala	Thr Gln Lys	Val Val Ile	Gly Asp His	Asp Gly Val	Val												
	25		30		35												
atg tgc tdt	ggc atg aag	aaa gga gaa	gca gca gca	gtg ttc aag	act											319	
Met Cys Xaa	Gly Met Lys	Lys Gly Glu	Ala Ala Ala	Val Phe Lys	Thr												
	40		45		50												
tta ccc cgg	cca a															332	
Leu Pro Arg	Pro																
	55																

<210> 3539
 <211> 246
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> 82..246

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cttctctctc	agagactgca	g atg gct	ttt ccc	tgc cgc	arg tcc	ctg act										111	

	Met	Ala	Phe	Pro	Cys	Arg	Xaa	Ser	Leu	Thr	
	1				5					10	
gcc maa gac tct ggc ctg cct cct ggt ggg cgt gag tkt ctt agc act											159
Ala Xaa Asp Ser Gly Leu Pro Pro Gly Gly Arg Glu Xaa Leu Ser Thr											
	15				20					25	
gca gca gtg gtt cct cca ggc gcc aag gtc ccc gcg gga gga gag gtc											207
Ala Ala Val Val Pro Pro Gly Ala Lys Val Pro Ala Gly Gly Glu Val											
	30				35					40	
ccc gca gga gga gac gcc aga ggg tcc cac cga cga cta											246
Pro Ala Gly Gly Asp Ala Arg Gly Ser His Arg Arg Leu											
	45				50					55	

<210> 3540

<211> 245

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 39..245

<400> 3540

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					Met	Pro	His	Trp	Gly	Lys	
					1					5	
gtc cac gct tcc ccc atc tgc agg ggt ctt ttg gca cca gcc gca aga											104
Val His Ala Ser Pro Ile Cys Arg Gly Leu Leu Ala Pro Ala Ala Arg											
	10				15					20	
cat aag acc agt atc ctt gga ata gcg cas cag gga aag tcc ttg agc											152
His Lys Thr Ser Ile Leu Gly Ile Ala Xaa Gln Gly Lys Ser Leu Ser											
	25				30					35	
cag gag gtc tgg aag gag cat tgg agc ttc tgc att aga gac ttg ggc											200
Gln Glu Val Trp Lys Glu His Trp Ser Phe Cys Ile Arg Asp Leu Gly											
	40				45					50	
cgc gcg agg gna agt gct gga cag wmt ctc ctt cgc cag ccc ctc											245
Arg Ala Arg Xaa Ser Ala Gly Gln Xaa Leu Leu Arg Gln Pro Leu											
	55				60					65	

<210> 3541

<211> 318

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 151..318

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ttggattgtc tggcaatgat tactgtgttg ctaactcatt ttctttgagt taaagctgtg											120
tatacatTTTT aaaaggcata tagatagtgt atg cat atg tat atg tac ata ggg											174
					Met	His	Met	Tyr	Met	Tyr	Ile
											Gly

							1				5						
aag	ccc	cat	atg	tat	ata	gta	tgt	tgt	aca	ctg	cac	atg	tac	aaa	gaa		222
Lys	Pro	His	Met	Tyr	Ile	Val	Cys	Cys	Thr	Leu	His	Met	Tyr	Lys	Glu		
	10						15					20					
tgt	ctt	cag	atc	aaa	gaa	aat	tta	tct	ctt	ttt	ata	aac	tta	agg	aca		270
Cys	Leu	Gln	Ile	Lys	Glu	Asn	Leu	Ser	Leu	Phe	Ile	Asn	Leu	Arg	Thr		
	25				30					35				40			
ggt	gca	aaa	ggc	ttc	aag	gaa	ttt	atc	tca	aca	tta	ttc	ttt	cta	tgt		318
Val	Ala	Lys	Gly	Phe	Lys	Glu	Phe	Ile	Ser	Thr	Leu	Phe	Phe	Leu	Cys		
			45						50					55			

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 <213> Homo sapiens

<220>
 <221> CDS
 <222> 8..211

<400> 3542																	
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	Met	Ile	Tyr	Val	Thr	Asp	Lys	Gly	Gln	Lys	Lys	His	Phe	Gln			
	1				5					10							
caa	gta	ttc	caa	atg	ctg	aag	atc	atg	gga	tat	gac	tg	gca	gaa	agg		97
Gln	Val	Phe	Gln	Met	Leu	Lys	Ile	Met	Gly	Tyr	Asp	Trp	Ala	Glu	Arg		
	15				20					25				30			
tgc	cag	cac	gtg	ccc	ttt	gga	gta	gta	cag	gga	atg	aag	act	cga	aga		145
Cys	Gln	His	Val	Pro	Phe	Gly	Val	Val	Gln	Gly	Met	Lys	Thr	Arg	Arg		
			35						40					45			
gga	gat	gtc	act	ttc	ctg	gaa	gat	gtt	tta	aat	gag	att	caa	tta	agg		193
Gly	Asp	Val	Thr	Phe	Leu	Glu	Asp	Val	Leu	Asn	Glu	Ile	Gln	Leu	Arg		
		50					55						60				
atg	cya	cag	aac	atg	gca	cc											213
Met	Xaa	Gln	Asn	Met	Ala												
		65															

<210> 3543
 <211> 384
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 84..383

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ggttgcgaggg	gcggtgttga	aga	atg	tgt	ggg	cga	aca	tcc	tgt	cac	tta	cct		113			
		Met	Cys	Gly	Arg	Thr	Ser	Cys	His	Leu	Pro						
			1			5				10							
aga	gat	gtt	ctc	acg	aga	gct	tgc	gcc	tac	cag	gat	cgg	cgg	ggc	cag		161

004220-0567560

Arg	Asp	Val	Leu	Thr	Arg	Ala	Cys	Ala	Tyr	Gln	Asp	Arg	Arg	Gly	Gln	
				15					20					25		
cag	cgg	ctc	ccg	gag	tgg	agg	gac	cct	gat	aag	tac	tgc	ccc	tct	tac	209
Gln	Arg	Leu	Pro	Glu	Trp	Arg	Asp	Pro	Asp	Lys	Tyr	Cys	Pro	Ser	Tyr	
		30						35				40				
aac	aag	agt	cct	caa	tcc	aac	agc	cca	gtg	ctt	ctg	tct	cga	ctg	cac	257
Asn	Lys	Ser	Pro	Gln	Ser	Asn	Ser	Pro	Val	Leu	Leu	Ser	Arg	Leu	His	
		45					50					55				
ttt	gag	aag	gat	gca	gac	tca	tct	gag	cgt	atc	att	gct	ccc	atg	cgc	305
Phe	Glu	Lys	Asp	Ala	Asp	Ser	Ser	Glu	Arg	Ile	Ile	Ala	Pro	Met	Arg	
	60					65				70						
tgg	ggc	ttg	gtc	cct	tct	trg	ttc	aaa	gaa	agt	gat	cct	tcc	aag	ctg	353
Trp	Gly	Leu	Val	Pro	Ser	Xaa	Phe	Lys	Glu	Ser	Asp	Pro	Ser	Lys	Leu	
	75				80					85				90		
cag	ttc	aat	act	amc	aac	tgt	cgt	agt	gat	a						384
Gln	Phe	Asn	Thr	Xaa	Asn	Cys	Arg	Ser	Asp							
				95					100							

<210> 3544
 <211> 359
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 140..358

<400> 3544															
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ttataackac	ccagaaggta	caagtgctat	caggacaagt	tcctcatagc	acagtcatgt		120								
catttggaac	acaagctgt	atg ttg atg	tct cat ctt	gag gaa cca	aaa gta		172								
		Met Leu Met	Ser His Leu	Glu Glu Pro	Lys Val										
		1	5	10											
aca gaa gat	gaa gaa cca	ccc aca	gaa caa	gat aag	agg aaa	mnc atg	220								
Thr Glu Asp	Glu Glu Pro	Pro Thr	Glu Gln	Asp Lys	Arg Lys	Xaa Met									
	15		20		25										
ctg gcc ctg	aag gac cct	gtt cat	aca gtg	tca ctg	cag cag	ttc atc	268								
Leu Ala Leu	Lys Asp Pro	Val His	Thr Val	Ser Leu	Gln Gln	Phe Ile									
	30		35		40										
kac gag aag	ckc aag gca	cag cag	gag atg	cta rgm	saa caa	ggc ttc	316								
Xaa Glu Lys	Xaa Lys Ala	Gln Gln	Glu Met	Leu Xaa	Xaa Gln	Gly Phe									
	45		50		55										
cag tcc ctc	atg gaa aca	gtg gat	acg gag	att gtc	acc cag	c	359								
Gln Ser Leu	Met Glu Thr	Val Asp	Thr Glu	Ile Val	Thr Gln										
	60		65		70										

<210> 3545
 <211> 340
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS

<222> 14..340

<400> 3545

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Met Gln Lys Ile Glu Glu Asn Arg Asp Cys Gln Leu
1 5 10
gaa aaa caa ata aaa gaa gaa act ctg gag caa aga gat ttt acc act 97
Glu Lys Gln Ile Lys Glu Glu Thr Leu Glu Gln Arg Asp Phe Thr Thr
15 20 25
aaa agc gaa aag ttt caa gaa gaa gaa ttt cag aat gac ata gag aaa 145
Lys Ser Glu Lys Phe Gln Glu Glu Glu Phe Gln Asn Asp Ile Glu Lys
30 35 40
gca att gat act cat aat cag aat gac ttg act ttc aga gta tct tgk 193
Ala Ile Asp Thr His Asn Gln Asn Asp Leu Thr Phe Arg Val Ser Xaa
45 50 55 60
cgc tgc agt gga act att gga aag gcc ttc act gca cag gta tgc ttg 241
Arg Cys Ser Gly Thr Ile Gly Lys Ala Phe Thr Ala Gln Val Cys Leu
65 70 75
cat cct aaa gtg gag tct gtc gcc cag gct gga atg cat trg cac aat 289
His Pro Lys Val Glu Ser Val Ala Gln Ala Gly Met His Xaa His Asn
80 85 90
ctg gct cac tgc aac cts cac cts cca ggt tca ggt gat tct ttt gcc 337
Leu Ala His Cys Asn Leu His Leu Pro Gly Ser Gly Asp Ser Phe Ala
95 100 105
tca 340
Ser

<210> 3546

<211> 301

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 54..299

<400> 3546

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Met
1
tat cag cac att tca cct gat ttg agt cga cgc ttt cct ccc cgt tca 104
Tyr Gln His Ile Ser Pro Asp Leu Ser Arg Arg Phe Pro Pro Arg Ser
5 10 15
gaa gtg acg aga ctg tat gga tgc gtt tgt gat tta agg acg aac aaa 152
Glu Val Thr Arg Leu Tyr Gly Ser Val Cys Asp Leu Arg Thr Asn Lys
20 25 30
ctt ccc ggt tcc cct ggg cta agc aaa tct atg ttt gat ctt aca aac 200
Leu Pro Gly Ser Pro Gly Leu Ser Lys Ser Met Phe Asp Leu Thr Asn
35 40 45
tca tct cag cga ttc atc cag aga cat gat tca ttg tcc agt gta ccc 248
Ser Ser Gln Arg Phe Ile Gln Arg His Asp Ser Leu Ser Ser Val Pro
50 55 60 65

agt agt tct tct tca agg aaa aak nct cag ggg agt aac aga agc ctg 296
 Ser Ser Ser Ser Ser Arg Lys Xaa Xaa Gln Gly Ser Asn Arg Ser Leu
 70 75 80

gat at 301
 Asp

<210> 3547
 <211> 438
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 53..436

<400> 3547
 tatttgcccc ttactttatc ttgtgccttg agaaattgct ggggagagag gt atg tcc 58
 Met Ser
 1
 act ggg cag ctg tac agg atg gag gat ata ggg cgt ttc cac tcc cag 106
 Thr Gly Gln Leu Tyr Arg Met Glu Asp Ile Gly Arg Phe His Ser Gln
 5 10 15
 cag cca ggt tcc ctc acc cca agc tca ccc act gtt ggg gag att atc 154
 Gln Pro Gly Ser Leu Thr Pro Ser Ser Pro Thr Val Gly Glu Ile Ile
 20 25 30
 tac aat aac acc aga aac aca ttg ggg tgg att ggg ggt atc ctt atg 202
 Tyr Asn Asn Thr Arg Asn Thr Leu Gly Trp Ile Gly Gly Ile Leu Met
 35 40 45 50
 ggt tct ttt cag gga acc att gct gga caa ggc aca gga gcc acc tcc 250
 Gly Ser Phe Gln Gly Thr Ile Ala Gly Gln Gly Thr Gly Ala Thr Ser
 55 60 65
 att tct gag ctc tgc aag gga caa gaa cta gag cca tca ggg gct ggg 298
 Ile Ser Glu Leu Cys Lys Gly Gln Glu Leu Glu Pro Ser Gly Ala Gly
 70 75 80
 ctc act gtg gcc cca ccc caa gcc gtc agc ctc cag gga tca cac cct 346
 Leu Thr Val Ala Pro Pro Gln Ala Val Ser Leu Gln Gly Ser His Pro
 85 90 95
 gcc ttg gct gct aca gct ttt tca ctc cas tgc cct agg gga gtt cag 394
 Ala Leu Ala Ala Thr Ala Phe Ser Leu Xaa Cys Pro Arg Gly Val Gln
 100 105 110
 cas cta atg atc tct atc tct gaa cat ctc ttc atc cat gct cc 438
 Xaa Leu Met Ile Ser Ile Ser Glu His Leu Phe Ile His Ala
 115 120 125

<210> 3548
 <211> 398
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 125..397

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<400> 3548
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attagaatcc aaacaaggaa aacgaatcaa aaacaggggt gagataaagg tcaatattca      120
gttt atg agg aac aat atg acc gca agt atg ttt gac tta tca atg aag      169
    Met Arg Asn Asn Met Thr Ala Ser Met Phe Asp Leu Ser Met Lys
      1          5          10          15
gac aaa acc aga tct cct ttt gca aag tta aaa gat aag atg aag ggt      217
Asp Lys Thr Arg Ser Pro Phe Ala Lys Leu Lys Asp Lys Met Lys Gly
      20          25          30
aga aaa aat gat gga aca ttt tct gat acg tct tct gca atc att cca      265
Arg Lys Asn Asp Gly Thr Phe Ser Asp Thr Ser Ser Ala Ile Ile Pro
      35          40          45
agt act cac atg ccc gat gcc aat agt gaa ttt tca agt ggt gaa ata      313
Ser Thr His Met Pro Asp Ala Asn Ser Glu Phe Ser Ser Gly Glu Ile
      50          55          60
cag atg aaa tcc aaa cca aaa aag cct ttt ctc ttg ggt cct cag cga      361
Gln Met Lys Ser Lys Pro Lys Lys Pro Phe Leu Leu Gly Pro Gln Arg
      65          70          75
ctc tcg tca gcg cat tca atg tct gat tta tct ggg t      398
Leu Ser Ser Ala His Ser Met Ser Asp Leu Ser Gly
      80          85          90

<210> 3549
<211> 314
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 100..312

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gctgaagagt tttatactgt gaggtgccaa gtggctgat atg aag aac att tat      114
                                Met Lys Asn Ile Tyr
                                  1          5
gaa tct ctt gat gaa gtt act ata aaa gac act ttg gaa ggt gat aac      162
Glu Ser Leu Asp Glu Val Thr Ile Lys Asp Thr Leu Glu Gly Asp Asn
                                  10          15          20
atg tat act tgt tct cat tgt ggg aag aaa gta cga gct gaa aaa agg      210
Met Tyr Thr Cys Ser His Cys Gly Lys Lys Val Arg Ala Glu Lys Arg
                                  25          30          35
gca tgt ttt aag aaa ttg cct cgc att ttg agt ttc aat act atg aga      258
Ala Cys Phe Lys Lys Leu Pro Arg Ile Leu Ser Phe Asn Thr Met Arg
                                  40          45          50
tac aca ttt aat atg gtc acg atg atg aaa gag aaa gtg aat aca cac      306
Tyr Thr Phe Asn Met Val Thr Met Met Lys Glu Lys Val Asn Thr His
                                  55          60          65
ttt tcc tt      314
Phe Ser
70

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<210> 3550
 <211> 278
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 70..276

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 tcactgtag atg gct tta cag acc cat caa att cag aga ggg ttc tgc tta 111
 Met Ala Leu Gln Thr His Gln Ile Gln Arg Gly Phe Cys Leu
 1 5 10
 ggt tca ctc tcc aat gtt aac cga aat gcc acg gta gaa atg aca aga 159
 Gly Ser Leu Ser Asn Val Asn Arg Asn Ala Thr Val Glu Met Thr Arg
 15 20 25 30
 agg cat ata gga aga gga gtg cgc tta tac tac ata ggt ggg gaa gtt 207
 Arg His Ile Gly Arg Gly Val Arg Leu Tyr Tyr Ile Gly Gly Glu Val
 35 40 45
 ttt gct gag tgc cta agt gat agt gca atc ttt gtg cag agc ccc aat 255
 Phe Ala Glu Cys Leu Ser Asp Ser Ala Ile Phe Val Gln Ser Pro Asn
 50 55 60
 tgt aat cag aga tat ggc tgg cg 278
 Cys Asn Gln Arg Tyr Gly Trp
 65

<210> 3551
 <211> 220
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 45..218

<400> 3551
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 Met Arg Ala Pro
 1
 aga aac tct agc cta ctc tca tat tct cca gct agc aam cct cag caa 104
 Arg Asn Ser Ser Leu Leu Ser Tyr Ser Pro Ala Ser Xaa Pro Gln Gln
 5 10 15 20
 tac aaa agc cag ttt ttc cca aag tcc cgg caa aaa tcc caa acc ctg 152
 Tyr Lys Ser Gln Phe Phe Pro Lys Ser Arg Gln Lys Ser Gln Thr Leu
 25 30 35
 att cta atc agg gtt gta tcc tca gtc ctg aaa aag atc ctt gag gca 200
 Ile Leu Ile Arg Val Val Ser Ser Val Leu Lys Lys Ile Leu Glu Ala
 40 45 50
 aag gaa tat gcc cat cgg tg 220
 Lys Glu Tyr Ala His Arg
 55

SECRET

SECRET

[illegible]

SECRET

[illegible]

SECRET

[illegible]

<211> 384
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 121..384

<400> 3554
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 tgcttggtggt gcaacgagaa agggaagtcc ttctactcca cagaagctgt acaggcacat 120
 atg aat gac aaa agc cac tgt aag ctc ttc aca gat ggc gat gct gct 168
 Met Asn Asp Lys Ser His Cys Lys Leu Phe Thr Asp Gly Asp Ala Ala
 1 5 10 15
 ttg gaa ttt gca gac ttc tat gat ttt agg agt agc tat cca gat cac 216
 Leu Glu Phe Ala Asp Phe Tyr Asp Phe Arg Ser Ser Tyr Pro Asp His
 20 25 30
 aag gaa ggg gag gac ccc aat aag gct gag gag ttg ccc tca gaa aag 264
 Lys Glu Gly Glu Asp Pro Asn Lys Ala Glu Glu Leu Pro Ser Glu Lys
 35 40 45
 aac ttg gaa tat gat gat gaa acc atg gaa ttg att ctg cct tct ggt 312
 Asn Leu Glu Tyr Asp Asp Glu Thr Met Glu Leu Ile Leu Pro Ser Gly
 50 55 60
 gcc aga gtg ggt cat gnn tcc ttg atg aga tac tac aaa cag cga ttt 360
 Ala Arg Val Gly His Xaa Ser Leu Met Arg Tyr Tyr Lys Gln Arg Phe
 65 70 75 80
 ggc ttg tca aga gct gtg gca gtt 384
 Gly Leu Ser Arg Ala Val Ala Val
 85

<210> 3555
 <211> 286
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 59..286

<400> 3555
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 atg aat gga agt agg act cta acg cac agc att agt gat gga caa ctt 106
 Met Asn Gly Ser Arg Thr Leu Thr His Ser Ile Ser Asp Gly Gln Leu
 1 5 10 15
 caa ggt ggc cag tcc aat agt gaa cta ttt cag cag gag ssa cag aca 154
 Gln Gly Gly Gln Ser Asn Ser Glu Leu Phe Gln Gln Glu Xaa Gln Thr
 20 25 30
 gca cca gct caa gtt cct caa ggc ttt aat gtt ttt gga atg tcc agt 202
 Ala Pro Ala Gln Val Pro Gln Gly Phe Asn Val Phe Gly Met Ser Ser
 35 40 45
 tcc tct ggt gct tca aat tca gca cca cat ctt gga ttt cac tta ggc 250
 Ser Ser Gly Ala Ser Asn Ser Ala Pro His Leu Gly Phe His Leu Gly

50 55 60
 agc aaa gga aca tct agc ctt tct caa caa act ccc 286
 Ser Lys Gly Thr Ser Ser Leu Ser Gln Gln Thr Pro
 65 70 75

<210> 3556
 <211> 260
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 50..259

<400> 3556
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 Met Ala Ala
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 ttg gga gca ggt gag atg gaa tat aga ttt atg cta aaa caa gga gaa 106
 Leu Gly Ala Gly Glu Met Glu Tyr Arg Phe Met Leu Lys Gln Gly Glu
 5 10 15
 agg aga gag gag caa tca gct tat gat gaa aag gca tca acc ata caa 154
 Arg Arg Glu Glu Gln Ser Ala Tyr Asp Glu Lys Ala Ser Thr Ile Gln
 20 25 30 35
 cag aag ttt tat tgg cca aac tgg aag cag gaa tca agg gga gat caa 202
 Gln Lys Phe Tyr Trp Pro Asn Trp Lys Gln Glu Ser Arg Gly Asp Gln
 40 45 50
 gag gga tta gac aat gtg gtg ggc tgg aaa gct gaa aat aca aat caa 250
 Glu Gly Leu Asp Asn Val Val Gly Trp Lys Ala Glu Asn Thr Asn Gln
 55 60 65
 ctg aag agg a 260
 Leu Lys Arg
 70

<210> 3557
 <211> 309
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 72..308

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 agaatggcgc t atg tgc agt tkg gcc cct ggc acc atg ggc ctt tgg ctt 110
 Met Cys Ser Xaa Ala Pro Gly Thr Met Gly Leu Trp Pro
 1 5 10
 gcc tgc tgc aga gta gcc ctg cct ggg cag tct cca ggc act gag cag 158
 Ala Cys Cys Arg Val Ala Leu Pro Gly Gln Ser Pro Gly Thr Glu Gln
 15 20 25
 gcc atc tgt ggc cag gct gag aga atg act ggc tgc ctt acc agc gtg 206

Ala	Ile	Cys	Gly	Gln	Ala	Glu	Arg	Met	Thr	Gly	Ser	Leu	Thr	Ser	Val		
30					35					40					45		
cat	ggg	aca	agg	agc	ttt	gga	gcv	tca	agg	ggg	tgt	tgc	tgg	cct	ggg	254	
His	Gly	Thr	Arg	Ser	Phe	Gly	Ala	Ser	Arg	Gly	Cys	Cys	Trp	Pro	Gly		
				50					55					60			
cta	gag	gga	aag	gtg	acc	atc	cgt	ctg	tcc	tcc	tgt	ctt	tct	att	agc	302	
Leu	Glu	Gly	Lys	Val	Thr	Ile	Arg	Leu	Ser	Ser	Cys	Leu	Ser	Ile	Ser		
			65					70					75				
gcc	tcc	t														309	
Ala	Ser																

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<220>
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 <222> 127..432

<400>	3558																
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ttatttttga	gctcgtgtga	agactgagaa	atcacgtagt	ccttcctgaa	accactaaga											120	
ggaaaa	atg	tct	gtg	aca	ctg	cat	aca	gat	gta	ggg	gat	att	aaa	att		168	
	Met	Ser	Val	Thr	Leu	His	Thr	Asp	Val	Gly	Asp	Ile	Lys	Ile			
	1				5					10							
gaa	gtc	ttc	tgt	gag	agg	aca	ccc	aaa	aca	tgt	gag	aat	ttc	ttg	gct	216	
Glu	Val	Phe	Cys	Glu	Arg	Thr	Pro	Lys	Thr	Cys	Glu	Asn	Phe	Leu	Ala		
15					20					25				30			
ctt	tgt	gcc	agt	aat	tac	tac	aat	ggc	tgt	ata	tty	cat	agg	aat	atc	264	
Leu	Cys	Ala	Ser	Asn	Tyr	Tyr	Asn	Gly	Cys	Ile	Phe	His	Arg	Asn	Ile		
				35				40					45				
aag	ggg	ttc	atg	ggt	caa	aca	gga	gat	cca	aca	gga	act	gga	aga	gga	312	
Lys	Gly	Phe	Met	Val	Gln	Thr	Gly	Asp	Pro	Thr	Gly	Thr	Gly	Arg	Gly		
			50				55					60					
ggc	aac	agt	att	tgg	ggc	aag	aag	ttt	gag	gat	gaa	tac	agt	gaa	tat	360	
Gly	Asn	Ser	Ile	Trp	Gly	Lys	Lys	Phe	Glu	Asp	Glu	Tyr	Ser	Glu	Tyr		
		65					70					75					
ctt	aag	cac	aat	ggt	aga	ggg	ggt	gta	tct	atg	gct	aat	aat	ggc	cga	408	
Leu	Lys	His	Asn	Val	Arg	Gly	Val	Val	Ser	Met	Ala	Asn	Asn	Gly	Arg		
		80				85					90						
aca	cca	atg	gat	ctc	agt	tct	tca	tc								434	
Thr	Pro	Met	Asp	Leu	Ser	Ser	Ser										
95						100											

<210> 3559
 <211> 243
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 24..242

004220 "022400" 0951399

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                        Met Gln Asp Leu Arg Met Leu Met Pro His
                        1           5           10

tct aaa gca gat act aaa atg gat cgt aag gat aag cta ttt gtg att      101
Ser Lys Ala Asp Thr Lys Met Asp Arg Lys Asp Lys Leu Phe Val Ile
                        15           20           25

aac gag gtt tgt gaa atg aag aac tgt aat aaa tgc atc tat ttt gaa      149
Asn Glu Val Cys Glu Met Lys Asn Cys Asn Lys Cys Ile Tyr Phe Glu
                        30           35           40

gct aag aaa aaa cag gat ctc tat atg tgg ctt tca aat tca cct cac      197
Ala Lys Lys Lys Gln Asp Leu Tyr Met Trp Leu Ser Asn Ser Pro His
                        45           50           55

gga cca tct gct aaa ttc ctt gtt caa aat att cat acc ctc gct a      243
Gly Pro Ser Ala Lys Phe Leu Val Gln Asn Ile His Thr Leu Ala
                        60           65           70
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<210> 3560
<211> 211
<212> DNA
<213> Homo sapiens
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<220>
<221> CDS
<222> 22..210
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<400> 3560
taagcaggta agtatcaaaa a atg atg gac ttc cta cag act att ttt tat      51
                        Met Met Asp Phe Leu Gln Thr Ile Phe Tyr
                        1           5           10

tat tat tat act tta agt tct agg gta cat gtg cag aac atg cag gtt      99
Tyr Tyr Tyr Thr Leu Ser Ser Arg Val His Val Gln Asn Met Gln Val
                        15           20           25

tgt tac ata ggt ata cac gtg cca tgg tgg ttt gct gca ccc atc aac      147
Cys Tyr Ile Gly Ile His Val Pro Trp Trp Phe Ala Ala Pro Ile Asn
                        30           35           40

ccg tca tct aca tta ggt att act cct aat ttt ccc cta ctc ccc aac      195
Pro Ser Ser Thr Leu Gly Ile Thr Pro Asn Phe Pro Leu Leu Pro Asn
                        45           50           55

ccc ctg aca ggc cct a      211
Pro Leu Thr Gly Pro
                        60
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<210> 3561
<211> 333
<212> DNA
<213> Homo sapiens
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<220>
<221> CDS
<222> 55..333
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tgc aac ggt cat tca ccc agg tca cat tac ctt cct tct ctc cct cag c 341
 Cys Asn Gly His Ser Pro Arg Ser His Tyr Leu Pro Ser Leu Pro Gln
 90 95 100

<210> 3563
 <211> 358
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 99..356

<400> 3563
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 ccaggagcat cttacccgac ctcttggtcac cgtaccaa atg gcg atc cga gca aaa 116
 Met Ala Ile Arg Ala Lys
 1 5
 aga ctg gaa gag agc cga gcg gcg rcg ctc cga gag ctc cag gag aag 164
 Arg Leu Glu Glu Ser Arg Ala Ala Xaa Leu Arg Glu Leu Gln Glu Lys
 10 15 20
 cag gct ctg atg gag cag cag aga cga gag ama agg gca ctg cag gag 212
 Gln Ala Leu Met Glu Gln Gln Arg Arg Glu Xaa Arg Ala Leu Gln Glu
 25 30 35
 tgg aga gag cga gcc cag agg atg agg aag agg aag gaa gag ctc agc 260
 Trp Arg Glu Arg Ala Gln Arg Met Arg Lys Arg Lys Glu Glu Leu Ser
 40 45 50
 aaa ctc ctg cct ccg cgg agg agc atg gtg gca tca aag att ccc tct 308
 Lys Leu Leu Pro Pro Arg Arg Ser Met Val Ala Ser Lys Ile Pro Ser
 55 60 65 70
 gcc aca gnb bcg ata gat aac agg aaa gta cca ctg aat ccg cct gga 356
 Ala Thr Xaa Xaa Ile Asp Asn Arg Lys Val Pro Leu Asn Pro Pro Gly
 75 80 85
 aa 358

<210> 3564
 <211> 359
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 91..357

<400> 3564
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 gtcattaggg aaatataaat ttaaaccata atg aga tac cac tgc ata ctc cct 114
 Met Arg Tyr His Cys Ile Leu Pro
 1 5
 aga atg gct gta atg aat agg att agt cac atg gtg aca aga atg gag 162
 Arg Met Ala Val Met Asn Arg Ile Ser His Met Val Thr Arg Met Glu
 10 15 20

gat cat ctg gaa ctc tca tac act gac gat agg aat gtg aaa tgg atc	210
Asp His Leu Glu Leu Ser Tyr Thr Asp Asp Arg Asn Val Lys Trp Ile	
25 30 35 40	
aac tac ttt gga aga caa ttg ggc agt ttc ttt caa agt aaa tgt gaa	258
Asn Tyr Phe Gly Arg Gln Leu Gly Ser Phe Phe Gln Ser Lys Cys Glu	
45 50 55	
gat gcc ata cga ttc atc cat tcc att tct gmt tat tca aga gah atg	306
Asp Ala Ile Arg Phe Ile His Ser Ile Ser Xaa Tyr Ser Arg Xaa Met	
60 65 70	
aaa ctg tat atc cac aaa aga gac ttg tac aca arc att cac agc agc	354
Lys Leu Tyr Ile His Lys Arg Asp Leu Tyr Thr Xaa Ile His Ser Ser	
75 80 85	
tat ta	359
Tyr	

<210> 3565
 <211> 341
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 22..339

<400> 3565	
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Met Leu Glu Thr Ala Ser Lys Leu Leu Leu	
1 5 10	
tca ggt act gct gat ggt gca gac ctc agg aca gta gat cca gaa aca	99
Ser Gly Thr Ala Asp Gly Ala Asp Leu Arg Thr Val Asp Pro Glu Thr	
15 20 25	
cag gct aga ctg gaa gct tta cta gaa gct gca gga ata gga aaa ttg	147
Gln Ala Arg Leu Glu Ala Leu Leu Glu Ala Ala Gly Ile Gly Lys Leu	
30 35 40	
tcc acg gct gat ggt aaa gcc ttt gca gat cct gaa gta ctt cgg agg	195
Ser Thr Ala Asp Gly Lys Ala Phe Ala Asp Pro Glu Val Leu Arg Arg	
45 50 55	
ttg aca tcg tct gtt agt tgt gcg ttg gat gaa gct gct gct gca ctt	243
Leu Thr Ser Ser Val Ser Cys Ala Leu Asp Glu Ala Ala Ala Leu	
60 65 70	
acc cgt atg aga gct gaa agc aca gca aat gca ggg cag tcg gac aac	291
Thr Arg Met Arg Ala Glu Ser Thr Ala Asn Ala Gly Gln Ser Asp Asn	
75 80 85 90	
cgc agt ttg gca gaa gcc tgt tca gaa gga gat gta aat gct gtg cga	339
Arg Ser Leu Ala Glu Ala Cys Ser Glu Gly Asp Val Asn Ala Val Arg	
95 100 105	
aa	341

<210> 3566
 <211> 342
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 157..342

<400> 3566
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 ctgtagatcc tattccagtt cccaggacat attccaacct cgacctccag ccaactttga 120
 acccctgaag ttgtgtgctg atgtgtttct aacaac atg gtc tca ccc aaa gat 174
 Met Val Ser Pro Lys Asp
 1 5
 ctt cct ctt gtg ctt ttg cag gac att aaa gtt ccc agc tcc atg act 222
 Leu Pro Leu Val Leu Leu Gln Asp Ile Lys Val Pro Ser Ser Met Thr
 10 15 20
 gga tca cat gct gga aac cct cat ata gaa agg aat gat ctc ccc aga 270
 Gly Ser His Ala Gly Asn Pro His Ile Glu Arg Asn Asp Leu Pro Arg
 25 30 35
 cat ggt tct cct caa ttt ttt aca ggh hyg act tgt gct tct rca aac 318
 His Gly Ser Pro Gln Phe Phe Thr Gly Xaa Thr Cys Ala Ser Xaa Asn
 40 45 50
 cca tct cag tgt ctg gca gca ttt 342
 Pro Ser Gln Cys Leu Ala Ala Phe
 55 60

<210> 3567
 <211> 182
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 22..180

<400> 3567
 gcaggaaatg cagccgggag g atg ggc agg ttg tgg gat gct ccg ccg ttc 51
 Met Gly Arg Leu Trp Asp Ala Pro Pro Phe
 1 5 10
 cgc gac cac ccg cct ccc cgg ccc agc aga acc ggg tcc agg ctg ggg 99
 Arg Asp His Pro Pro Pro Arg Pro Ser Arg Thr Gly Ser Arg Leu Gly
 15 20 25
 gag gtg cta gcg gtg tat gca cct aag tcc acc tgg gcc tgg agg agg 147
 Glu Val Leu Ala Val Tyr Ala Pro Lys Ser Thr Trp Ala Trp Arg Arg
 30 35 40
 aca ggt gtg caa aag aaa ata tct cgg gac ccc cc 182
 Thr Gly Val Gln Lys Lys Ile Ser Arg Asp Pro
 45 50

<210> 3568
 <211> 306
 <212> DNA
 <213> Homo sapiens

<220>

<221> CDS
<222> 95..304

<400> 3568
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actggccatc agagaamsmc aaatcaaaac caca atg aga tac cat ctc aca cca 115
Met Arg Tyr His Leu Thr Pro
1 5
ggt agr atg gca atc att aar aag tcm bga aac aac agg tgc tgg aga 163
Val Arg Met Ala Ile Ile Lys Lys Ser Xaa Asn Asn Arg Cys Trp Arg
10 15 20
gga tgt gga gam ata gga aca ctt tta cac tgt tgg tgg gac tgt aaa 211
Gly Cys Gly Xaa Ile Gly Thr Leu Leu His Cys Trp Trp Asp Cys Lys
25 30 35
cta gtt caa cca ttg tgg aag tca gtg tgg cga ttc ctc agg gat cta 259
Leu Val Gln Pro Leu Trp Lys Ser Val Trp Arg Phe Leu Arg Asp Leu
40 45 50 55
gaa cta gaa ata cca ttt gac cca gcc atc cca tta ctg ggt ata ta 306
Glu Leu Glu Ile Pro Phe Asp Pro Ala Ile Pro Leu Leu Gly Ile
60 65 70

<210> 3569
<211> 399
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 233..397

<400> 3569
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aattgattcg gaaggccatg cagctaactt tgtagaaaca gaacaaattg tacactacaa 120
tgggagcaaa gcttcgtttg tacagactcg aggatcaata cctgttttct ggtcccaaag 180
accaaaccctc aagtacaaac cactgccaca gatcagcaaa gtagcaaatac ac atg gac 238
Met Asp
1
ggt ttc caa agg cat ttt gat tcc caa gta att att tat gga aaa caa 286
Gly Phe Gln Arg His Phe Asp Ser Gln Val Ile Ile Tyr Gly Lys Gln
5 10 15
ggt ata atc aat ctg att aac cag aag ggc tgc gag aag cca ctt gag 334
Val Ile Ile Asn Leu Ile Asn Gln Lys Gly Ser Glu Lys Pro Leu Glu
20 25 30
cag aca ttt gca aca atg gtg tct tcc ttg gga agt gga atg atg aga 382
Gln Thr Phe Ala Thr Met Val Ser Ser Leu Gly Ser Gly Met Met Arg
35 40 45 50
tac att gcc ttt gac tt 399
Tyr Ile Ala Phe Asp
55

<210> 3570
<211> 333

<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 171..332

<400> 3570
agaatctttc gggtccccctt cgggctgggc tccccgcagg aaccaggaac gggctggcca 60
ggaggacmww atggaccggg agaaggtgac agaggcaaag ccagaccctt cctgttccat 120
cttgacagagg ctgtcccaac gcgaggggct atcaaggact cacaactgc atg atg 176
Met Met
1
gcc gcc ctg ccg gag gac act gta gtt ttt gag aag cct gtg aag acc 224
Ala Ala Leu Pro Glu Asp Thr Val Val Phe Glu Lys Pro Val Lys Thr
5 10 15
atc cac tgg aac ggg tcc ttc cag gag gca gcc ttt ccc ggg gag acc 272
Ile His Trp Asn Gly Ser Phe Gln Glu Ala Ala Phe Pro Gly Glu Thr
20 25 30
ttt cca gtg tgc gta gag tgt gag gat gga gac cgg ttc ccg gcg cac 320
Phe Pro Val Ser Val Glu Cys Glu Asp Gly Asp Arg Phe Pro Ala His
35 40 45 50
cat gtc atc gtc a 333
His Val Ile Val

<210> 3571
<211> 359
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 93..359

<400> 3571
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ggaaagtga gttgtgtgat gaaggagctt ct atg cac cct tgt gat grc aca 113
Met His Pro Cys Asp Xaa Thr
1 5
tac tgt ggc cct ttt cca gaa tct gag ccg gaa gtg aag gct gta gct 161
Tyr Cys Gly Pro Phe Pro Glu Ser Glu Pro Glu Val Lys Ala Val Ala
10 15 20
aac ttc ctt cga aaa cac aga aag cac att agg gct tat ctc tcc ttt 209
Asn Phe Leu Arg Lys His Arg Lys His Ile Arg Ala Tyr Leu Ser Phe
25 30 35
cat gca tat gct cag atg tta ctg tat ccc tat tct tac aaa tat gca 257
His Ala Tyr Ala Gln Met Leu Leu Tyr Pro Tyr Ser Tyr Lys Tyr Ala
40 45 50 55
aca att ccc aat ttt aga tgt gtg gaa tct gca gst tat aaa gct gtg 305
Thr Ile Pro Asn Phe Arg Cys Val Glu Ser Ala Xaa Tyr Lys Ala Val
60 65 70
gat gca ctt cag tca gta tac ggg gta cga tac aga tat ggr cca gcc 353

Asp Ala Leu Gln Ser Val Tyr Gly Val Arg Tyr Arg Tyr Gly Pro Ala
 75 80 85

tcc aca
 Ser Thr

359

<210> 3572
 <211> 299
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 59..298

<400> 3572
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 atg agg cag cat cga caa ttt atg gac cgc acg cat tat ctg ctt aca 106
 Met Arg Gln His Arg Gln Phe Met Asp Arg Thr His Tyr Leu Leu Thr
 1 5 10 15
 ttc agc tct tca gaa amc ttg gcy waa ggc tat tgc tac gga cac ggt 154
 Phe Ser Ser Ser Glu Xaa Leu Ala Xaa Gly Tyr Cys Tyr Gly His Gly
 20 25 30
 agc caa cct gag cag agg tcc aga acc tcc ctt ttt caa aca att ata 202
 Ser Gln Pro Glu Gln Arg Ser Arg Thr Ser Leu Phe Gln Thr Ile Ile
 35 40 45
 gtt cca tta att cct agt att gtg gat aga gca cca aaa ggc aga act 250
 Val Pro Leu Ile Pro Ser Ile Val Asp Arg Ala Pro Lys Gly Arg Thr
 50 55 60
 ttc ggg gat gtc ctg cag cca gca aaa cct gaa tac aga gtg ggg gaa a 299
 Phe Gly Asp Val Leu Gln Pro Ala Lys Pro Glu Tyr Arg Val Gly Glu
 65 70 75 80

<210> 3573
 <211> 226
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 69..224

<400> 3573
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 gtaacgac atg gta cct acc atg agg gtg gtt gtg atg att aag caa gat 110
 Met Val Pro Thr Met Arg Val Val Val Met Ile Lys Gln Asp
 1 5 10
 aag gct tgt aaa rgg ctt amc tts agg grc cta caa aaa gtg cgt aaa 158
 Lys Ala Cys Lys Xaa Leu Xaa Xaa Arg Xaa Leu Gln Lys Val Arg Lys
 15 20 25 30
 aca tgg ttc cag ctg ggc gtg atg gct cgc gtc tgt ggt ctc aca ctt 206
 Thr Trp Phe Gln Leu Gly Val Met Ala Arg Val Cys Gly Leu Thr Leu
 35 40 45

tgg gag gcc ggg gcg ggc at
 Trp Glu Ala Gly Ala Gly
 50

226

<210> 3574
 <211> 306
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 70..306

<400> 3574
 gtagtagtga gtacgtgctg aggagcaaag gagtaaccaa gagatccagt gaccgacaga 60
 gcaagagcc atg ccg cgc cgg ggc ctg gtg gct ggg cca gac ttg gag tat 111
 Met Pro Arg Arg Gly Leu Val Ala Gly Pro Asp Leu Glu Tyr
 1 5 10
 ttt cag sgt cgc taw ttc acg ccg gcg gag gtg gcc caa cat aac agg 159
 Phe Gln Xaa Arg Xaa Phe Thr Pro Ala Glu Val Ala Gln His Asn Arg
 15 20 25 30
 ccc gaa gac ctc tgg gta tct tac ctg gga cgc gtg tac gac cta acg 207
 Pro Glu Asp Leu Trp Val Ser Tyr Leu Gly Arg Val Tyr Asp Leu Thr
 35 40 45
 tca ttg gca cag gaa tac aag ggg aac ctg ctg ctg aaa ccc atc gtg 255
 Ser Leu Ala Gln Glu Tyr Lys Gly Asn Leu Leu Leu Lys Pro Ile Val
 50 55 60
 gaa gtt gca ggc cag gat atc agc cac tgg ttt gat cca aag acc aga 303
 Glu Val Ala Gly Gln Asp Ile Ser His Trp Phe Asp Pro Lys Thr Arg
 65 70 75
 gtc 306
 Val

<210> 3575
 <211> 283
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 60..281

<400> 3575
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 atg gcg gac aaa acg cca ggc gga tct cag aag gcc agt tca aag acg 107
 Met Ala Asp Lys Thr Pro Gly Gly Ser Gln Lys Ala Ser Ser Lys Thr
 1 5 10 15
 aga tca tca gat gtt cat tca tck gga tct tca gat gca cat atg gat 155
 Arg Ser Ser Asp Val His Ser Ser Gly Ser Ser Asp Ala His Met Asp
 20 25 30
 gca tct gga ccc tca gat agt gat atg cca agt cgg aca cga cct aag 203
 Ala Ser Gly Pro Ser Asp Ser Asp Met Pro Ser Arg Thr Arg Pro Lys

35	40	45	
agc cca aga aaa cat aat tat agg aat gaa agt gcc cgt gaa agc ctt	251		
Ser Pro Arg Lys His Asn Tyr Arg Asn Glu Ser Ala Arg Glu Ser Leu			
50	55	60	
tgt gat tct cct cat cag aat ctc tca aga cc	283		
Cys Asp Ser Pro His Gln Asn Leu Ser Arg			
65	70		

<210> 3576
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 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 61..369

<400> 3576	
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atg aac ccg gac ctg cgc agg gag cgg gat tcc gcc agc ttc aac ccg	108
Met Asn Pro Asp Leu Arg Arg Glu Arg Asp Ser Ala Ser Phe Asn Pro	
1 5 10 15	
gag ctg ctt aca cac atc ctg gac ggc agc ccc gag aaa acc cgg cgc	156
Glu Leu Leu Thr His Ile Leu Asp Gly Ser Pro Glu Lys Thr Arg Arg	
20 25 30	
cgc cga gag atc gag aac atg atc ctg aac gac cca gac ttc cag cat	204
Arg Arg Glu Ile Glu Asn Met Ile Leu Asn Asp Pro Asp Phe Gln His	
35 40 45	
gag gac ttg aac ttc ctc act cgc agc cag cgt tat gag gtg gct gtc	252
Glu Asp Leu Asn Phe Leu Thr Arg Ser Gln Arg Tyr Glu Val Ala Val	
50 55 60	
agg aaa agt gcc atc atg gtg aag aag atg agg gag ttt ggc atc gct	300
Arg Lys Ser Ala Ile Met Val Lys Lys Met Arg Glu Phe Gly Ile Ala	
65 70 75 80	
gac cct tat gaa att atg tgg ttt aaa aat ttt gtg cac cga ggg cgg	348
Asp Pro Tyr Glu Ile Met Trp Phe Lys Asn Phe Val His Arg Gly Arg	
85 90 95	
cct gag cct ctg gat ctt cac tt	371
Pro Glu Pro Leu Asp Leu His	
100	

<210> 3577
 <211> 380
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 125..379

<400> 3577	
actagaccaa gtggccccctt atctcctttc tgaaccgctt gaataggcca cccttccttc	60

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aaactatctt cacaaaacaa tttttttaag catctaggat acctgctccc acacataatt 120
ttct atg tct cat ttc ttg gcc ttg gat ttt ata ctg ctg ctt ttc tac 169
    Met Ser His Phe Leu Ala Leu Asp Phe Ile Leu Leu Leu Phe Tyr
      1           5           10           15
ctg aag act aga atc cga att cct cat cta gct gta agg cca ctc tac 217
Leu Lys Thr Arg Ile Arg Ile Pro His Leu Ala Val Arg Pro Leu Tyr
      20           25           30
tac cag tta tcc ttc ttg gcc tcc ttt tct ttc cca act cca agg tct 265
Tyr Gln Leu Ser Phe Leu Ala Ser Phe Ser Phe Pro Thr Pro Arg Ser
      35           40           45
cca tca act tct gtt tcc ctg gaa tgg aat gaa caa gag ctt tgg ctt 313
Pro Ser Thr Ser Val Ser Leu Glu Trp Asn Glu Gln Glu Leu Trp Leu
      50           55           60
agc att ggt aat ctt tac aaa ctg gtt cct cat gca tcc cca tgc ccc 361
Ser Ile Gly Asn Leu Tyr Lys Leu Val Pro His Ala Ser Pro Cys Pro
      65           70           75
tgt agt tan ccc nct aam c 380
Cys Ser Xaa Pro Xaa Xaa
80           85

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<210> 3578
 <211> 357
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 <213> Homo sapiens

<220>
 <221> CDS
 <222> 158..355

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aagaccctgt tcctgggtgt cacgctcggc ctggccgctg cctgtcctt caaccytgga 120
ggaggaggat atcacagga cctggtacgt gaaggcc atg gtg gtc gat aag gac 175
                      Met Val Val Asp Lys Asp
                        1           5
ttt ccg gag gac agg agg ccc agg aag gtg tcc cca gtg aag gtg aca 223
Phe Pro Glu Asp Arg Arg Pro Arg Lys Val Ser Pro Val Lys Val Thr
      10           15           20
gcc ctg ggc ggt ggg aag ttg gaa gcc acg ttc acc ttc atg agg gag 271
Ala Leu Gly Gly Gly Lys Leu Glu Ala Thr Phe Thr Phe Met Arg Glu
      25           30           35
gat cgg tgc atc cag aag aaa atc ctg atg cgg aag acg gag gag cmt 319
Asp Arg Cys Ile Gln Lys Lys Ile Leu Met Arg Lys Thr Glu Glu Xaa
      40           45           50
ggc aaa tac agc gcc tat ggg ggc agg aag ctc atg ta 357
Gly Lys Tyr Ser Ala Tyr Gly Gly Arg Lys Leu Met
55           60           65

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<210> 3579
 <211> 329
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> 109..327

<400> 3579
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 gaattattgtg tggtttgtga tgagmcacat gtgtttcaaa atggccct atg ctt agg 117
 Met Leu Arg
 1
 cct acc gta tgt gaa cgg gag ctg tgt gtg ttt gct ttt caa acc ctg 165
 Pro Thr Val Cys Glu Arg Glu Leu Cys Val Phe Ala Phe Gln Thr Leu
 5 10 15
 gga gta atg aat gaa gct gct gat gaa ata gca act gga gct cag gtg 213
 Gly Val Met Asn Glu Ala Asp Glu Ile Ala Thr Gly Ala Gln Val
 20 25 30 35
 gta gat cta cta gta tcc atg tgt agg tct gcg ttg gaa tct cct aga 261
 Val Asp Leu Leu Val Ser Met Cys Arg Ser Ala Leu Glu Ser Pro Arg
 40 45 50
 aaa gtt gtg att ttc grg cca tat cct tct gtg gta gat cct aat gat 309
 Lys Val Val Ile Phe Xaa Pro Tyr Pro Ser Val Val Asp Pro Asn Asp
 55 60 65
 cct cag atg ttg gcc ttc aa 329
 Pro Gln Met Leu Ala Phe
 70

<210> 3580
 <211> 297
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 5..295

<400> 3580
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 Met Asn Phe Cys Lys Lys Pro Arg Xaa Cys His Ala Leu Leu Leu
 1 5 10 15
 ccg ccc tgg gct gga ctg gag gtg ggc atg cga ccc tca caa yac aca 97
 Pro Pro Trp Ala Gly Leu Glu Val Gly Met Arg Pro Ser Gln Xaa Thr
 20 25 30
 gct ggg gcm aaa gcc mgw hng ctg gcv agc amg sca gst tgg atg gga 145
 Ala Gly Ala Lys Ala Xaa Xaa Leu Ala Ser Xaa Xaa Xaa Trp Met Gly
 35 40 45
 gtg ggc acc tca gaa agt cac cag gac ttk ggg tca gga aca gtg gct 193
 Val Gly Thr Ser Glu Ser His Gln Asp Xaa Gly Ser Gly Thr Val Ala
 50 55 60
 ggg tgg gcc cag aac tgc ccc cac tgt scc cct acm cac cga tgg agc 241
 Gly Trp Ala Gln Asn Cys Pro His Cys Xaa Pro Thr His Arg Trp Ser
 65 70 75
 ccc cag ata gag ctg ggt ggc ctg ttt ctg cag ccc ttg ggc agt tct 289
 Pro Gln Ile Glu Leu Gly Gly Leu Phe Leu Gln Pro Leu Gly Ser Ser

297

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<210> 3581
<211> 293
<212> DNA
<213> Homo sapiens
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<220>  
<221> CDS  
<222> 72..293
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aacttgactc c atg tgc ctt act gtg tta ttg cac aag tgc tgg agt aag																110
Met Cys Leu Thr Val Leu Leu His Lys Cys Trp Ser Lys																
1 5 10																
gtt gga gtt ttc cca gat tcc agg tac cca atg act aca gta gat tat																158
Val Gly Val Phe Pro Asp Ser Arg Tyr Pro Met Thr Thr Val Asp Tyr																
15 20 25																
gaa aga gca gtt cag gtg aga gcc aag mta gaa aca cac aca tgc aaa																206
Glu Arg Ala Val Gln Val Arg Ala Lys Xaa Glu Thr His Thr Cys Lys																
30 35 40 45																
cct cag aaa aaa aag gat tcc caa aag tcc tct att ttg tca tgg aga																254
Pro Gln Lys Lys Lys Asp Ser Gln Lys Ser Ser Ile Leu Ser Trp Arg																
50 55 60																
ctt ttt tct cca ttt cac tgg tcc cac gaa aag gcc ctc																293
Leu Phe Ser Pro Phe His Trp Ser His Glu Lys Ala Leu																
65 70																

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<210> 3582
<211> 302
<212> DNA
<213> Homo sapiens
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<220>  
<221> CDS  
<222> 60..302
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atg	gcg	gga	mct	ggg	ggc	tsg	agg	gac	agg	gas	stc	acg	gat	ctg	ggc	107
Met	Ala	Gly	Xaa	Gly	Gly	Xaa	Arg	Asp	Arg	Xaa	Xaa	Thr	Asp	Leu	Gly	
1				5				10						15		
cac	ctg	ccg	gat	cca	act	gga	ata	ttc	tca	cta	gat	aaa	acc	att	ggc	155
His	Leu	Pro	Asp	Pro	Thr	Gly	Ile	Phe	Ser	Leu	Asp	Lys	Thr	Ile	Gly	
			20					25					30			
ctt	ggt	act	tat	ggc	aga	atc	tat	ttg	gga	ctt	cat	gag	aag	act	ggt	203
Leu	Gly	Thr	Tyr	Gly	Arg	Ile	Tyr	Leu	Gly	Leu	His	Glu	Lys	Thr	Gly	
		35					40					45				
gca	ttt	aca	gct	gtt	aaa	gtg	atg	aac	gct	cgt	aag	acc	cct	tta	cct	251

Ala	Phe	Thr	Ala	Val	Lys	Val	Met	Asn	Ala	Arg	Lys	Thr	Pro	Leu	Pro	
50						55					60					
gaa	ata	sga	agg	cga	gtg	aga	gtg	aat	aaa	tat	caa	aaa	tct	gtt	ggg	299
Glu	Ile	Xaa	Arg	Arg	Val	Arg	Val	Asn	Lys	Tyr	Gln	Lys	Ser	Val	Gly	
65					70					75					80	
tgc																302
Cys																

<210> 3583
 <211> 322
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 83..322

<400> 3583	
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aagaggagaa agaggcggaa aa atg twt ttg ttc ata aga agk aaa cgc tcc	112
Met Xaa Leu Phe Ile Arg Xaa Lys Arg Ser	
1 5 10	
tct gca tct gtt gat aat acc cca gcg ggc tct ccc cag gga agt ggg	160
Ser Ala Ser Val Asp Asn Thr Pro Ala Gly Ser Pro Gln Gly Ser Gly	
15 20 25	
ggg gaa gat gag gat gac cca gat gaa ggg gat gat gat tcc cta agt	208
Gly Glu Asp Glu Asp Asp Pro Asp Glu Gly Asp Asp Asp Ser Leu Ser	
30 35 40	
gaa ggc agt aca tcc gag cag cag gat gag cta cag gaa gaa tca gaa	256
Glu Gly Ser Thr Ser Glu Gln Gln Asp Glu Leu Gln Glu Glu Ser Glu	
45 50 55	
atg tca gaa aaa aag tca tgc tcc tct tct ccc acc caa agt gag ata	304
Met Ser Glu Lys Lys Ser Cys Ser Ser Ser Pro Thr Gln Ser Glu Ile	
60 65 70	
tcc aca tcg ctg cct caa	322
Ser Thr Ser Leu Pro Gln	
75 80	

<210> 3584
 <211> 259
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 82..258

<400> 3584	
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ggcgctggga agtcgtccaa g atg att aaa aaa ttc gac aag aag gac gag	111
Met Ile Lys Lys Phe Asp Lys Lys Asp Glu	
1 5 10	

gag tct ggt agt ggc tcc aat cct ttc cag cat ctg gag aag agt gct	159
Glu Ser Gly Ser Gly Ser Asn Pro Phe Gln His Leu Glu Lys Ser Ala	
15 20 25	
ggt tta cag gag gct cgt ata ttc aat gaa act cca atc aat cca aga	207
Val Leu Gln Glu Ala Arg Ile Phe Asn Glu Thr Pro Ile Asn Pro Arg	
30 35 40	
aga tgt ttg cat att ctt aca aag att ctt tac tta ctg aac cag ggt	255
Arg Cys Leu His Ile Leu Thr Lys Ile Leu Tyr Leu Leu Asn Gln Gly	
45 50 55	
aac c	259
Asn	

<210> 3585
 <211> 295
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 141..293

<400> 3585	
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tkaaggytgc hnngttgctg gggagcgtcg gcgatgctct tggstacaga aatgtctgca	120
aggagaacag cactgtaggc atg aag atc cag gag gag ctg caa cgt tcc ggg	173
Met Lys Ile Gln Glu Glu Leu Gln Arg Ser Gly	
1 5 10	
ggc ctg gac crs ctc gta ctc tgc cca kga gaa tgg ccc gtg adt bac	221
Gly Leu Asp Xaa Leu Val Leu Ser Pro Xaa Glu Trp Pro Val Xaa Xaa	
15 20 25	
aac acc atc atg cac atc gca acc gcc gag gcc ctc acc aca gac tac	269
Asn Thr Ile Met His Ile Ala Thr Ala Glu Ala Leu Thr Thr Asp Tyr	
30 35 40	
tgg tgc ctg gat gat ctg tac cgg ga	295
Trp Cys Leu Asp Asp Leu Tyr Arg	
45 50	

<210> 3586
 <211> 337
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 116..337

<400> 3586	
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gctgcagcct gacttcaatg ctgaaaagtt ctcaggcctc tgggtacgtgg tckcc atg	118
Met	
1	
gca tct gac tgc agg gtc ttc ctg ggc aag aag gac cac ctg tcc atg	166

Ala	Ser	Asp	Cys	Arg	Val	Phe	Leu	Gly	Lys	Lys	Asp	His	Leu	Ser	Met	
			5					10					15			
tcc	acc	agg	gcc	atc	agg	ccc	aca	gag	gag	ggc	ggc	ctc	cac	gtc	cac	214
Ser	Thr	Arg	Ala	Ile	Arg	Pro	Thr	Glu	Glu	Gly	Gly	Leu	His	Val	His	
		20					25					30				
atg	gag	ttc	ccg	ggg	ncg	gac	ggc	tgt	aac	cag	gtg	gat	gcc	gag	tac	262
Met	Glu	Phe	Pro	Gly	Xaa	Asp	Gly	Cys	Asn	Gln	Val	Asp	Ala	Glu	Tyr	
		35				40					45					
ctg	aag	gtg	ggc	kcc	gag	gga	cac	ttc	aga	gtc	ccg	gcc	ttg	ggc	tac	310
Leu	Lys	Val	Gly	Xaa	Glu	Gly	His	Phe	Arg	Val	Pro	Ala	Leu	Gly	Tyr	
50					55					60					65	
ctg	gac	gtg	cgc	atc	gtg	gac	aca	gac								337
Leu	Asp	Val	Arg	Ile	Val	Asp	Thr	Asp								
					70											

<210> 3587

<211> 426

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 3..425

<400> 3587

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Met	Asp	Met	Asp	His	Ile	Met	Thr	Trp	Ala	Thr	Asp	Val	Ala	Lys		
1				5					10				15			
gga	atg	cat	tat	tta	cat	atg	gag	gct	cct	gtc	aag	gtg	att	cac	aga	95
Gly	Met	His	Tyr	Leu	His	Met	Glu	Ala	Pro	Val	Lys	Val	Ile	His	Arg	
			20					25				30				
gac	ctc	aag	tca	aga	aac	gtt	gtt	ata	gct	gct	gat	gga	gta	ctg	aag	143
Asp	Leu	Lys	Ser	Arg	Asn	Val	Val	Ile	Ala	Ala	Asp	Gly	Val	Leu	Lys	
		35				40						45				
atc	tgt	gac	ttt	ggg	gcc	tct	cgg	ttc	cat	aac	cat	aca	aca	cac	atg	191
Ile	Cys	Asp	Phe	Gly	Ala	Ser	Arg	Phe	His	Asn	His	Thr	Thr	His	Met	
		50				55					60					
tcc	ttg	gtt	gga	act	ttc	cca	tgg	atg	gct	cca	gaa	gtt	atc	cag	agt	239
Ser	Leu	Val	Gly	Thr	Phe	Pro	Trp	Met	Ala	Pro	Glu	Val	Ile	Gln	Ser	
		65				70				75						
ctc	cct	gtg	tca	gaa	act	tgt	gac	aca	tat	tcc	tat	ggg	gtg	gtt	ctc	287
Leu	Pro	Val	Ser	Glu	Thr	Cys	Asp	Thr	Tyr	Ser	Tyr	Gly	Val	Val	Leu	
80					85				90				95			
tgg	gag	atg	cta	aca	agg	gag	gtc	ccc	ttt	aaa	ggg	ttg	gaa	gga	tta	335
Trp	Glu	Met	Leu	Thr	Arg	Glu	Val	Pro	Phe	Lys	Gly	Leu	Glu	Gly	Leu	
				100				105				110				
caa	gta	gct	tgg	ctt	gta	gtg	gma	aaa	aac	gag	aga	tta	acc	att	cca	383
Gln	Val	Ala	Trp	Leu	Val	Val	Xaa	Lys	Asn	Glu	Arg	Leu	Thr	Ile	Pro	
		115				120						125				
agc	agt	tgy	bcc	aga	agt	ttt	gct	gaa	ctg	tta	cat	cag	tgt	t		426
Ser	Ser	Cys	Xaa	Arg	Ser	Phe	Ala	Glu	Leu	Leu	His	Gln	Cys			
		130				135						140				

<210> 3588
 <211> 361
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 113..361

<400> 3588
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 attttttaaa acactgcttt cttcctcacc agagtatggg gcagagataa ta atg gac 118
 Met Asp
 1
 atc aat aca gct ggt att gat atg ccc atg ttt tct gct ttg tta cac 166
 Ile Asn Thr Ala Gly Ile Asp Met Pro Met Phe Ser Ala Leu Leu His
 5 10 15
 tac ctt tat aca gga gag ttt gga atg gag gac tca agg ttt caa aat 214
 Tyr Leu Tyr Thr Gly Glu Phe Gly Met Glu Asp Ser Arg Phe Gln Asn
 20 25 30
 gtc gat atc ctt gtt cag ctt agt gaa gaa ttt gga aca cca aat tcc 262
 Val Asp Ile Leu Val Gln Leu Ser Glu Glu Phe Gly Thr Pro Asn Ser
 35 40 45 50
 ctt gat gta gat atg cgt gga ctc ttt gak tac atg tgt tat taw ntg 310
 Leu Asp Val Asp Met Arg Gly Leu Phe Xaa Tyr Met Cys Tyr Xaa Xaa
 55 60 65
 tcg tmc tta gtt dat ctt cag act ctg aac tgg ttg aag ctt ttg gtg 358
 Ser Xaa Leu Val Xaa Leu Gln Thr Leu Asn Trp Leu Lys Leu Leu Val
 70 75 80
 gaa 361
 Glu

<210> 3589
 <211> 308
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 129..308

<400> 3589
 atcttggatc cgcgggacaa gaaaattcat gcgagggaga cgtggtgggc ggtccttcct 60
 gtgacacgac ccttgagtga cagtbckatt tgattgcctc cggtactgtg aggaaaggac 120
 acgactct atg gtg agg act gat gga cat aca tta tct gag aaa aga aac 170
 Met Val Arg Thr Asp Gly His Thr Leu Ser Glu Lys Arg Asn
 1 5 10
 tac cag gtg aca aac agc atg ttt ggt gct tca aga aag aag ttt gta 218
 Tyr Gln Val Thr Asn Ser Met Phe Gly Ala Ser Arg Lys Lys Phe Val
 15 20 25 30
 gag ggg gtc gac agt gac tac cat gac gaa aac atg tac tac agc cag 266
 Glu Gly Val Asp Ser Asp Tyr His Asp Glu Asn Met Tyr Tyr Ser Gln

35 40 45 308
 tct tct atg tdt cca cat cnd kca gaa aaa gat atg ctg gcc
 Ser Ser Met Xaa Pro His Xaa Xaa Glu Lys Asp Met Leu Ala
 50 55 60

<210> 3590
 <211> 311
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 116..310

<400> 3590
 aacagaagga gcagaaagaa ccaatgatga tagctcagct gaaactattg aaaagaaaga 60
 aaaagccaac ctagaggaac gggccatttg tgagtacaat gaaaacccaa aaggt atg 118
 Met
 1
 agc aca ttt gat aac ata cat ata tac ata cat aca tac aca cat ata 166
 Ser Thr Phe Asp Asn Ile His Ile Tyr Ile His Thr Tyr Thr His Ile
 5 10 15
 tat gtg tat gta tgc cat aat tgg gta att ata agc tta cat ata agt 214
 Tyr Val Tyr Val Cys His Asn Trp Val Ile Ile Ser Leu His Ile Ser
 20 25 30
 tta cat ata tgc tat aat ttt tac tgt cac atg atc ctc ata aca agc 262
 Leu His Ile Cys Tyr Asn Phe Tyr Cys His Met Ile Leu Ile Thr Ser
 35 40 45
 tat gaa ata tgt gat aca gac tta tct gtt ctt ata tat aac cac cag c 311
 Tyr Glu Ile Cys Asp Thr Asp Leu Ser Val Leu Ile Tyr Asn His Gln
 50 55 60 65

<210> 3591
 <211> 383
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 170..382

<400> 3591
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 atttagggaa atcaccagta acttgactga ccaattgatt ttagagagaa agtaaccaa 120
 ccaaataattt atctgggcaa agtcataaat tctccacttg aatgcgctc atg aaa aat 178
 Met Lys Asn
 1
 aag gcc aaa aca aga gtt ctg ggc cac agc tca gcc cag agg gtt cct 226
 Lys Ala Lys Thr Arg Val Leu Gly His Ser Ser Ala Gln Arg Val Pro
 5 10 15
 ggg gat ggg agg cct ctc tct ccc cac ccc ctg act cta gag aac tgg 274
 Gly Asp Gly Arg Pro Leu Ser Pro His Pro Leu Thr Leu Glu Asn Trp

20 25 30 35
 gtt ttc tcc cag tac tcc agc aat tca ttt ctg aaa gca gtt gag cca 322
 Val Phe Ser Gln Tyr Ser Ser Asn Ser Phe Leu Lys Ala Val Glu Pro
 40 45 50
 ctt tat tcc aaa gta cac tgc aga tgt tca aac tct cca ttt ctc ttt 370
 Leu Tyr Ser Lys Val His Cys Arg Cys Ser Asn Ser Pro Phe Leu Phe
 55 60 65
 ccc ctc cca cct a 383
 Pro Leu Pro Pro
 70

<210> 3592
 <211> 312
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 130..312

<400> 3592
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 gatgtttgat ggctgttgaa tgaacgtaag tgaatctgtt cagttttagg gttttattgc 120
 atttttgat atg gat tgt gcc agt ata tct gta aag ttc act tct atg gct 171
 Met Asp Cys Ala Ser Ile Ser Val Lys Phe Thr Ser Met Ala
 1 5 10
 acc atg cat gac ttg agt cag ttc tgg gct tct aga gga gag gtt aca 219
 Thr Met His Asp Leu Ser Gln Phe Trp Ala Ser Arg Gly Glu Val Thr
 15 20 25 30
 aac tgg tgg cca gta gga caa act agc cta cca ctg ttt tat ttg gct 267
 Asn Trp Trp Pro Val Gly Gln Thr Ser Leu Pro Leu Phe Tyr Leu Ala
 35 40 45
 ttc atg gtg ttt ggt tct ttt ttt cct tta att tcc tgc cag ccc 312
 Phe Met Val Phe Gly Ser Phe Phe Pro Leu Ile Ser Cys Gln Pro
 50 55 60

<210> 3593
 <211> 315
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 10..315

<400> 3593
 agagaaaaa atg aag agc aat gaa gct gca tcc aag gaa cta gct tct aaa 51
 Met Lys Ser Asn Glu Ala Ala Ser Lys Glu Leu Ala Ser Lys
 1 5 10
 aaa tcc cta cct atg aat tat tac aca gta ttc tac cat gtt caa gaa 99
 Lys Ser Leu Pro Met Asn Tyr Tyr Thr Val Phe Tyr His Val Gln Glu
 15 20 25 30

caa cta cct aga gac tgt ttc gtg gta agt gaa gga gca aat act atg	147
Gln Leu Pro Arg Asp Cys Phe Val Val Ser Glu Gly Ala Asn Thr Met	
35 40 45	
gac att gga cgg act gtg ctt cag aac tac ctt cct cgt cac agg ctt	195
Asp Ile Gly Arg Thr Val Leu Gln Asn Tyr Leu Pro Arg His Arg Leu	
50 55 60	
gat gct ggt act ttc gga aca atg gga gtt ggt ttg gga ttt gct att	243
Asp Ala Gly Thr Phe Gly Thr Met Gly Val Gly Leu Gly Phe Ala Ile	
65 70 75	
gca gct gcc gtg gtg gct aaa gat aga agc cct ggg caa tgg atc atc	291
Ala Ala Ala Val Val Ala Lys Asp Arg Ser Pro Gly Gln Trp Ile Ile	
80 85 90	
tgt gtg gaa gga gac agt gca ttt	315
Cys Val Glu Gly Asp Ser Ala Phe	
95 100	

<210> 3594

<211> 385

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 55..384

<400> 3594

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Met	
1	
aga caa aca rat cgg gat gta ata aca gca tta act cac aga cct tgg	105
Arg Gln Thr Xaa Arg Asp Val Ile Thr Ala Leu Thr His Arg Pro Trp	
5 10 15	
agc cta agc cat aca gga gat ggg aaa cca cgc tat gat act ttc tgg	153
Ser Leu Ser His Thr Gly Asp Gly Lys Pro Arg Tyr Asp Thr Phe Trp	
20 25 30	
aaa cat ttt ata ttt gtt atg atg gac att ttg ctc gat tgg agc atg	201
Lys His Phe Ile Phe Val Met Met Asp Ile Leu Leu Asp Trp Ser Met	
35 40 45	
cat aat atc ttg tgg tac ctg tgt gga att tca gct ttc ccc atg caa	249
His Asn Ile Leu Trp Tyr Leu Cys Gly Ile Ser Ala Phe Pro Met Gln	
50 55 60 65	
aag gat ttt gta tcc ccg gcc tac ttg aag rwg tgg tca gct aaa gga	297
Lys Asp Phe Val Ser Pro Ala Tyr Leu Lys Xaa Trp Ser Ala Lys Gly	
70 75 80	
atc cag gtt gtt ggt tgg act gtt aat acc ttt gat gaa aga gtt act	345
Ile Gln Val Val Gly Trp Thr Val Asn Thr Phe Asp Glu Arg Val Thr	
85 90 95	
acg aat ccc atc ttg gtt cca gct ata tca ctg aca gca t	385
Thr Asn Pro Ile Leu Val Pro Ala Ile Ser Leu Thr Ala	
100 105 110	

<210> 3595

<211> 311

<212> DNA
<213> Homo sapiens

<220>
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<222> 62..310

<400> 3595
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a atg aag cgg cgt ttg gat gac cag gag tca ccg gtg tat gca gcc cag 109
Met Lys Arg Arg Leu Asp Asp Gln Glu Ser Pro Val Tyr Ala Ala Gln
1 5 10 15
cag cgt cgg atc cct ggc agc aca gag gct ttt cct cac cag cac cgg 157
Gln Arg Arg Ile Pro Gly Ser Thr Glu Ala Phe Pro His Gln His Arg
20 25 30
gtg ctt gcc cct gcc cct cct gtg tat gaa gca gtg tct gag acc atg 205
Val Leu Ala Pro Ala Pro Val Tyr Glu Ala Val Ser Glu Thr Met
35 40 45
cag tca gct acg gga att cag tac tct gta aca ccc agc tac cag gtt 253
Gln Ser Ala Thr Gly Ile Gln Tyr Ser Val Thr Pro Ser Tyr Gln Val
50 55 60
tca gcc atg cca cag agc tcc ggc agt cat ggg ccc gct ata gca gca 301
Ser Ala Met Pro Gln Ser Ser Gly Ser His Gly Pro Ala Ile Ala Ala
65 70 75 80
gtt cat agc a 311
Val His Ser

<210> 3596
<211> 316
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 87..314

<400> 3596
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atcgcatcttc tacagcaatt gacgac atg gaa gcc tat act aag ctg aca gat 113
Met Glu Ala Tyr Thr Lys Leu Thr Asp
1 5
aac att ttt ctg gag att tta tac tct act gat ccc aaa ttg aaa gac 161
Asn Ile Phe Leu Glu Ile Leu Tyr Ser Thr Asp Pro Lys Leu Lys Asp
10 15 20 25
gca cga gag att tta aaa caa att gaa tac cgt aat cta ttc aag tat 209
Ala Arg Glu Ile Leu Lys Gln Ile Glu Tyr Arg Asn Leu Phe Lys Tyr
30 35 40
gtg ggt gag acg cag cca aca gga caa ata aag att aan agg gag gac 257
Val Gly Glu Thr Gln Pro Thr Gly Gln Ile Lys Ile Xaa Arg Glu Asp
45 50 55
tat gaa tct ctt cca aaa gag gtt gcc agt gct aaa ccc aaa gta ttg 305
Tyr Glu Ser Leu Pro Lys Glu Val Ala Ser Ala Lys Pro Lys Val Leu

004220"6667560

60 65 70 316
 cta gac gtg aa
 Leu Asp Val
 75

<210> 3597
 <211> 261
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 24..260

<400> 3597
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 Met Met Ile Ile Pro Lys Lys Ala Ser Thr
 1 5 10
 cta ttc att cgt tgr arg cat gaa tat gca ttc agc ttc gag ctt cca 101
 Leu Phe Ile Arg Xaa Xaa His Glu Tyr Ala Phe Ser Phe Glu Leu Pro
 15 20 25
 cag aca cca ctc gct acc tca ttc gaa ggc cga cat ggc agt gtg cgc 149
 Gln Thr Pro Leu Ala Thr Ser Phe Glu Gly Arg His Gly Ser Val Arg
 30 35 40
 tat tgg gtg aaa gcc gaa ttg cac agg cct tgg cta cta cca gta aaa 197
 Tyr Trp Val Lys Ala Glu Leu His Arg Pro Trp Leu Leu Pro Val Lys
 45 50 55
 tta aag aag gaa ttt aca gtc ttt gag cat ata gat atc aac act cct 245
 Leu Lys Lys Glu Phe Thr Val Phe Glu His Ile Asp Ile Asn Thr Pro
 60 65 70
 tca tta ctg tca ccc c 261
 Ser Leu Leu Ser Pro
 75

<210> 3598
 <211> 399
 <212> DNA
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<220>
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 <222> 60..398

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 atg ggg ctg ggg gcc gtc ccc ggg aga cag gcg gcc ttc cga gag gga 107
 Met Gly Leu Gly Ala Val Pro Gly Arg Gln Ala Ala Phe Arg Glu Gly
 1 5 10 15
 ctg gag cag gcc gtg cgg tat gcc aaa gcc ctg ggc tgt ccc agg atc 155
 Leu Glu Gln Ala Val Arg Tyr Ala Lys Ala Leu Gly Cys Pro Arg Ile
 20 25 30
 cac ctg atg gct ggc cga gta ccc cag gga gct gat cga ata gca gtc 203

004220"66667560

His	Leu	Met	Ala	Gly	Arg	Val	Pro	Gln	Gly	Ala	Asp	Arg	Ile	Ala	Val		
		35					40				45						
aag	gct	gag	atg	gag	gcc	gtt	ttt	ctg	gag	aac	ctg	agg	cat	gca	gct	251	
Lys	Ala	Glu	Met	Glu	Ala	Val	Phe	Leu	Glu	Asn	Leu	Arg	His	Ala	Ala		
		50					55				60						
ggg	gtt	ttg	gct	cag	gag	gac	ctc	gtg	gga	ctg	ctg	gag	ccc	atc	aac	299	
Gly	Val	Leu	Ala	Gln	Glu	Asp	Leu	Val	Gly	Leu	Leu	Glu	Pro	Ile	Asn		
65					70				75					80			
acc	cgc	atc	act	gac	ccc	cag	tac	ttc	ctg	gac	acg	ccc	agc	agg	cgg	347	
Thr	Arg	Ile	Thr	Asp	Pro	Gln	Tyr	Phe	Leu	Asp	Thr	Pro	Ser	Arg	Arg		
				85					90					95			
cag	cat	ctt	aca	gaa	ggg	agg	aag	acc	caa	cct	cca	att	aca	aat	gga	395	
Gln	His	Leu	Thr	Glu	Gly	Arg	Lys	Thr	Gln	Pro	Pro	Ile	Thr	Asn	Gly		
			100					105						110			
caa	c															399	
Gln																	

<210> 3599

<211> 314

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 11..313

<400> 3599

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	Met	Val	Asn	Phe	Pro	Gln	Lys	Ile	Ala	Gly	Glu	Leu	Tyr				
	1				5					10							
gga	cct	ctc	atg	ctg	gtc	ttc	act	ctg	gtt	gct	atc	cta	ctc	cat	ggg	97	
Gly	Pro	Leu	Met	Leu	Val	Phe	Thr	Leu	Val	Ala	Ile	Leu	Leu	His	Gly		
	15				20					25							
atg	aag	acg	tct	gac	act	att	atc	cgg	gag	ggc	acc	ctg	atg	ggc	aca	145	
Met	Lys	Thr	Ser	Asp	Thr	Ile	Ile	Arg	Glu	Gly	Thr	Leu	Met	Gly	Thr		
30					35				40					45			
gcc	att	ggc	acc	tgc	ttc	ggc	tac	tgg	ctg	gga	gtc	tca	tcc	ttc	att	193	
Ala	Ile	Gly	Thr	Cys	Phe	Gly	Tyr	Trp	Leu	Gly	Val	Ser	Ser	Phe	Ile		
				50					55					60			
tac	ttc	ctt	gcc	tac	ctg	tgc	aac	gcc	cag	atc	acc	atg	ctg	cag	atg	241	
Tyr	Phe	Leu	Ala	Tyr	Leu	Cys	Asn	Ala	Gln	Ile	Thr	Met	Leu	Gln	Met		
			65				70					75					
ttg	gca	ctg	ctg	ggc	tat	ggc	ctc	ttt	ggg	cat	tgc	att	gtc	ctg	ttc	289	
Leu	Ala	Leu	Leu	Gly	Tyr	Gly	Leu	Phe	Gly	His	Cys	Ile	Val	Leu	Phe		
			80				85				90						
atc	acc	tat	aat	atc	cac	ctc	cgc	c								314	
Ile	Thr	Tyr	Asn	Ile	His	Leu	Arg										
			95				100										

<210> 3600

<211> 319

<212> DNA

<213> Homo sapiens

<220>
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 <222> 2..319

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 Met Ser Ile Ile Gln Trp Lys Leu Val Glu Lys Leu Ser Leu Pro Gln
 1 5 10 15
 aat gag act gta gcg gat act act cta acc aaa gcc ccc gtc tct tcc 97
 Asn Glu Thr Val Ala Asp Thr Thr Leu Thr Lys Ala Pro Val Ser Ser
 20 25 30
 act gaa agt gtc atc caa tct aat act ccc aca ccg cct cct tct cag 145
 Thr Glu Ser Val Ile Gln Ser Asn Thr Pro Thr Pro Pro Ser Gln
 35 40 45
 ccc tta aat gag aca gct gaa gag gaa agt aga ata agc agt tct ccc 193
 Pro Leu Asn Glu Thr Ala Glu Glu Glu Ser Arg Ile Ser Ser Ser Pro
 50 55 60
 aca ctt ctg gag aac agc ctg gaa caa act gtg gag cca agt gaa gac 241
 Thr Leu Leu Glu Asn Ser Leu Glu Gln Thr Val Glu Pro Ser Glu Asp
 65 70 75 80
 cac agc gag gag gag agt gaa gag ggc agc gga gac ctt ggt gag cct 289
 His Ser Glu Glu Glu Ser Glu Glu Gly Ser Gly Asp Leu Gly Glu Pro
 85 90 95
 ctt tat gaa gag cca tgc aac gag ata agc 319
 Leu Tyr Glu Glu Pro Cys Asn Glu Ile Ser
 100 105

<210> 3601
 <211> 296
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 108..296

<400> 3601
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 tcttgctact ggctgggctc tttgggtcca cactgctttt atgagct atg aca ctc 116
 Met Thr Leu
 1
 acc gca aag gtc tgc agc ttc act cct gaa gcc agc gag acc acg agc 164
 Thr Ala Lys Val Cys Ser Phe Thr Pro Glu Ala Ser Glu Thr Thr Ser
 5 10 15
 cca ctg gga gga agg aac aag tcc aga ggc gcc acc tta aga gct gta 212
 Pro Leu Gly Gly Arg Asn Lys Ser Arg Gly Ala Thr Leu Arg Ala Val
 20 25 30 35
 gca ctc acc gcg agg gtc cgc ggc ttc att ctt gaa gtc agt gag acc 260
 Ala Leu Thr Ala Arg Val Arg Gly Phe Ile Leu Glu Val Ser Glu Thr
 40 45 50
 aag aac cca cca att cca gac aca act gcg ccc agc 296

Lys Asn Pro Pro Ile Pro Asp Thr Thr Ala Pro Ser
55 60

<210> 3602
<211> 311
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 140..310

<400> 3602
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tattacagag aggagcaacg gcggctatat atatgccttt aaattacacc aatgtaaact 120
gagtgcggca gctgtgaat atg gtc ggc aga cat cta ttc cct ccc cca cca 172
Met Val Gly Arg His Leu Phe Pro Pro Pro Pro
1 5 10
agt tct ttc tcc ctc tgt gat ttt tct ccc aaa ttt ctt ggt ttg ctt 220
Ser Ser Phe Ser Leu Cys Asp Phe Ser Pro Lys Phe Leu Gly Leu Leu
15 20 25
aaa ata agc tac ccc tct ctt ccc ctg tat tgt ctc ttc gcc acc tct 268
Lys Ile Ser Tyr Pro Ser Leu Pro Leu Tyr Cys Leu Phe Ala Thr Ser
30 35 40
tcc aaa aar att aat ttt cat ttt aga cct tta acc cca gaa g 311
Ser Lys Lys Ile Asn Phe His Phe Arg Pro Leu Thr Pro Glu
45 50 55

<210> 3603
<211> 303
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 68..301

<400> 3603
ttggctccgg atcgtgcgtg aggcggcttc gtgggcagcg agagtcacag acaagacagc 60
aagcagg atg gag cac tac cgg aaa gct ggc tct gta gag ctc cca gcg 109
Met Glu His Tyr Arg Lys Ala Gly Ser Val Glu Leu Pro Ala
1 5 10
cct tcc cca atg ccc cag cta cct cct gat acc ctt gag atg cgg gtc 157
Pro Ser Pro Met Pro Gln Leu Pro Pro Asp Thr Leu Glu Met Arg Val
15 20 25 30
cga gat ggc agc aaa att cgc aac ctg ctg ggg ttg gct ctg ggt cgg 205
Arg Asp Gly Ser Lys Ile Arg Asn Leu Leu Gly Leu Ala Leu Gly Arg
35 40 45
ttg gag ggc ggc agt gct cgg cat gta gtg ttc tca ggt tct ggc agg 253
Leu Glu Gly Gly Ser Ala Arg His Val Val Phe Ser Gly Ser Gly Arg
50 55 60
gct gca gga aag gct gtc agc tgc gct gag att gtc aag cgg cgg gtc 301

Ala Ala Gly Lys Ala Val Ser Cys Ala Glu Ile Val Lys Arg Arg Val
65 70 75

cc

303

<210> 3604
<211> 262
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 105..260

<400> 3604
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ccacatttcc tccttttctt ttcgacaaaa ccaccatcgt catc atg gcc cgt tct 116
Met Ala Arg Ser
1
cga tgg tca ctg tct ctt cgg agc tgt tgg gta cac ctg cag aaa ggc 164
Arg Trp Ser Leu Ser Leu Arg Ser Cys Trp Val His Leu Gln Lys Gly
5 10 15 20
tgt cac ttc aca ctt gga aga ttg cac agc ggc cag gca gag gcg ctc 212
Cys His Phe Thr Leu Gly Arg Leu His Ser Gly Gln Ala Glu Ala Leu
25 30 35
ctc act tcc cag cca agg cgg ccg ggc aga ggc gct cct cac ttc cca 260
Leu Thr Ser Gln Pro Arg Arg Pro Gly Arg Gly Ala Pro His Phe Pro
40 45 50
ga 262

<210> 3605
<211> 298
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 77..298

<400> 3605
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atattatttta ctttct atg cat cat ggc ctc aca cca ctg tta ctt ggt gta 112
Met His His Gly Leu Thr Pro Leu Leu Leu Gly Val
1 5 10
cat gag caa aaa cag caa gtg gtg aaa ttt tta atc aag aaa aaa gca 160
His Glu Gln Lys Gln Gln Val Val Lys Phe Leu Ile Lys Lys Lys Ala
15 20 25
aat tta aat gca ctg gat aga tat gga aga act gct ctc ata ctt gct 208
Asn Leu Asn Ala Leu Asp Arg Tyr Gly Arg Thr Ala Leu Ile Leu Ala
30 35 40
gta tgt tgt gga tcg gca agt ata gtc agc ctt cta ctt gag caa aac 256
Val Cys Cys Gly Ser Ala Ser Ile Val Ser Leu Leu Leu Glu Gln Asn
45 50 55 60

att gat gta tct tct caa gat cta tct gga cag acg gcc ccc 298
 Ile Asp Val Ser Ser Gln Asp Leu Ser Gly Gln Thr Ala Pro
 65 70

<210> 3606
 <211> 362
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 58..360

<400> 3606
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 atg gca gcc aga cga att aca cag gag act ttt gat gct gta tta caa 105
 Met Ala Ala Arg Arg Ile Thr Gln Glu Thr Phe Asp Ala Val Leu Gln
 1 5 10 15
 gaa aaa gcc aaa cga tat cac atg gat gcc agt ggt gag gct gta agc 153
 Glu Lys Ala Lys Arg Tyr His Met Asp Ala Ser Gly Glu Ala Val Ser
 20 25 30
 gaa act ctt cag ttt aaa gct caa gat ctc tta agg gca gtc cca aga 201
 Glu Thr Leu Gln Phe Lys Ala Gln Asp Leu Leu Arg Ala Val Pro Arg
 35 40 45
 tcc aga gca gag atg tat gat gac gtc cac agc gat ggc aga tac tcc 249
 Ser Arg Ala Glu Met Tyr Asp Asp Val His Ser Asp Gly Arg Tyr Ser
 50 55 60
 ctc agt gga tct gta gct cac tct aga gat gcc gga aga gaa ggc ctg 297
 Leu Ser Gly Ser Val Ala His Ser Arg Asp Ala Gly Arg Glu Gly Leu
 65 70 75 80
 aga agt gac gta ttt cca ggg cct tcc ttc aga tca agc aac cck kby 345
 Arg Ser Asp Val Phe Pro Gly Pro Ser Phe Arg Ser Ser Asn Pro Xaa
 85 90 95
 atc agt gat gac agc cg 362
 Ile Ser Asp Asp Ser
 100

<210> 3607
 <211> 358
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 41..358

<400> 3607
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 Met Glu Lys Leu Pro
 1 5
 agt ggc atg gaa att tct ttt gcc cct gcc acg tcc cat gag gcc cca 103
 Ser Gly Met Glu Ile Ser Phe Ala Pro Ala Thr Ser His Glu Ala Pro

	10		15		20	
gcc atg atg gat agt cac atc agc agc agt gat gct gct acc gag atg						151
Ala Met Met Asp Ser His Ile Ser Ser Ser Asp Ala Ala Thr Glu Met						
	25		30		35	
ctc agc cag ccc aac cac ccc agc ggc gaa gtc aag gct gaa aat aac						199
Leu Ser Gln Pro Asn His Pro Ser Gly Glu Val Lys Ala Glu Asn Asn						
	40		45		50	
att gag atg gtg ggc gag tcc cag gcg gcc aag gtc att gtc tct gtc						247
Ile Glu Met Val Gly Glu Ser Gln Ala Ala Lys Val Ile Val Ser Val						
	55		60		65	
gaa gat gct gtg cct acc ata ttc tgt ggc aag atc aaa ggc ctc tca						295
Glu Asp Ala Val Pro Thr Ile Phe Cys Gly Lys Ile Lys Gly Leu Ser						
70		75		80		85
ggg tgt cca cca aaa act tct cct tca aaa gag aag act ccg tgc ttc						343
Gly Cys Pro Pro Lys Thr Ser Pro Ser Lys Glu Lys Thr Pro Cys Phe						
	90		95		100	
agg gct atg aca tca						358
Arg Ala Met Thr Ser						
	105					

<210> 3608
 <211> 317
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 14..316

<400> 3608	
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Met Asp Phe Val Leu Leu Asn Phe Ala Glu Met Asn	
	10
aag ctc tgg gtg cga atg cag cat cag gga cat agc cga gat aga gaa	97
Lys Leu Trp Val Arg Met Gln His Gln Gly His Ser Arg Asp Arg Glu	
	15
aaa aga gaa cga gaa aga caa gaa ctg aga att tta gtg gga aca aat	145
Lys Arg Glu Arg Glu Arg Gln Glu Leu Arg Ile Leu Val Gly Thr Asn	
	30
ttg gtg cgc ctc agt cag ttg gaa ggt gta aat gtg gaa cgt tac aaa	193
Leu Val Arg Leu Ser Gln Leu Glu Gly Val Asn Val Glu Arg Tyr Lys	
	45
cag att gtt ttg act ggc ata ttg gag caa gtt gta aac tgt agg gat	241
Gln Ile Val Leu Thr Gly Ile Leu Glu Gln Val Val Asn Cys Arg Asp	
	65
gct ttg gct caa gaa tat ctc atg gag tgt att att cag gtt ttc mmt	289
Ala Leu Ala Gln Glu Tyr Leu Met Glu Cys Ile Ile Gln Val Phe Xaa	
	80
gat gaa ttt cac ctc cag act ttg aat c	317
Asp Glu Phe His Leu Gln Thr Leu Asn	
	95
	100

<210> 3609

<211> 168
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 7..168

<400> 3609
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 1 5 10
 gtg gaa ttt tac aaa atg ctc act aga gat cac tgc agt cat ttc cta 96
 Val Glu Phe Tyr Lys Met Leu Thr Arg Asp His Cys Ser His Phe Leu
 15 20 25 30
 agt gct tcc ttt gcc aca gac tgg cct ggg tcc ttt att tac ctt ccc 144
 Ser Ala Ser Phe Ala Thr Asp Trp Pro Gly Ser Phe Ile Tyr Leu Pro
 35 40 45
 tca ttc act ttc cct cgg cca ccc 168
 Ser Phe Thr Phe Pro Arg Pro Pro
 50

<210> 3610
 <211> 287
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 38..286

<400> 3610
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 Met Lys Val Thr Leu Ser
 1 5
 gct ttg gat act tct gag agt tct ttc aca cct ttg gtg gtc ata gaa 103
 Ala Leu Asp Thr Ser Glu Ser Ser Phe Thr Pro Leu Val Val Ile Glu
 10 15 20
 ctt gct cag gat gtc aaa gaa gaa acc aaa gaa tgg ctg aaa aac aga 151
 Leu Ala Gln Asp Val Lys Glu Glu Thr Lys Glu Trp Leu Lys Asn Arg
 25 30 35
 att ata gct aaa aaa aaa gat gga ggt gcc cag ttg ttg ttt aga cca 199
 Ile Ile Ala Lys Lys Lys Asp Gly Gly Ala Gln Leu Leu Phe Arg Pro
 40 45 50
 ttg tta aat aaa tat gaa caa gaa aca cta gaa aat cag aac tta tat 247
 Leu Leu Asn Lys Tyr Glu Gln Glu Thr Leu Glu Asn Gln Asn Leu Tyr
 55 60 65 70
 ctt gtt ggt gcc tcc aag att aga atg tta cta ggg gct c 287
 Leu Val Gly Ala Ser Lys Ile Arg Met Leu Leu Gly Ala
 75 80

<210> 3611

<211> 394
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 139..393

<400> 3611
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 ccaggcagaa agaaaccgtc tgctgctcaa gacccacagg acgccgggaa gactaaatga 120
 tcaactgcccc cagtgaat atg gtg aag aag ctg gtg atg gcc cag aag cgg 171
 Met Val Lys Lys Leu Val Met Ala Gln Lys Arg
 1 5 10
 gga gag aca cga gcc ctt tgc ctg ggt gta acc atg gtg gtg tgt gcc 219
 Gly Glu Thr Arg Ala Leu Cys Leu Gly Val Thr Met Val Val Cys Ala
 15 20 25
 gtc atc acc tac tac atc ctg gtc acg act gtg ctg ccc ctc tac cag 267
 Val Ile Thr Tyr Tyr Ile Leu Val Thr Thr Val Leu Pro Leu Tyr Gln
 30 35 40
 aaa agc gtg tgg acc cag gaa tcc aag tgc cac ctg att gag acc aac 315
 Lys Ser Val Trp Thr Gln Glu Ser Lys Cys His Leu Ile Glu Thr Asn
 45 50 55
 atc agg gac cag gag gag ctg aag ggc aag aag gtg ccc cag tac cca 363
 Ile Arg Asp Gln Glu Glu Leu Lys Gly Lys Lys Val Pro Gln Tyr Pro
 60 65 70 75
 tgc ctg tgg gtc aac gtg tca gct gcc ggc a 394
 Cys Leu Trp Val Asn Val Ser Ala Ala Gly
 80 85

<210> 3612
 <211> 461
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 103..459

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 catcccaact agagaagaag ggacaccttc ccctcctaac aa atg aat gag cgg 114
 Met Asn Glu Arg
 1
 gca att gca ggg gct ctc att gct gac ttc ttg tct ggc ctg gta cac 162
 Ala Ile Ala Gly Ala Leu Ile Ala Asp Phe Leu Ser Gly Leu Val His
 5 10 15 20
 tgg ggt gct gac aca tgg ggc tct gtg gag ctg ccc att gtg ggg aag 210
 Trp Gly Ala Asp Thr Trp Gly Ser Val Glu Leu Pro Ile Val Gly Lys
 25 30 35
 gct ttc atc cga ccc ttc cgg gag cac cac att gac cca aca gct atc 258
 Ala Phe Ile Arg Pro Phe Arg Glu His His Ile Asp Pro Thr Ala Ile

aca	cg	cac	gac	ttc	atc	gag	acc	aac	ggg	gac	aac	tgc	ctg	gtg	aca	306
Thr	Arg	His	Asp	Phe	Ile	Glu	Thr	Asn	Gly	Asp	Asn	Cys	Leu	Val	Thr	
	55						60				65					
ctg	ctg	ccg	ctg	cta	aac	atg	gcc	tac	aag	ttc	cg	acc	cac	agc	cct	354
Leu	Leu	Pro	Leu	Leu	Asn	Met	Ala	Tyr	Lys	Phe	Arg	Thr	His	Ser	Pro	
	70					75				80						
gaa	gcc	ctg	gag	cag	cta	tac	ccc	tgg	gag	tgc	ttc	gtc	ttc	tgc	ctg	402
Glu	Ala	Leu	Glu	Gln	Leu	Tyr	Pro	Trp	Glu	Cys	Phe	Val	Phe	Cys	Leu	
85					90				95						100	
atc	atc	ttc	ggc	acc	ttc	acc	aac	cag	atc	cac	aag	tgg	tcg	cac	acg	450
Ile	Ile	Phe	Gly	Thr	Phe	Thr	Asn	Gln	Ile	His	Lys	Trp	Ser	His	Thr	
				105					110					115		
tac	ttt	ggg	ct													461
Tyr	Phe	Gly														

<210> 3613
 <211> 457
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 158..457

<400> 3613																
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agctccaaca	tatgcattct	gaagaaagat	ggctgagatg	gacagaatgc	tttattttgg											120
aaagaaacaa	tgttctaggt	caaactgagt	ctaccaa	atg	cag	act	ttc	aca	atg							175
			Met	Gln	Thr	Phe	Thr	Met								
			1				5									
ggt	cta	gaa	gaa	atc	tgg	aca	agt	ctt	ttc	atg	tgg	ttt	ttc	tac	gca	223
Val	Leu	Glu	Glu	Ile	Trp	Thr	Ser	Leu	Phe	Met	Trp	Phe	Phe	Tyr	Ala	
		10					15					20				
ttg	att	cca	tn	ttg	ctc	aca	gat	gaa	gtg	gcc	att	ctg	cct	gcc	cct	271
Leu	Ile	Pro	Xaa	Leu	Leu	Thr	Asp	Glu	Val	Ala	Ile	Leu	Pro	Ala	Pro	
		25				30					35					
cag	aac	ctc	tct	gta	ctc	tca	acc	aac	atg	nag	cat	ctc	ttg	atg	tgg	319
Gln	Asn	Leu	Ser	Val	Leu	Ser	Thr	Asn	Met	Xaa	His	Leu	Leu	Met	Trp	
	40					45				50						
agc	cca	gtg	atc	gcg	cct	gga	gaa	aca	gtg	tac	tat	tct	gtc	gaa	tac	367
Ser	Pro	Val	Ile	Ala	Pro	Gly	Glu	Thr	Val	Tyr	Tyr	Ser	Val	Glu	Tyr	
55					60				65					70		
cag	ggg	gag	tac	gag	agc	ctg	tac	acg	agc	cac	atc	tgg	atc	ccc	agc	415
Gln	Gly	Glu	Tyr	Glu	Ser	Leu	Tyr	Thr	Ser	His	Ile	Trp	Ile	Pro	Ser	
				75				80						85		
agc	tgg	tgc	tca	ctc	act	gaa	ggt	cct	gag	tgt	gat	gtc	act			457
Ser	Trp	Cys	Ser	Leu	Thr	Glu	Gly	Pro	Glu	Cys	Asp	Val	Thr			
			90					95					100			

<210> 3614
 <211> 239
 <212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 63..239

<400> 3614

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ag atg gct tcc atg cac ata tca tct tta tgc tat agg aag tca cct      107
  Met Ala Ser Met His Ile Ser Ser Leu Cys Tyr Arg Lys Ser Pro
    1         5         10        15
gta tgc tct aag gtg ctc aaa ccc att act tcc agc cta ggc atc tct      155
Val Cys Ser Lys Val Leu Lys Pro Ile Thr Ser Ser Leu Gly Ile Ser
    20        25        30
cct tac att caa act tac ctg atc tct cat agc tgg tta atc aca aag      203
Pro Tyr Ile Gln Thr Tyr Leu Ile Ser His Ser Trp Leu Ile Thr Lys
    35        40        45
tac tgc cac atc tgc ctc ctg agt gtt ttg cca gcc      239
Tyr Cys His Ile Cys Leu Leu Ser Val Leu Pro Ala
    50        55
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<210> 3615

<211> 296

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 71..295

<400> 3615

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agagcctggc tgctggcggc cgggagcgcc gggacggggc gcgaascgga gstccgggac      60
gtggatacag atg aaa aga asc ama gaa ttg ata act mma aat cat agt      109
  Met Lys Arg Xaa Xaa Glu Leu Ile Thr Xaa Asn His Ser
    1         5         10
caa gag gha aca agt att ctt cgk tgn hgg aaa tgt aga maa tgt ata      157
Gln Glu Xaa Thr Ser Ile Leu Arg Xaa Xaa Lys Cys Arg Xaa Cys Ile
    15        20        25
gca agc tct ggt tgt ttt atg gag tat ctt gag aat caa gtg att aag      205
Ala Ser Ser Gly Cys Phe Met Glu Tyr Leu Glu Asn Gln Val Ile Lys
    30        35        40        45
gat ava gat gmt tca gtt gat gct caa aat att tgt cat gtg tgg cac      253
Asp Xaa Asp Xaa Ser Val Asp Ala Gln Asn Ile Cys His Val Trp His
    50        55        60
atg amt gta gaa gcc ctt cca gaa tgg ata agc tgc cta atc c      296
Met Xaa Val Glu Ala Leu Pro Glu Trp Ile Ser Cys Leu Ile
    65        70        75
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<210> 3616

<211> 358

<212> DNA

<213> Homo sapiens

<220>
 <221> CDS
 <222> 168..356

<400> 3616
 caaaaagcac ttacctgaaa attaaagctg aagggttttct ttactgattt gaagggcatc 60
 tgggaatttc atttcgtaga aactccactt aamcatggca agagtttctc aagatataaa 120
 aattctccct gattgtaaca agtactgaga cagtgaacaa atcctgt atg tca cat 176
 Met Ser His
 1
 ttg atg acc tta gca att ata cag aca ggg aaa atg ttt atc ttg att 224
 Leu Met Thr Leu Ala Ile Ile Gln Thr Gly Lys Met Phe Ile Leu Ile
 5 10 15
 tct gct aca gca aca ctg aag cca gag gtg tct gag ctt tgg cta atg 272
 Ser Ala Thr Ala Thr Leu Lys Pro Glu Val Ser Glu Leu Trp Leu Met
 20 25 30 35
 tca ctt gat gta ggt cag ccc tay tgt gag tgt caa ccc tgg ttt cta 320
 Ser Leu Asp Val Gly Gln Pro Tyr Cys Glu Cys Gln Pro Trp Phe Leu
 40 45 50
 aat gtg ctg ctg gag gaa tcc act tca ctt cca gtt ta 358
 Asn Val Leu Leu Glu Glu Ser Thr Ser Leu Pro Val
 55 60

<210> 3617
 <211> 228
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 70..228

<400> 3617
 agaaattgtt ccggatctcg ggtcggacac ggaagtcttc ctgcagtgtt tctggatgcg 60
 gggacaggg atg cgc agg aat tcc agt ctc agt ttc cag atg gag cga ccc 111
 Met Arg Arg Asn Ser Ser Leu Ser Phe Gln Met Glu Arg Pro
 1 5 10
 ctc gag gag caa gtc cag agc aag tss tgc tct agt caa ggc cgc aca 159
 Leu Glu Glu Gln Val Gln Ser Lys Xaa Ser Ser Ser Gln Gly Arg Thr
 15 20 25 30
 kka aca gga ggg tct gat gtc ctc cag atg cag aac agt gaa cac cat 207
 Xaa Thr Gly Gly Ser Asp Val Leu Gln Met Gln Asn Ser Glu His His
 35 40 45
 gga caa agc atc aag act cac 228
 Gly Gln Ser Ile Lys Thr His
 50

<210> 3618
 <211> 395
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 209..394

<400> 3618
 aatgtttaac gtgcccgaagt cccggcccac tgatactgga ggctgctgcc ccaggttggtg 60
 gaggggtgtgc ggtgcctggc gttggctcct gtggcccac ctgccaccgc ggctgctgga 120
 actgccttga aggaaggcgg acagcctgag ggcctgagt gtcagggttac caaggaaacc 180
 aagccagcca accaaggtct ggagaagg atg atg ccc cgt gtg gcc ccc gtg 232
 Met Met Pro Arg Val Ala Pro Val
 1 5
 gcc ctg cct gca gtg tgc agt gtg ggg ctg ggc aga gag gaa gav tcc 280
 Ala Leu Pro Ala Val Cys Ser Val Gly Leu Gly Arg Glu Glu Xaa Ser
 10 15 20
 tgg tta gcc aga ggt gcc acc gca gac tcc cca ggc agg gtt gat ggc 328
 Trp Leu Ala Arg Gly Ala Thr Ala Asp Ser Pro Gly Arg Val Asp Gly
 25 30 35 40
 cct gct ggg gtt ccc ctg gct cca ctg gct tgc tgt gac tgg gga cat 376
 Pro Ala Gly Val Pro Leu Ala Pro Leu Ala Cys Cys Asp Trp Gly His
 45 50 55
 tcc tta gct ttg agg caa c 395
 Ser Leu Ala Leu Arg Gln
 60

<210> 3619
 <211> 353
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 140..352

<400> 3619
 tactttkctc ttaaagtctc atgaagcaaa cagcaatgca gtgagattta gagtgtgcct 60
 gtcataaac aagcttttgg gaagtatdcc agaaaatgcw cagattgatg atgatgtgtt 120
 tgataaaatk aataaagcc atg ctt atk aga ttg aaa gat aag att cca aat 172
 Met Leu Xaa Arg Leu Lys Asp Lys Ile Pro Asn
 1 5 10
 gtg aga ata cag gca gtt ctg gcg ctt tca cga ctt cag gat ccc aag 220
 Val Arg Ile Gln Ala Val Leu Ala Leu Ser Arg Leu Gln Asp Pro Lys
 15 20 25
 gat gat gaa tgc cca gtg gtt aat gca tat gcd act ttg att gaa aat 268
 Asp Asp Glu Cys Pro Val Val Asn Ala Tyr Ala Thr Leu Ile Glu Asn
 30 35 40
 gat tca aat cca gaa gtt aga cgg gca gtg tta tca tgt att gca cca 316
 Asp Ser Asn Pro Glu Val Arg Arg Ala Val Leu Ser Cys Ile Ala Pro
 45 50 55
 tca gca aag act ttg cbd vaa att rta ggg cgc aca c 353
 Ser Ala Lys Thr Leu Xaa Xaa Ile Xaa Gly Arg Thr
 60 65 70

<210> 3620
 <211> 322
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 67..321

<400> 3620
 acaaagcttg cagggtaagt gacacaactt gaaactgctt ggccctcttt aaaaagaaat 60
 aataaa atg gga gag aat gaa gca agt tta cct aac acg tct ttg caa 108
 Met Gly Glu Asn Glu Ala Ser Leu Pro Asn Thr Ser Leu Gln
 1 5 10
 ggt aaa aag atg gcc tat cag aag gtc cat gca gat caa aga gct cca 156
 Gly Lys Lys Met Ala Tyr Gln Lys Val His Ala Asp Gln Arg Ala Pro
 15 20 25 30
 gga cac tca cag tac tta gac aat gat gac ctt caa gcc act gcc ctt 204
 Gly His Ser Gln Tyr Leu Asp Asn Asp Asp Leu Gln Ala Thr Ala Leu
 35 40 45
 gac tta gag tgg gac atg gag aag gaa cta gag gag tct ggt ttt gac 252
 Asp Leu Glu Trp Asp Met Glu Lys Glu Leu Glu Glu Ser Gly Phe Asp
 50 55 60
 caa ttc cag ctn nac agt gct gag aat cag aac cta ggg cat tca gag 300
 Gln Phe Gln Leu Xaa Ser Ala Glu Asn Gln Asn Leu Gly His Ser Glu
 65 70 75
 nct ata gac ctc aat ctt gat t 322
 Xaa Ile Asp Leu Asn Leu Asp
 80 85

<210> 3621
 <211> 437
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 58..435

<400> 3621
 agttagtgcc tggaccagga ccatcacact ggggaccggc ttctctgctc tcccggtt 57
 atg ggg gtc ggg gga atg atg ggt caa ggg tct tyc cga aga rrg cga 105
 Met Gly Val Gly Gly Met Met Gly Gln Gly Ser Xaa Arg Arg Xaa Arg
 1 5 10 15
 gaa agg aac agg cgc ctt caa aag ccc act tgg cga tgg gtt aca gta 153
 Glu Arg Asn Arg Arg Leu Gln Lys Pro Thr Trp Arg Trp Val Thr Val
 20 25 30
 aga gga agt ctg cat tat cac gag gag ctt gga aag gag gta aca cac 201
 Arg Gly Ser Leu His Tyr His Glu Glu Leu Gly Lys Glu Val Thr His
 35 40 45
 tca agg caa att tca agt aac tca tcc tgg agg cag ctg cct act ctg 249

Ser	Arg	Gln	Ile	Ser	Ser	Asn	Ser	Ser	Trp	Arg	Gln	Leu	Pro	Thr	Leu	
50						55					60					
cag	ctg	tgg	ttc	tcc	acc	aca	gag	aga	aga	aaa	ggg	agg	gag	atg	gag	297
Gln	Leu	Trp	Phe	Ser	Thr	Thr	Glu	Arg	Arg	Lys	Gly	Arg	Glu	Met	Glu	
65					70					75					80	
tgc	gca	ggt	ctg	aga	agg	ctt	tca	ttc	tgg	agc	atc	tgc	agg	agc	ctg	345
Cys	Ala	Gly	Leu	Arg	Arg	Leu	Ser	Phe	Trp	Ser	Ile	Cys	Arg	Ser	Leu	
				85					90					95		
cac	cat	ggc	cca	gta	gca	ccc	ctt	ttt	ctc	cat	gag	ctg	ctg	gtg	ggt	393
His	His	Gly	Pro	Val	Ala	Pro	Leu	Phe	Leu	His	Glu	Leu	Leu	Val	Gly	
			100					105						110		
tcc	ccc	tcc	cgg	ata	gcg	cct	cct	tcc	aga	aag	agg	atg	tgg	tc		437
Ser	Pro	Ser	Arg	Ile	Ala	Pro	Pro	Ser	Arg	Lys	Arg	Met	Trp			
			115					120					125			

<210> 3622

<211> 362

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 168..362

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atttccacaa	ctttaaaggg	ccaagattag	gcattcttgg	gctggaaatt	caaattcccca											60	
taaggaagag	aggctgcca	ccttggtcaa	acaatwaaga	vgamaagarg	aaattgatca											120	
gggattttga	tgaaaagcaa	caggaagcaa	atgaaacgct	ggcagag	atg	gag	gag									176	
					Met	Glu	Glu										
					1												
gag	cta	cgt	tat	gca	ccc	ctg	tct	ttc	cga	aac	ccc	atg	atg	tct	aag	224	
Glu	Leu	Arg	Tyr	Ala	Pro	Leu	Ser	Phe	Arg	Asn	Pro	Met	Met	Ser	Lys		
	5					10					15						
ctt	cga	aac	tac	cgg	aag	gac	ctt	gct	aaa	ctc	cat	cgg	gag	gtg	aga	272	
Leu	Arg	Asn	Tyr	Arg	Lys	Asp	Leu	Ala	Lys	Leu	His	Arg	Glu	Val	Arg		
20				25						30				35			
agc	aca	cct	ttg	aca	gcc	aca	cct	gga	ggc	cga	gga	gac	atg	aaa	tat	320	
Ser	Thr	Pro	Leu	Thr	Ala	Thr	Pro	Gly	Gly	Arg	Gly	Asp	Met	Lys	Tyr		
				40				45						50			
ggc	ata	tat	gct	gta	gag	aat	gag	cat	atg	aat	cgg	cta	ctt			362	
Gly	Ile	Tyr	Ala	Val	Glu	Asn	Glu	His	Met	Asn	Arg	Leu	Leu				
			55					60					65				

<210> 3623

<211> 374

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 77..373

<400> 3623

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agcgccgaga ttgattcacc ttcacctgtg ctgcactcca gctgacccaa gtaggaagcc      60
agacgagctg taaaac atg aac gga aga gtg gat tat ttg gtc act gag gaa      112
          Met Asn Gly Arg Val Asp Tyr Leu Val Thr Glu Glu
                1          5          10

gag atc aat ctt acc aga ggg ccc tca ggg ctg ggc ttc aac atc gtc      160
Glu Ile Asn Leu Thr Arg Gly Pro Ser Gly Leu Gly Phe Asn Ile Val
          15          20          25

ggt ggg aca gat cag cag tat gtc tcc aac gac agt ggc atc tac gtc      208
Gly Gly Thr Asp Gln Gln Tyr Val Ser Asn Asp Ser Gly Ile Tyr Val
          30          35          40

agc cgc atc aaa gaa aat ggg gct gcg gcc ctg gat ggg cgg ctc cag      256
Ser Arg Ile Lys Glu Asn Gly Ala Ala Ala Leu Asp Gly Arg Leu Gln
          45          50          55          60

gag ggt gat aag atc ctt tcg gta aat ggc caa gac cta aag aac ctg      304
Glu Gly Asp Lys Ile Leu Ser Val Asn Gly Gln Asp Leu Lys Asn Leu
          65          70          75

ctg cac cag gat gct gta gac ctc ttt cgt aat gca ggc tat gct gtg      352
Leu His Gln Asp Ala Val Asp Leu Phe Arg Asn Ala Gly Tyr Ala Val
          80          85          90

tct ctg aga gtg cag cac agg t      374
Ser Leu Arg Val Gln His Arg
          95

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<210> 3624

<211> 288

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 50..286

<400> 3624

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tggaaaatac ttgtattcgg cagttgacgg ccakcccct cgaagagga atg gac tcc      58
          Met Asp Ser
                1

gcc cag agg gaa gcc ttg gac gac att gyc atr cag gtc atg gag ats      106
Ala Gln Arg Glu Ala Leu Asp Asp Ile Xaa Xaa Gln Val Met Glu Xaa
          5          10          15

atc aat gcc aac gcc aag acc aga ggg cgc atc att gac ttc aaa gag      154
Ile Asn Ala Asn Ala Lys Thr Arg Gly Arg Ile Ile Asp Phe Lys Glu
          20          25          30          35

atc cag tac ggc tac cgc cgg gtg aac ccc atg tat ggg gct gag tac      202
Ile Gln Tyr Gly Tyr Arg Arg Val Asn Pro Met Tyr Gly Ala Glu Tyr
          40          45          50

atc ctg gac ctg ctg ctt ctg tac aaa aag cac aaa ggg aag aaa atg      250
Ile Leu Asp Leu Leu Leu Leu Tyr Lys Lys His Lys Gly Lys Lys Met
          55          60          65

acg gtc cct gtg agg asg cac gcg tat tta cag cct ca      288
Thr Val Pro Val Arg Xaa His Ala Tyr Leu Gln Pro
          70          75

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<210> 3625
 <211> 341
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 156..341

<400> 3625
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 tctctgctct agttttggct gaaaacactc taaatggacc aagcaciaag caacggcgac 120
 ttattgtttc ttggcacta agtggtggca cacaa atg aaa aca ttt aaa gat 173
 Met Lys Thr Phe Lys Asp
 1 5
 gaa gaa ctc ttt cca ctt caa gta gtc atg aaa aaa ctg gat ctt att 221
 Glu Glu Leu Phe Pro Leu Gln Val Val Met Lys Lys Leu Asp Leu Ile
 10 15 20
 agw gaa ctt aga gaa cga gtc caa aca caa tgt gac tgt tgt ttt tta 269
 Xaa Glu Leu Arg Glu Arg Val Gln Thr Gln Cys Asp Cys Cys Phe Leu
 25 30 35
 tac tgg cat cga gct gtc ttc cca att twt tta gat grt gta tat gaa 317
 Tyr Trp His Arg Ala Val Phe Pro Ile Xaa Leu Asp Xaa Val Tyr Glu
 40 45 50
 atg ctg ttg atg cag cag ata cat 341
 Met Leu Leu Met Gln Gln Ile His
 55 60

<210> 3626
 <211> 382
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 103..381

<400> 3626
 cccatctccc caccctctct tctccaccag ccaacgtccg ggaaaaacga gtttttcacg 60
 actgaaataa catagcaaaa taagccaaga tgtctggatc ca atg acc tac gag 114
 Met Thr Tyr Glu
 1
 gcc cag ttc ttt ggc ttc acg cca caa acg tgc atg ctt cgg atc tac 162
 Ala Gln Phe Phe Gly Phe Thr Pro Gln Thr Cys Met Leu Arg Ile Tyr
 5 10 15 20
 att gca ttt caa gac tac cta ttt gaa gtg atg cag gcc gtt gad cag 210
 Ile Ala Phe Gln Asp Tyr Leu Phe Glu Val Met Gln Ala Val Xaa Gln
 25 30 35
 gtt att ctg aag aag ctg gat ggc atc cca gac tgt gac att agc cca 258
 Val Ile Leu Lys Lys Leu Asp Gly Ile Pro Asp Cys Asp Ile Ser Pro
 40 45 50
 gtg cag att cgc aaa tgc aca gag aag ttt ctt tgc ttc atg aaa gga 306

Val	Gln	Ile	Arg	Lys	Cys	Thr	Glu	Lys	Phe	Leu	Cys	Phe	Met	Lys	Gly	
	55						60				65					
cat	ttt	gat	aac	ctt	ttt	agc	aaa	atg	gag	caa	ctg	ttt	ttg	cag	ctg	354
His	Phe	Asp	Asn	Leu	Phe	Ser	Lys	Met	Glu	Gln	Leu	Phe	Leu	Gln	Leu	
	70					75					80					
att	tta	cgt	att	ccc	tca	aac	atc	ttg	c							382
Ile	Leu	Arg	Ile	Pro	Ser	Asn	Ile	Leu								
85					90											

<210> 3627
 <211> 423
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 72..422

<400> 3627																
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aatctgaagg	g	atg	atg	gat	gca	tca	aaa	gag	ctg	caa	gtt	ctc	cac	att		110
		Met	Met	Asp	Ala	Ser	Lys	Glu	Leu	Gln	Val	Leu	His	Ile		
	1					5					10					
gac	ttc	ttg	aat	cag	gac	aac	gcc	gtt	tct	cac	cac	aca	tg	gag	ttc	158
Asp	Phe	Leu	Asn	Gln	Asp	Asn	Ala	Val	Ser	His	His	Thr	Trp	Glu	Phe	
	15					20				25						
caa	acg	agc	agt	cct	gtg	ttc	cgg	cga	gga	cag	gtg	ttt	cac	ctg	cgg	206
Gln	Thr	Ser	Ser	Pro	Val	Phe	Arg	Arg	Gly	Gln	Val	Phe	His	Leu	Arg	
	30				35				40					45		
ctg	gtg	ctg	aac	cag	ccc	cta	caa	tcc	tac	cac	caa	ctg	aaa	ctg	gaa	254
Leu	Val	Leu	Asn	Gln	Pro	Leu	Gln	Ser	Tyr	His	Gln	Leu	Lys	Leu	Glu	
			50					55					60			
ttc	agc	aca	ggg	ccg	aat	cct	agc	atc	gcc	aaa	cac	acc	ctg	gtg	gtg	302
Phe	Ser	Thr	Gly	Pro	Asn	Pro	Ser	Ile	Ala	Lys	His	Thr	Leu	Val	Val	
			65				70						75			
ctc	gac	ccg	agg	acg	ccc	tca	gac	cac	tac	aac	tg	cag	gca	acc	ctt	350
Leu	Asp	Pro	Arg	Thr	Pro	Ser	Asp	His	Tyr	Asn	Trp	Gln	Ala	Thr	Leu	
		80				85					90					
caa	aat	gag	tct	ggc	aaa	gag	gtc	aca	gtv	gct	gtc	acc	agt	tcc	ccc	398
Gln	Asn	Glu	Ser	Gly	Lys	Glu	Val	Thr	Val	Ala	Val	Thr	Ser	Ser	Pro	
	95					100					105					
aat	gcc	atc	ctg	ggc	aag	tac	caa	c								423
Asn	Ala	Ile	Leu	Gly	Lys	Tyr	Gln									
110						115										

<210> 3628
 <211> 386
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 121..384

<400> 3628

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aaactgaagc ccaacctagg caacggggca gacctgcca attaccgctg gacccagacc      60
ctgtcggagc tggacctggc ggtccctttc tgtgtgaact tccggctgaa aggggaaggac    120
atg gtg gtg gac atc cag cgg cgg cac ctc cgg gtg ggg ctc aag ggg      168
Met Val Val Asp Ile Gln Arg Arg His Leu Arg Val Gly Leu Lys Gly
1           5           10           15
cag cca gcg atc att gat ggg gag ctc tac aat gaa gtg aag gtg gag      216
Gln Pro Ala Ile Ile Asp Gly Glu Leu Tyr Asn Glu Val Lys Val Glu
           20           25           30
gag agc tcg tgg ctc att gag gac ggc aag gtg gtg act gtg cat ctg      264
Glu Ser Ser Trp Leu Ile Glu Asp Gly Lys Val Val Thr Val His Leu
           35           40           45
gag aag atc aat aag atg gag tgg tgg agc cgc ttg gtg tcc agt gac      312
Glu Lys Ile Asn Lys Met Glu Trp Trp Ser Arg Leu Val Ser Ser Asp
           50           55           60
ctg aga tca aca cca aga aga tta acc ctg aag aat tcc aag ctg tca      360
Leu Arg Ser Thr Pro Arg Arg Leu Thr Leu Lys Asn Ser Lys Leu Ser
65           70           75           80
gac ctg gac agt gag act cgc agc at      386
Asp Leu Asp Ser Glu Thr Arg Ser
           85

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<210> 3629

<211> 391

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 6..389

<400> 3629

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tggga atg aag ctg tca gaa atc ccc ttg act ctg cat tct gtt tca gag      50
Met Lys Leu Ser Glu Ile Pro Leu Thr Leu His Ser Val Ser Glu
1           5           10           15
ctg gtg cgg ctc tgc ttg cgc aga tct gat gtt cag gag gaa agc gag      98
Leu Val Arg Leu Cys Leu Arg Arg Ser Asp Val Gln Glu Glu Ser Glu
           20           25           30
ggc tca gac aca gat gac aat aaa gat tca gct gca ttt gag gat aat      146
Gly Ser Asp Thr Asp Asp Asn Lys Asp Ser Ala Ala Phe Glu Asp Asn
           35           40           45
gag gta caa gat gag ttc cta gaa aag ctg gag acc tct gaa ttt ttt      194
Glu Val Gln Asp Glu Phe Leu Glu Lys Leu Glu Thr Ser Glu Phe Phe
           50           55           60
gag ctg acg tca gag gag aag cta cag atc ttg aca gya ctg tgc cac      242
Glu Leu Thr Ser Glu Glu Lys Leu Gln Ile Leu Thr Xaa Leu Cys His
           65           70           75
cgg atc ctc atg aca tac tca gtg caa gac cac atg gag acc aga cag      290
Arg Ile Leu Met Thr Tyr Ser Val Gln Asp His Met Glu Thr Arg Gln
80           85           90           95
cag atg tct gca gag ttg tgg aag gaa cgg ctt gct gtg ttg aag gaa      338

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Gln Met Ser Ala Glu Leu Trp Lys Glu Arg Leu Ala Val Leu Lys Glu
 100 105 110
 gaa aat gat aag aag aga gca gag aaa cag aaa cgg aaa gaa atg gaa 386
 Glu Asn Asp Lys Lys Arg Ala Glu Lys Gln Lys Arg Lys Glu Met Glu
 115 120 125
 gcc gt 391
 Ala

<210> 3630
 <211> 401
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 205..399

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 tccactcttc tctaccacag acttctccta agaatttctt cttctcattt ttgccttttt 120
 attgtattga acaatgggtg cmatccctag cctaccact tggccgattc tgcacatag 180
 aaactagctt agcagcatat tatc atg gat gtg aat ata ttt ttg agt agg 231
 Met Asp Val Asn Ile Phe Leu Ser Arg
 1 5
 gaa tat gat caa gag ttc tat agt atc ttt cca aaa aca ttt ttt aga 279
 Glu Tyr Asp Gln Glu Phe Tyr Ser Ile Phe Pro Lys Thr Phe Phe Arg
 10 15 20 25
 gac aaa tct ttt ctc cca aat att cat tta gtt tgg aac atc tct gct 327
 Asp Lys Ser Phe Leu Pro Asn Ile His Leu Val Trp Asn Ile Ser Ala
 30 35 40
 ctt act gta aat cac agt gac att atc cag ggg gta tct agg gah ncc 375
 Leu Thr Val Asn His Ser Asp Ile Ile Gln Gly Val Ser Arg Xaa Xaa
 45 50 55
 ccc tgg ata gtc tgc ttt ttg atc ac 401
 Pro Trp Ile Val Cys Phe Leu Ile
 60 65

<210> 3631
 <211> 247
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 55..246

<400> 3631
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 Met
 1
 gca cca tct cgg ctc act gca acc tcc acc tcc tgg ttc aag cga ttc 105
 Ala Pro Ser Arg Leu Thr Ala Thr Ser Thr Ser Trp Phe Lys Arg Phe

	5		10		15	
tca ggc ctc agc ttc cca agt agt tgg gat tac agg sgc stg cca cca						153
Ser Gly Leu Ser Phe Pro Ser Ser Trp Asp Tyr Arg Xaa Xaa Pro Pro						
	20		25		30	
cac ctg gct aat ttt gta ttt tta gta gag atg ggg ttt ctc cat gtt						201
His Leu Ala Asn Phe Val Phe Leu Val Glu Met Gly Phe Leu His Val						
	35		40		45	
ggg cag gct ggt ctc aaa ctc ccg acc tca agt gat cta ccc gca c						247
Gly Gln Ala Gly Leu Lys Leu Pro Thr Ser Ser Asp Leu Pro Ala						
50		55		60		

<210> 3632
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 <212> DNA
 <213> Homo sapiens

<220>
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 <222> 130..363

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tcatgagtga actccattc acaattgctt caaagagaac aaaatacata ggaatccaac	120
ttacaaggg atg ttg aag gac ctc ttc aag gag aac tac aaa cca ctg ctc	171
Met Leu Lys Asp Leu Phe Lys Glu Asn Tyr Lys Pro Leu Leu	
	1 5 10
agt gaa ata aaa gag gat aca aac aaa tgg aag aac att cca tgc tca	219
Ser Glu Ile Lys Glu Asp Thr Asn Lys Trp Lys Asn Ile Pro Cys Ser	
15 20 25 30	
tgg ata gga aga atc aat atc atg aaa atg ccc ata ctg ccc aag gta	267
Trp Ile Gly Arg Ile Asn Ile Met Lys Met Pro Ile Leu Pro Lys Val	
	35 40 45
att tat aga ttc aat gcc atc ccc atc aag cta cca atg act ttc ttc	315
Ile Tyr Arg Phe Asn Ala Ile Pro Ile Lys Leu Pro Met Thr Phe Phe	
	50 55 60
aca gaa ttg gaa aaa act aaa gtt cat atg gaa cca aaa aag agc cca	363
Thr Glu Leu Glu Lys Thr Lys Val His Met Glu Pro Lys Lys Ser Pro	
	65 70 75
ca	365

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 <211> 219
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 <213> Homo sapiens

<220>
 <221> CDS
 <222> 62..217

<400> 3633	
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c atg caa tct gat ggt ctt ggt tgc cac ttt agg cag agt ata tat acc	109

Met Gln Ser Asp Gly Leu Gly Cys His Phe Arg Gln Ser Ile Tyr Thr
 1 5 10 15
 acc ccc cac cca mtc cts kcc ama mcc sac cca btc ttt cct tct ttc 157
 Thr Pro His Pro Xaa Leu Xaa Xaa Xaa Xaa Pro Xaa Phe Pro Ser Phe
 20 25 30
 cta ctt tat cag gtg aag aca tdc agt gaa gct tgc ctg atg gta agg 205
 Leu Leu Tyr Gln Val Lys Thr Xaa Ser Glu Ala Cys Leu Met Val Arg
 35 40 45
 aaa cca gcc cat tc 219
 Lys Pro Ala His
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<210> 3634
 <211> 469
 <212> DNA
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<220>
 <221> CDS
 <222> 216..467

<400> 3634
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 gctgcaggca agggtttcca tccccgctgc ctaggcact ctcttcccaa ggccagggtg 120
 ggacacctggg grangtcagt tcagaaatat ctagcagaga cctcttaaac ccccatccca 180
 gcaccccatc ctgttgttcc cagagctggg ctccc atg agt gtg cta gag cca 233
 Met Ser Val Leu Glu Pro
 1 5
 gat agc cgt ggc ccc cca ccc atc tca ctc aca cac aca ggc atc cat 281
 Asp Ser Arg Gly Pro Pro Pro Ile Ser Leu Thr His Thr Gly Ile His
 10 15 20
 aca ccc cag aag act tcc caa atg agg cca gac tca ggg tca cgg gga 329
 Thr Pro Gln Lys Thr Ser Gln Met Arg Pro Asp Ser Gly Ser Arg Gly
 25 30 35
 atg tgc ttc tgc ccc tgt aag ggc ttt ggg gaa ggg ggc aac ata gta 377
 Met Cys Phe Cys Pro Cys Lys Gly Phe Gly Glu Gly Gly Asn Ile Val
 40 45 50
 gag gct gga aag agc ccc caa acc tgt gcv bat gmc cct cca gcc ctg 425
 Glu Ala Gly Lys Ser Pro Gln Thr Cys Ala Xaa Xaa Pro Pro Ala Leu
 55 60 65 70
 cgt ttc cat tct gcc ttc tca gag tgc cct tgc tgc acc cag ac 469
 Arg Phe His Ser Ala Phe Ser Glu Cys Pro Cys Cys Thr Gln
 75 80

<210> 3635
 <211> 460
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 121..459

<400> 3635

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cagaatgaaa ccagcgctct tcagcgctct gtgtgagatc aaagagaaaa caggcatgta      120
atg aat tta mtw cca cat gtg akg aac ctt ctc cga gaa cag agt aga      168
Met Asn Leu Xaa Pro His Val Xaa Asn Leu Leu Arg Glu Gln Ser Arg
1          5          10          15
aca cgt ccc att tct cca aaa gag att gaa aga atg gtg ggc atc atc      216
Thr Arg Pro Ile Ser Pro Lys Glu Ile Glu Arg Met Val Gly Ile Ile
          20          25          30
cat cga aaa ttt agt tcc att cag atg cag ctc aaa caa agc act tgt      264
His Arg Lys Phe Ser Ser Ile Gln Met Gln Leu Lys Gln Ser Thr Cys
          35          40          45
gaa gca gtt atg att tta aga tca agg ttc ctt gat gcc aga cgg aaa      312
Glu Ala Val Met Ile Leu Arg Ser Arg Phe Leu Asp Ala Arg Arg Lys
          50          55          60
agg cgt aac ttc agt aaa cag dhs aca gaa atc ttg aat gaa tat ttt      360
Arg Arg Asn Phe Ser Lys Gln Xaa Thr Glu Ile Leu Asn Glu Tyr Phe
65          70          75          80
tac tca cac ctc agc aac ccc tac ccc agt gaa gaa gcc aaa gag gag      408
Tyr Ser His Leu Ser Asn Pro Tyr Pro Ser Glu Glu Ala Lys Glu Glu
          85          90          95
ctg gcc aag aaa tgc agc atc aca gtg tca cag gta tcc aat tgg ttt      456
Leu Ala Lys Lys Cys Ser Ile Thr Val Ser Gln Val Ser Asn Trp Phe
          100          105          110
ggc a      460
Gly

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<210> 3636

<211> 417

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 163..417

<400> 3636

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gcgccccgcg cggcgggtta ctgcgttacc ggaggettca gtccccggcg gcgcggcgac      120
agctagggtt cacggccact ggggcagagg agccgcgaga ag atg tgg gtt ttt      174
Met Trp Val Phe
1
ggt tac ggg tcc ctg atc tgg aag gtg gat ttc ccc tat cag gac aag      222
Gly Tyr Gly Ser Leu Ile Trp Lys Val Asp Phe Pro Tyr Gln Asp Lys
5          10          15          20
ctg gtc gga tac atc acc aac tac agc agg cgc ttc tgg cag ggc agc      270
Leu Val Gly Tyr Ile Thr Asn Tyr Ser Arg Arg Phe Trp Gln Gly Ser
          25          30          35
acg aac cac cgc ggg gtc ccc ggc aag cct kda aga gtt gtg act ctt      318
Thr Asn His Arg Gly Val Pro Gly Lys Pro Xaa Arg Val Val Thr Leu
          40          45          50
gtt gaa gat cct gcg gga tgt gta tgg ggt gtt gct tac agr ttg cca      366

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Val Glu Asp Pro Ala Gly Cys Val Trp Gly Val Ala Tyr Arg Leu Pro
55 60 65
gta gga aag gaa gaa gaa gta aaa gca tac ctt gac ttc aga gaa aaa 414
Val Gly Lys Glu Glu Glu Val Lys Ala Tyr Leu Asp Phe Arg Glu Lys
70 75 80
gga 417
Gly
85

<210> 3637
<211> 361
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 175..360

<400> 3637
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gtctgcacat gatgtgtgcc acacacccaa acatagttca gattattgaa gtgtttgcta 120
acagtgtcca gttttcccca tgagtccagc cctagggccc gactcttaat tgta atg 177
Met
1
gag atg atg gaa ggg gga gag cta ttt cac aga atc agc cag cac cgg 225
Glu Met Met Glu Gly Gly Glu Leu Phe His Arg Ile Ser Gln His Arg
5 10 15
cac ttt aca gag aag caa gcc agc caa gta aca aag cag ata gct ttg 273
His Phe Thr Glu Lys Gln Ala Ser Gln Val Thr Lys Gln Ile Ala Leu
20 25 30
gct ctg cgg cac tgt cac ttg tta aac att gcg cac aga gac ctc aag 321
Ala Leu Arg His Cys His Leu Leu Asn Ile Ala His Arg Asp Leu Lys
35 40 45
cct gaa aat ctg ctt hnb aag gat aac tct ttg gat gcc c 361
Pro Glu Asn Leu Leu Xaa Lys Asp Asn Ser Leu Asp Ala
50 55 60

<210> 3638
<211> 409
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 203..409

<400> 3638
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gaggctgtcg gggtaatggc cacacgctga cagaaccagc cgagtggaaa aggggagcga 120
ascgttcctc tgsaaccct tccccaggcc tgaggccttc ccgcttggtg ctgccgccgc 180
cactgccggc tgaggagggg cg atg agt tgg ttc aac gcc tcc cag ctc tcc 232
Met Ser Trp Phe Asn Ala Ser Gln Leu Ser

						1					5					10	
agc	ttc	sct	aag	cag	gcc	ctg	tcc	cag	gcc	cag	aag	tct	att	gac	agg		280
Ser	Phe	Xaa	Lys	Gln	Ala	Leu	Ser	Gln	Ala	Gln	Lys	Ser	Ile	Asp	Arg		
				15					20					25			
gtt	ctg	gac	atc	cag	gaa	gag	gag	chg	agc	atc	tgg	gcc	gag	acc	att		328
Val	Leu	Asp	Ile	Gln	Glu	Glu	Glu	Xaa	Ser	Ile	Trp	Ala	Glu	Thr	Ile		
				30				35					40				
ccg	tat	gga	gag	ccg	gga	ata	agt	tcc	cct	gtc	agt	gga	gga	tgg	gat		376
Pro	Tyr	Gly	Glu	Pro	Gly	Ile	Ser	Ser	Pro	Val	Ser	Gly	Gly	Trp	Asp		
		45				50					55						
act	tca	acc	tgg	ggg	ttg	aaa	tca	aac	act	gaa							409
Thr	Ser	Thr	Trp	Gly	Leu	Lys	Ser	Asn	Thr	Glu							
	60					65											

<210> 3639
 <211> 214
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 27..212

<400> 3639	
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Met Phe Asn Gly Gln Phe Leu Phe Asp	
aga cct atg cat gtg aaa atg gat gac aag tct gtt cct cat aaa gag	101
Arg Pro Met His Val Lys Met Asp Asp Lys Ser Val Pro His Lys Glu	
10	15
20	25
tac cgt tca cat gat ggt aaa aca cca caa tta cca cgt gkt ctt gga	149
Tyr Arg Ser His Asp Gly Lys Thr Pro Gln Leu Pro Arg Xaa Leu Gly	
	30
	35
	40
ggc att ggg atg gga ctt ggt ccg ggt gga cag cct att agt gcc agc	197
Gly Ile Gly Met Gly Leu Gly Pro Gly Gly Gln Pro Ile Ser Ala Ser	
	45
	50
	55
cag ttg aac ata ggc cc	214
Gln Leu Asn Ile Gly	
	60

<210> 3640
 <211> 193
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 6..191

<400> 3640	
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Met Phe Lys Tyr Leu Ile Ser His Phe Gly Gly Phe Leu Phe Phe	

1	5	10	15	
tat ttt tta gat ggt gtc tca cgc tat cgc cca ggc tgg agt gca gtg	98			
Tyr Phe Leu Asp Gly Val Ser Arg Tyr Arg Pro Gly Trp Ser Ala Val				
20	25	30		
gcg cga act cgg ctc act gca acc tcc gcc tcc tgg ggw wma agc aat	146			
Ala Arg Thr Arg Leu Thr Ala Thr Ser Ala Ser Trp Gly Xaa Ser Asn				
35	40	45		
tct cct tcc tca gcc tcc caa gta gct ggg att aca ggc atg cac ca	193			
Ser Pro Ser Ser Ala Ser Gln Val Ala Gly Ile Thr Gly Met His				
50	55	60		

<210> 3641
 <211> 491
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 157..489

<400> 3641			
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acctaattga tcagcagcag cagaaaatca ttgccctgca gagtgggtta caagctgggtg	120		
agctgtcagg grggaawtgt cgaavcaggt caagag atg ttc tgc tca ggt ttc	174		
Met Phe Cys Ser Gly Phe			
1	5		
cag aca tgt gcc cgg gag gtg ctt cag tat ctg gcc aag cac gag aac	222		
Gln Thr Cys Ala Arg Glu Val Leu Gln Tyr Leu Ala Lys His Glu Asn			
10	15	20	
act cgg gac ctg aag tct tcg cag ctt gtc acc cac ctc cac cgg gtg	270		
Thr Arg Asp Leu Lys Ser Ser Gln Leu Val Thr His Leu His Arg Val			
25	30	35	
gtc tcg gag ctg ctg cag ggt ggt acc tcc agg aag cca tca gac cca	318		
Val Ser Glu Leu Leu Gln Gly Gly Thr Ser Arg Lys Pro Ser Asp Pro			
40	45	50	
gct ccc aaa gtg atg gac ttc aag gaa aaa ccc agc tct ccg gcc aaa	366		
Ala Pro Lys Val Met Asp Phe Lys Glu Lys Pro Ser Ser Pro Ala Lys			
55	60	65	70
ggg tcg gaa ggt cct ggg aaa aac tgc gtg mna gtc atc cag cgg act	414		
Gly Ser Glu Gly Pro Gly Lys Asn Cys Val Xaa Val Ile Gln Arg Thr			
75	80	85	
ttc gct cac tcg agt ggg gag cag agc ggc agc rtc acg gac aca gac	462		
Phe Ala His Ser Ser Gly Glu Gln Ser Gly Ser Xaa Thr Asp Thr Asp			
90	95	100	
agt ggc tat gga gga gat cgg aga agg gc	491		
Ser Gly Tyr Gly Gly Asp Arg Arg Arg			
105	110		

<210> 3642
 <211> 276
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 115..276

<400> 3642

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ttttagacct gggctggtaa gaagtgtga agatgttttt tagagatttg tggg atg      117
                                         Met
                                         1
aca aat tcc act ggg gtt tct gas ctt ctc agt cat gct tgt ctt ggg      165
Thr Asn Ser Thr Gly Val Ser Xaa Leu Leu Ser His Ala Cys Leu Gly
          5                      10                      15
gtc acc act cct tgg ccc tct cct atg gca cct gtc cct cat tct gct      213
Val Thr Thr Pro Trp Pro Ser Pro Met Ala Pro Val Pro His Ser Ala
          20                      25                      30
caa gcc cct atg cct tcc caa caa ctt gcc ttt agc tct ggg cag atg      261
Gln Ala Pro Met Pro Ser Gln Gln Leu Ala Phe Ser Ser Gly Gln Met
          35                      40                      45
tct ttg ctt gca ctc      276
Ser Leu Leu Ala Leu
50

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<210> 3643
 <211> 456
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 135..455

<400> 3643

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cccgcctgga aatgatggta ttgctgtgag ttttattatt actagtatat ttataaggct      120
ttacaactta taaa atg ctt tcc tat aaa tta cct cat ttg att ctt gtg      170
          Met Leu Ser Tyr Lys Leu Pro His Leu Ile Leu Val
          1                      5                      10
gct tgc ttt tct ttt ttg tac cca aag aga act agt atg cac ttt ttc      218
Ala Cys Phe Ser Phe Leu Tyr Pro Lys Arg Thr Ser Met His Phe Phe
          15                      20                      25
ttt tgt tct cct ggc aat tcc aat ttt ttg aac atg aat gag ggg gcc      266
Phe Cys Ser Pro Gly Asn Ser Asn Phe Leu Asn Met Asn Glu Gly Ala
          30                      35                      40
agc cgc ggt ggc tca tgc ctg tgg tcc cag cac ttt ggg agg ctg agg      314
Ser Arg Gly Gly Ser Cys Leu Trp Ser Gln His Phe Gly Arg Leu Arg
          45                      50                      55                      60
cgg gcg gat cac ctg agg tca gga gtt cga gac cgg cat ggc naa crk      362
Arg Ala Asp His Leu Arg Ser Gly Val Arg Asp Arg His Gly Xaa Xaa
          65                      70                      75
ggc gaa acc ctg tct cta cta gaa aat gcg aaa att atc tgg gtg tbg      410
Gly Glu Thr Leu Ser Leu Leu Glu Asn Ala Lys Ile Ile Trp Val Xaa
          80                      85                      90

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tgg cac tgc cct gtg rta cca gct act cgg gag gct gag gca ggg a	456
Trp His Ser Pro Val Xaa Pro Ala Thr Arg Glu Ala Glu Ala Gly	
95 100 105	

<210> 3644
 <211> 356
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 82..354

<400> 3644	
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gtctttgccc actgaacagc c atg aga agg caa ctc cgg tcc aga agg gct	111
Met Arg Arg Gln Leu Arg Ser Arg Arg Ala	
1 5 10	
cca tcc ttt cct tac agt tat cgc tac aga byc gat gat ccg gat gaa	159
Pro Ser Phe Pro Tyr Ser Tyr Arg Tyr Arg Xaa Asp Asp Pro Asp Glu	
15 20 25	
gcg aac cag aac tac tta gca gat gaa gag gag gaa gca gaa gaa gag	207
Ala Asn Gln Asn Tyr Leu Ala Asp Glu Glu Glu Glu Ala Glu Glu Glu	
30 35 40	
gct cgg gtg acg gtg gtg ccc aaa tgc gag gag gag gaa gaa gag gag	255
Ala Arg Val Thr Val Val Pro Lys Ser Glu Glu Glu Glu Glu Glu Glu	
45 50 55	
gag aaa gaa gag gag gaa gag gag gaa aag gah gag gaa gag ggt caa	303
Glu Lys Glu Glu Glu Glu Glu Glu Glu Lys Xaa Glu Glu Glu Gly Gln	
60 65 70	
ggt cag cca aca ggc aat gcc tgg tgg cag aaa ttg cag atc atg agt	351
Gly Gln Pro Thr Gly Asn Ala Trp Trp Gln Lys Leu Gln Ile Met Ser	
75 80 85 90	
gaa ta	356
Glu	

<210> 3645
 <211> 425
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 143..424

<400> 3645	
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tcccatgga gaagctggcg gcctctacag agccccaagg gcctcggccg gtccctgggc	120
gtgagagtgt ccaggkkgcc cr atg acc aag mmc ttt cgc agc ttc cgg tca	172
Met Thr Lys Xaa Phe Arg Ser Phe Arg Ser	
1 5 10	
gag tgt gag gct gag gtg ggc tgg aac ctg acc tat agc agg gct ggg	220

<221> CDS
<222> 78..350

<400> 3647
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ggaggcttct ctacaac atg acc caa agg agc att gca ggt cct att tgc 110
Met Thr Gln Arg Ser Ile Ala Gly Pro Ile Cys
1 5 10
aac ctg aag ttt gtg act ctc ctg gwt ggc ttw agk tca gam ctc cca 158
Asn Leu Lys Phe Val Thr Leu Leu Xaa Gly Xaa Xaa Ser Xaa Leu Pro
15 20 25
thc ctg gga gct gga gta cag ctt caa gac aat ggg tat aat gga ttg 206
Xaa Leu Gly Ala Gly Val Gln Leu Gln Asp Asn Gly Tyr Asn Gly Leu
30 35 40
ctc att gca att aat cct cag gta cct gag aat cag aac ctc atc tca 254
Leu Ile Ala Ile Asn Pro Gln Val Pro Glu Asn Gln Asn Leu Ile Ser
45 50 55
aac att aag gaa atg ata act gaa gct tca ttt tac cta ttt aat gct 302
Asn Ile Lys Glu Met Ile Thr Glu Ala Ser Phe Tyr Leu Phe Asn Ala
60 65 70 75
acc aag aga aga gta ttt ttc aga aat ata aag att tta ata cct gcc 350
Thr Lys Arg Arg Val Phe Phe Arg Asn Ile Lys Ile Leu Ile Pro Ala
80 85 90
aa 352

<210> 3648
<211> 321
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 61..321

<400> 3648
agcagcagac gctctgtccc gcccgggcag ctctgcgagg cagcggctgg agagggaacc 60
atg ggg act gtg cac gcc cgg agt ttg gag cct ctt cca tca agt gga 108
Met Gly Thr Val His Ala Arg Ser Leu Glu Pro Leu Pro Ser Ser Gly
1 5 10 15
cct gat ttt gga gga tta gga gaa gaa gct gaa ttt gtt gaa gtt gag 156
Pro Asp Phe Gly Gly Leu Gly Glu Glu Ala Glu Phe Val Glu Val Glu
20 25 30
cct gaa gct aaa cag gaa att ctt gaa aac aaa gat gtg gtt gtt caa 204
Pro Glu Ala Lys Gln Glu Ile Leu Glu Asn Lys Asp Val Val Val Gln
35 40 45
cat gtt cat ttt gat gga ctt gga agg act aaa gat gat atc atc att 252
His Val His Phe Asp Gly Leu Gly Arg Thr Lys Asp Asp Ile Ile Ile
50 55 60
tgt gaa att gga gat gtt ttc aag gcc aaa aac cta att gag gta atg 300
Cys Glu Ile Gly Asp Val Phe Lys Ala Lys Asn Leu Ile Glu Val Met
65 70 75 80
cgg aaa tct cat gaa gcc cgt 321

Arg Lys Ser His Glu Ala Arg
85

<210> 3649
<211> 189
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 28..189

<400> 3649
acacacttac tgagcgtcta acaatga atg ggt caa gcc ctt cgt agg cac tgg 54
Met Gly Gln Ala Leu Arg Arg His Trp
1 5
caa tgg gaa gat gac caa tac aga cgg ctg aac ctt gct ttc aag gcc 102
Gln Trp Glu Asp Asp Gln Tyr Arg Arg Leu Asn Leu Ala Phe Lys Ala
10 15 20 25
ttc ata aag cac tgg aag atg rcm aaa cac ggt ccg ata caa agg gtc 150
Phe Ile Lys His Trp Lys Met Xaa Lys His Gly Pro Ile Gln Arg Val
30 35 40
ggg ttc agg act cca acc att att atc aaa gag cca cga 189
Gly Phe Arg Thr Pro Thr Ile Ile Ile Lys Glu Pro Arg
45 50

<210> 3650
<211> 288
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 65..286

<400> 3650
aatcaaagag gacacaagca gatggaaaaa catccaatgc tcatggatag gaagaatcaa 60
tatc atg aaa atg gcc ata ctg ccc aaa gga att tat aga ttc aat gct 109
Met Lys Met Ala Ile Leu Pro Lys Gly Ile Tyr Arg Phe Asn Ala
1 5 10 15
att ccc att aaa cta cca tcg aca ttc ttc aca gaa tta gaa aag act 157
Ile Pro Ile Lys Leu Pro Ser Thr Phe Phe Thr Glu Leu Glu Lys Thr
20 25 30
aat tta aaa ttc ata tgg aac caa aaa aca gtt cac att gcc aag aca 205
Asn Leu Lys Phe Ile Trp Asn Gln Lys Thr Val His Ile Ala Lys Thr
35 40 45
atc cta agc aaa aag aag aaa gct gga ggt atc aca cta tcc aac ttc 253
Ile Leu Ser Lys Lys Lys Lys Ala Gly Gly Ile Thr Leu Ser Asn Phe
50 55 60
aaa cta tac tac aag tcc aca gta aaa aaa aaa aa 288
Lys Leu Tyr Tyr Lys Ser Thr Val Lys Lys Lys
65 70

<210> 3651
 <211> 310
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 144..308

<400> 3651
 tagtgcaaaa cagttgaaac tgtcttggtt acagtttata ggattgaata tggcagcttt 60
 acttgaagca aggtctcttg atgttttaag cgatgggtgtt ttgaaggatc tttctgagtt 120
 ttaccggaaa atkgatycca gca atg gat aga aga gtc att aca cca tat caa 173
 Met Asp Arg Arg Val Ile Thr Pro Tyr Gln
 1 5 10
 gat gga cca gat att agc tat ttg gaa gta gaa gat gga gat atc ttc 221
 Asp Gly Pro Asp Ile Ser Tyr Leu Glu Val Glu Asp Gly Asp Ile Phe
 15 20 25
 ttg aaa gaa gaa ata aat atg gaa caa aat cat tcg gaa act atg ttc 269
 Leu Lys Glu Glu Ile Asn Met Glu Gln Asn His Ser Glu Thr Met Phe
 30 35 40
 aag aaa gca aaa aca aaa gct aaa aag aag cca cgt aaa cg 310
 Lys Lys Ala Lys Thr Lys Ala Lys Lys Lys Pro Arg Lys
 45 50 55

<210> 3652
 <211> 412
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 114..410

<400> 3652
 agacacgaag cctccccgggt ggcttacaga cgctgccagc atcgccgccg ccagaggaga 60
 aatgtctgaa gtaagacccc tctccagaga catcttgatg gagaccctcc tgt atg 116
 Met
 1
 agc agg ctc ctg gaa ccc ccg acc atg gag gtt ctt ggc atg act gac 164
 Ser Arg Leu Leu Glu Pro Pro Thr Met Glu Val Leu Gly Met Thr Asp
 5 10 15
 tct gaa gag gac ctg gac cct atg gag gac ttc gat tct ttg gaa tgc 212
 Ser Glu Glu Asp Leu Asp Pro Met Glu Asp Phe Asp Ser Leu Glu Cys
 20 25 30
 atg gag ggc agt gac gca ttg gcc ctg cgg ctg gcc tgc atc ggg gac 260
 Met Glu Gly Ser Asp Ala Leu Ala Leu Arg Leu Ala Cys Ile Gly Asp
 35 40 45
 gag atg gac gtg agc ctc agg gcc ccg cgc ctg gcc cag ctc tcc gar 308
 Glu Met Asp Val Ser Leu Arg Ala Pro Arg Leu Ala Gln Leu Ser Glu
 50 55 60 65

ntg gcc atg cac agc ctg ggt ctg gct ttc atc tac gac cag act gag	356
Xaa Ala Met His Ser Leu Gly Leu Ala Phe Ile Tyr Asp Gln Thr Glu	
70 75 80	
gac atc agg gat gnt ctt aga agt ttc atg gac ggt ttc acc aca ctt	404
Asp Ile Arg Asp Xaa Leu Arg Ser Phe Met Asp Gly Phe Thr Thr Leu	
85 90 95	
aag gmg ca	412
Lys Xaa	

<210> 3653
 <211> 412
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 129..410

<400> 3653	
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gtgacagctc cactctgtcc aaaaagccac cttttgttcg aaactccctg gagcgacgsa	120
gcgctcgg atg aag cgg cct tcc tcg gtc aag tcg ctg cgc tcc gag cgt	170
Met Lys Arg Pro Ser Ser Val Lys Ser Leu Arg Ser Glu Arg	
1 5 10	
ctg atc cgt acc tcg ctg gac ctg gag tta gac ctg cag gcg aca aga	218
Leu Ile Arg Thr Ser Leu Asp Leu Glu Leu Asp Leu Gln Ala Thr Arg	
15 20 25 30	
acc tgg cac agc caa ttg acc cag gag atc tcg gtg ctg aag gag ctc	266
Thr Trp His Ser Gln Leu Thr Gln Glu Ile Ser Val Leu Lys Glu Leu	
35 40 45	
aag gag cag ctg gaa caa gcc aag agc cac ggg gag aag gag ctg cca	314
Lys Glu Gln Leu Glu Gln Ala Lys Ser His Gly Glu Lys Glu Leu Pro	
50 55 60	
cag tgg ttg cgt gag gac gag cgt ttc cgc ctg ctg ctg agg atg ctg	362
Gln Trp Leu Arg Glu Asp Glu Arg Phe Arg Leu Leu Arg Met Leu	
65 70 75	
gag aag cgg atg gac cga gcg gag mac aag ggt gag ctt cag aca gac	410
Glu Lys Arg Met Asp Arg Ala Glu Xaa Lys Gly Glu Leu Gln Thr Asp	
80 85 90	
aa	412

<210> 3654
 <211> 350
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 65..349

<400> 3654	
aacttctgca tccaatattg tctcagcaac ttcagtagag aattttcagg tagctacagg	60

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acaa atg gtt act att gct ggt gtc cca agt cca sra gcc tca agg gta      109
  Met Val Thr Ile Ala Gly Val Pro Ser Pro Xaa Ala Ser Arg Val
    1             5             10             15
ggg ttt cag rac att gca cca aaa cct ctc cct tct cag caa gtt tca      157
Gly Phe Gln Xaa Ile Ala Pro Lys Pro Leu Pro Ser Gln Gln Val Ser
              20             25             30
tct aca gtg gta cag cag cct att caa caa cca cag cag cca acc caa      205
Ser Thr Val Val Gln Gln Pro Ile Gln Gln Pro Gln Gln Pro Thr Gln
              35             40             45
caa agc gta gtg att gta agc cag csr gct caa caa ggt caa act tat      253
Gln Ser Val Val Ile Val Ser Gln Xaa Ala Gln Gln Gly Gln Thr Tyr
              50             55             60
gca cca gcc att cac caa att gtt ctt gct aat cca gca gct ctt cca      301
Ala Pro Ala Ile His Gln Ile Val Leu Ala Asn Pro Ala Ala Leu Pro
              65             70             75
gct ggt cag aca gtt cag cta act gga caa gct aac ata act cca tct t      350
Ala Gly Gln Thr Val Gln Leu Thr Gly Gln Ala Asn Ile Thr Pro Ser
    80             85             90             95

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<210> 3655
 <211> 164
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 9..164

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<400> 3655
ttaaaaaa atg aaa gta aag gaa aaa aaa aaa act gca aat cta gaa aac      50
  Met Lys Val Lys Glu Lys Lys Lys Thr Ala Asn Leu Glu Asn
    1             5             10
ttt ttr grg aaa aac tat tta aaa ctg tca gat cct gmc cag caa kcc      98
Phe Leu Xaa Lys Asn Tyr Leu Lys Leu Ser Asp Pro Xaa Gln Gln Xaa
    15             20             25             30
ccc ccc cag scc ccc ttc caa gtr rcy ccg ggc ctk rag tgk gyc tgs      146
Pro Pro Gln Xaa Pro Phe Gln Val Xaa Pro Gly Leu Xaa Xaa Xaa Xaa
              35             40             45
gkg ttt ama ccc gtc ccc      164
Xaa Phe Xaa Pro Val Pro
              50

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<210> 3656
 <211> 283
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 54..281

<400> 3656

gaagagagaa ttaagacttc aggcatttgt tttgtgcaaa tgcagtcagg tct atg 56
Met
1
atc aag act gcc ctt att gat aaa gct act aaa ccc cag cct gga agg 104
Ile Lys Thr Ala Leu Ile Asp Lys Ala Thr Lys Pro Gln Pro Gly Arg
5 10 15
gaa att ata aat acc atc tgc cgg ttt tta att gca aaa cag gga gga 152
Glu Ile Ile Asn Thr Ile Cys Arg Phe Leu Ile Ala Lys Gln Gly Gly
20 25 30
ccg aat agt ggg aac cct ctg aat ngg ttt tat cag tgc ttt gtc cct 200
Pro Asn Ser Gly Asn Pro Leu Asn Xaa Phe Tyr Gln Cys Phe Val Pro
35 40 45
gaa att agg aag tac ctt gcc agg gta gga ctg cct ttt aac gtt ttt 248
Glu Ile Arg Lys Tyr Leu Ala Arg Val Gly Leu Pro Phe Asn Val Phe
50 55 60 65
ttg ata ttg gat aat gcc cct ggc cac cca gca ct 283
Leu Ile Leu Asp Asn Ala Pro Gly His Pro Ala
70 75

<210> 3657
<211> 415
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 176..415

<400> 3657
gtctctggcc ttcccctttt aggaacaaaa ggacccgtgm cagagcctac ttatcccgtt 60
acagctoctg gtgagaaggc cgaasgatgt cagaaataat agaaaaggct ttttcctttg 120
aaattatcka aacgttcaaa gatgggaaca gccgcagggg ggagadtact gtgct atg 178
Met
1
caa gtt gat ctg att ttg tgg acc atc cat ttc caa ttg gga agc tca 226
Gln Val Asp Leu Ile Leu Trp Thr Ile His Phe Gln Leu Gly Ser Ser
5 10 15
ctt act ttc aac ttg aag cat cag aaa acc aga ctt aca gca gct tca 274
Leu Thr Phe Asn Leu Lys His Gln Lys Thr Arg Leu Thr Ala Ala Ser
20 25 30
gcc tat agg ggt tta ttt ttc tca tgt aac aag aag aac aga agt gga 322
Ala Tyr Arg Gly Leu Phe Phe Ser Cys Asn Lys Lys Asn Arg Ser Gly
35 40 45
cag agg ccg agt tct caa ggr ctc agt ttc ttt ctg tcc cac caa cct 370
Gln Arg Pro Ser Ser Gln Gly Leu Ser Phe Phe Leu Ser His Gln Pro
50 55 60 65
tac cat gtt gga ttg tca tct ttg tgc ttg ttg cct cat gat ggc 415
Tyr His Val Gly Leu Ser Ser Leu Cys Leu Leu Pro His Asp Gly
70 75 80

<210> 3658
<211> 347
<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 135..347

<400> 3658

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cacagccgaa ctagtcccaa cgcgtttgca aatattcccc tggtagccta cttccttacc 60
cccgaatatt ggtaagatcg atcaatggct tcaggacatg gggtctcttc tgtgatcatt 120
caagtgtctca ctgc atg aag act ggc ttg tct cag tgt ttc aac ctc acc 170
                Met Lys Thr Gly Leu Ser Gln Cys Phe Asn Leu Thr
                1          5          10
agg gct gtc tct tgg tcc aca cct cgc tcc ctg tta gtg ccg tat gac 218
Arg Ala Val Ser Trp Ser Thr Pro Arg Ser Leu Leu Val Pro Tyr Asp
        15          20          25
agc ccc cat caa atg acc ttg gcc aag tca cgg ttt ctc tgt ggt caa 266
Ser Pro His Gln Met Thr Leu Ala Lys Ser Arg Phe Leu Cys Gly Gln
        30          35          40
ggg tgg ttg gct gat tgg tgg aaa gta ggg tgg acc aaa gga ggc cac 314
Gly Trp Leu Ala Asp Trp Trp Lys Val Gly Trp Thr Lys Gly Gly His
45          50          55          60
gtg agc agt cag cac cag ttc tgc acc agc agc 347
Val Ser Ser Gln His Gln Phe Cys Thr Ser Ser
        65          70
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<210> 3659

<211> 454

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 276..452

<400> 3659

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aagcgagacc gtccatccag aggaaggcaa gtttttggct cgggcggctg agaagaccgc 60
gcggggctgg agacaggtag cagtacgggg gcggggcttc atgccggatg tgatagtctg 120
cagtcgtttc gggtggcagc ctggcggtg ggagatgcgg cggccacctg ctgcaaagaa 180
ccgaagggaa ggtagaagt acgaaggcag tttggagctg gggctaagca gctgtcgcac 240
ggtcagatca tgggctccac caagcactgg ggcga atg gct cct gaa ctt gaa 293
                Met Ala Pro Glu Leu Glu
                1          5
ggg ggc tcn nnc ggc gtc ttt ggt gtg gcc ttt cta gcc aga gtc gcc 341
Gly Gly Ser Xaa Gly Val Phe Gly Val Ala Phe Leu Ala Arg Val Ala
        10          15          20
ctg gtt ttc tat ggc gtc ttc cag gac cgg acc ctg cac gtg agg tat 389
Leu Val Phe Tyr Gly Val Phe Gln Asp Arg Thr Leu His Val Arg Tyr
        25          30          35
acg gac atc gac tac cag gtc ttc asc gac gcc gcg cgc ttc gtc acg 437
Thr Asp Ile Asp Tyr Gln Val Phe Xaa Asp Ala Ala Arg Phe Val Thr
        40          45          50
gag ggg cgc tcg cct ta 454
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Glu Gly Arg Ser Pro
55

<210> 3660
<211> 453
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 62..451

<400> 3660
gagggcccca ggacagaagc agacagacac ggctcctgct gtcgattccg atccagccag 60
a atg cct cca act cag gcc gaa agt gtt ata agg agt att ata cga gaa 109
Met Pro Pro Thr Gln Ala Glu Ser Val Ile Arg Ser Ile Ile Arg Glu
1 5 10 15
ata gga caa gaa tgt gca gcc cat gga gag att gtt tct gaa act ctg 157
Ile Gly Gln Glu Cys Ala Ala His Gly Glu Ile Val Ser Glu Thr Leu
20 25 30
att gct ttt atg gtg aaa gct gtt gtc ctg gat cca agt aat ggc ttt 205
Ile Ala Phe Met Val Lys Ala Val Val Leu Asp Pro Ser Asn Gly Phe
35 40 45
aac atg gat aga acc ctc atg aaa agt gat gtg cag aat ctt gtt aag 253
Asn Met Asp Arg Thr Leu Met Lys Ser Asp Val Gln Asn Leu Val Lys
50 55 60
ctt tgt atg act cgg cta ttg gat act aaa aat cca tcc ctg gac act 301
Leu Cys Met Thr Arg Leu Leu Asp Thr Lys Asn Pro Ser Leu Asp Thr
65 70 75 80
att aag atg caa gtc tac ttc gat atg aat tat acg aat cga gtg gaa 349
Ile Lys Met Gln Val Tyr Phe Asp Met Asn Tyr Thr Asn Arg Val Glu
85 90 95
ttt ctc gaa gaa cat cac cgg gtc cta gag tct aga tta ggc tct gtt 397
Phe Leu Glu Glu His His Arg Val Leu Glu Ser Arg Leu Gly Ser Val
100 105 110
acc cga gaa att aca gat aac aga gca tgt gct aaa gaa gaa ttg gaa 445
Thr Arg Glu Ile Thr Asp Asn Arg Ala Cys Ala Lys Glu Glu Leu Glu
115 120 125
agc ctc ta 453
Ser Leu
130

<210> 3661
<211> 366
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 81..365

<400> 3661

<211> 313
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 126..311

<400> 3663
 ccaagtcctc ccaagttatt aactgggtcaa aaaggmmttaa aggmmttagtt cttaatatgtt 60
 aagatgccac ccattcaggg ttttttgctt tctaagaggg aactttttaca ggcataattg 120
 agaga atg cat aca tgc tct cta cct tgt ctt ctc ttt gct cag ctg cta 170
 Met His Thr Cys Ser Leu Pro Cys Leu Leu Phe Ala Gln Leu Leu
 1 5 10 15
 gaa ttt tgt agc ttt cct cca gat gtg cct cat aac tgt gcg cct att 218
 Glu Phe Cys Ser Phe Pro Pro Asp Val Pro His Asn Cys Ala Pro Ile
 20 25 30
 gtc tca gtc agg ccg cct aat att gta gca gcc ttt gaa ggg tgc tct 266
 Val Ser Val Arg Pro Pro Asn Ile Val Ala Ala Phe Glu Gly Cys Ser
 35 40 45
 gta gcc act gct ctt ttt cct ccc ttg tgc atc tcc aca ggg aat ga 313
 Val Ala Thr Ala Leu Phe Pro Pro Leu Cys Ile Ser Thr Gly Asn
 50 55 60

<210> 3664
 <211> 191
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 27..191

<400> 3664
 gactggaggg gcgcgacgsg ggcgca atg gcg ggg acc cgg ggc ttg atg ctg 53
 Met Ala Gly Thr Arg Gly Leu Met Leu
 1 5
 ctt ggg cct ggc cca gtg gcg ggt cct agg gac gtg ggt acc tgc aga 101
 Leu Gly Pro Gly Pro Val Ala Gly Pro Arg Asp Val Gly Thr Cys Arg
 10 15 20 25
 ggc cgg cag atg gag att cag aaa cat aag gac aac aag aaa ctt ccc 149
 Gly Arg Gln Met Glu Ile Gln Lys His Lys Asp Asn Lys Lys Leu Pro
 30 35 40
 caa ggt atc att ata gtc ttt aga ctt cag aca cac acc tcc 191
 Gln Gly Ile Ile Ile Val Phe Arg Leu Gln Thr His Thr Ser
 45 50 55

<210> 3665
 <211> 422
 <212> DNA
 <213> Homo sapiens

<220>

<221> CDS

<222> 52..420

<400> 3665

gtcggccgct tgcgacgctc cggaagtgac gtgctttccc gagccggggc c atg gca 57
Met Ala
1
cct gca agg tgt ttc tca gca aga ttg agg acc gtg ttt cag ggc gtg 105
Pro Ala Arg Cys Phe Ser Ala Arg Leu Arg Thr Val Phe Gln Gly Val
5 10 15
ggg cat tgg gct ttg tcc acw kgg gct ggc ctg aag ccc agc cgg cta 153
Gly His Trp Ala Leu Ser Thr Xaa Ala Gly Leu Lys Pro Ser Arg Leu
20 25 30
ctg cca cag cgg gct tct ccc agg ctg ctc tcg gtc agc cgt gcg gac 201
Leu Pro Gln Arg Ala Ser Pro Arg Leu Leu Ser Val Ser Arg Ala Asp
35 40 45 50
ctc gcc aag cat cag gaa ctc ccg ggg aag aag ctg ctc tct gag aaa 249
Leu Ala Lys His Gln Glu Leu Pro Gly Lys Lys Leu Leu Ser Glu Lys
55 60 65
aag ctg aaa agg tac ttt gtg gac tat cgg aga gtg ctt gtc tgt gga 297
Lys Leu Lys Arg Tyr Phe Val Asp Tyr Arg Arg Val Leu Val Cys Gly
70 75 80
gga aac gga ggc gct ggg gca agc tgc ttc cac agt gag ccc cgc aag 345
Gly Asn Gly Gly Ala Gly Ala Ser Cys Phe His Ser Glu Pro Arg Lys
85 90 95
gag ttt wga ggc cct gat gga ggg gac gga ggc aac ggt gga cac gtm 393
Glu Phe Xaa Gly Pro Asp Gly Gly Asp Gly Gly Asn Gly Gly His Val
100 105 110
vtt ctg aga gtt gac cag caa gtc aag tc 422
Xaa Leu Arg Val Asp Gln Gln Val Lys
115 120

<210> 3666

<211> 421

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 80..421

<400> 3666

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ttgcagttat tcagtgtta atg tac cgc ggt gag gct ctt gaa gat ttc aca 112
Met Tyr Arg Gly Glu Ala Leu Glu Asp Phe Thr
1 5 10
ggc ccg gat tgt cgt ttt gtg aat ttt aaa aaa ggt gat cct gta tat 160
Gly Pro Asp Cys Arg Phe Val Asn Phe Lys Lys Gly Asp Pro Val Tyr
15 20 25
gtt tac tat aaa ctg gca aga gga tgg cct gaa gtt tgg gct gga agt 208
Val Tyr Tyr Lys Leu Ala Arg Gly Trp Pro Glu Val Trp Ala Gly Ser

30	35	40	
gtt gga cgc act ttt gga tat ttt cca aaa gat tta atc cag gta gtt	256		
Val Gly Arg Thr Phe Gly Tyr Phe Pro Lys Asp Leu Ile Gln Val Val			
45	50	55	
cat gaa tat acc aaa gaa gag cta caa gtt cca aca gat gag acg gat	304		
His Glu Tyr Thr Lys Glu Glu Leu Gln Val Pro Thr Asp Glu Thr Asp			
60	65	70	75
ttt gtt tgt ttt gat gga gga aga gat gat ttt cat aat tat aat gta	352		
Phe Val Cys Phe Asp Gly Gly Arg Asp Asp Phe His Asn Tyr Asn Val			
80	85	90	
gaa gaa ctt tta ggg ttt ttg gaa ctg tac aat tct gca gct aca gat	400		
Glu Glu Leu Leu Gly Phe Leu Glu Leu Tyr Asn Ser Ala Ala Thr Asp			
95	100	105	
tct gag aaa gct gta gaa aaa	421		
Ser Glu Lys Ala Val Glu Lys			
110			

<210> 3667
 <211> 419
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 21..419

<400> 3667	
ctttagatga cctcacttgg atg gat gcc gag aca aaa aag aga gct gaa gaa	53
Met Asp Ala Glu Thr Lys Lys Arg Ala Glu Glu	
1	5
aag gcc tta gca att aaa gaa agg atc ggc tat cct gat gac att gtt	101
Lys Ala Leu Ala Ile Lys Glu Arg Ile Gly Tyr Pro Asp Asp Ile Val	
15	20
tca aat gat aac aaa ctg art aat rag tac ctc gag ttg aac tac aaa	149
Ser Asn Asp Asn Lys Leu Xaa Asn Xaa Tyr Leu Glu Leu Asn Tyr Lys	
30	35
gaa gat gaa tac ttc gag aac ata att caa aat ttg aaa ttc agc caa	197
Glu Asp Glu Tyr Phe Glu Asn Ile Ile Gln Asn Leu Lys Phe Ser Gln	
45	50
agt aaa caa ctg aag aag ctc cga gaa aar rtg gac aaa gat gag tgg	245
Ser Lys Gln Leu Lys Lys Leu Arg Glu Lys Xaa Asp Lys Asp Glu Trp	
60	65
ata agt gga gca gct gta gtc aat gca ttt tac tct tca gga aga aat	293
Ile Ser Gly Ala Ala Val Val Asn Ala Phe Tyr Ser Ser Gly Arg Asn	
80	85
cag ata gtc ttc cca gcc ggc att ctg cag ccc ccc ttc ttt agt gcc	341
Gln Ile Val Phe Pro Ala Gly Ile Leu Gln Pro Pro Phe Phe Ser Ala	
95	100
cag cag tcc aac tca ttg aac tat ggg ggc atc ggc atg gtc ata gga	389
Gln Gln Ser Asn Ser Leu Asn Tyr Gly Gly Ile Gly Met Val Ile Gly	
110	115
cac gaa atc acc cat ggc ttc gat gac aat	419
His Glu Ile Thr His Gly Phe Asp Asp Asn	

125

130

<210> 3668
 <211> 320
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 140..319

<400> 3668
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 tgggtgctccc gttccccaga ccctaccctt atccccagtg gagccggagt gcgggcgcgc 120
 cccascaccg gccctcacc atg gtg ctg ttg gca gca gcg gtc tgc aca aaa 172
 Met Val Leu Leu Ala Ala Ala Val Cys Thr Lys
 1 5 10
 gca gga aag gct att gtt tct cga cag ttt gtg gaa atg acc cga act 220
 Ala Gly Lys Ala Ile Val Ser Arg Gln Phe Val Glu Met Thr Arg Thr
 15 20 25
 cgg att gag ggc tta tta gca gct ttt cca aag ctc atg aac act gga 268
 Arg Ile Glu Gly Leu Leu Ala Ala Phe Pro Lys Leu Met Asn Thr Gly
 30 35 40
 aaa caa cat acg ttt gtt gaa aca gag agt gta aga tat gtc tac cag 316
 Lys Gln His Thr Phe Val Glu Thr Glu Ser Val Arg Tyr Val Tyr Gln
 45 50 55
 cgt c 320
 Arg
 60

<210> 3669
 <211> 446
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 61..444

<400> 3669
 tattagaaaa aaaccgagta gtaaggcaaa atccccggga aaggaattat cacatatttt 60
 atg cac tgc tgg cag ggc tgg aac atg aag aaa gag aag aat ttt att 108
 Met His Cys Trp Gln Gly Trp Asn Met Lys Lys Glu Lys Asn Phe Ile
 1 5 10 15
 tat cta cgc cag aaa act amc act act ttg aaw cag tct gga tgt gta 156
 Tyr Leu Arg Gln Lys Thr Xaa Thr Thr Leu Xaa Gln Ser Gly Cys Val
 20 25 30
 gaa gac aag aca atc agt gac cag gaa tcc ttt agg gaa gtt att acg 204
 Glu Asp Lys Thr Ile Ser Asp Gln Glu Ser Phe Arg Glu Val Ile Thr
 35 40 45
 gca atg gac gtg atg cag ttc agc aag gag gaa gtt tgg gaa gtg tcg 252
 Ala Met Asp Val Met Gln Phe Ser Lys Glu Glu Val Trp Glu Val Ser

50	55	60	
agg ctg ctt gct ggt ata ctg cat ctt ggg aac ata gaa ttt atc act			300
Arg Leu Leu Ala Gly Ile Leu His Leu Gly Asn Ile Glu Phe Ile Thr			
65	70	75	80
gct ggt ggg gca cag gtt tcc ttc aaa aca gct ttg ggc aga tct gcg			348
Ala Gly Gly Ala Gln Val Ser Phe Lys Thr Ala Leu Gly Arg Ser Ala			
	85	90	95
gag tta ctt ggg ctg gac cca aca cag ctc aca gat gct ttg acc cag			396
Glu Leu Leu Gly Leu Asp Pro Thr Gln Leu Thr Asp Ala Leu Thr Gln			
	100	105	110
aga tca atg ttc ctc agg gga gaa gag atc ctc acg cct ctc aat gtt			444
Arg Ser Met Phe Leu Arg Gly Glu Glu Ile Leu Thr Pro Leu Asn Val			
	115	120	125
ca			446

<210> 3670
 <211> 483
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 296..481

<400> 3670	
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gacttcagag gaacctcttt gggaagctaa tgattcaggg tattgaagac attagcatag	120
aacattaagt kggtcctttt kgtttcagaa gttcattggt gtgattaaat tgccatctga	180
taatttttat agaacagatg cttaattttt agagcatttt tctattttcc agcctttgca	240
aaatgtagc acagtgtctgc agaagcctaa tcctctctat aatcagaata cagat atg	298
	Met
	1
gtc cag aaa tca gtc agc aaa acc ttg ccc tct act tgg tct gac ccc	346
Val Gln Lys Ser Val Ser Lys Thr Leu Pro Ser Thr Trp Ser Asp Pro	
	5
agt gta aac atc agc cta gac aac tta cta cct ggt atg cag cct tcc	394
Ser Val Asn Ile Ser Leu Asp Asn Leu Leu Pro Gly Met Gln Pro Ser	
	20
aaa ccc cag cag cca tca ctg aat aca atg att cag caa cag aat atg	442
Lys Pro Gln Gln Pro Ser Leu Asn Thr Met Ile Gln Gln Gln Asn Met	
	35
cag sag cct atg aat gtg atg act caa agt ttt gga gct gt	483
Gln Xaa Pro Met Asn Val Met Thr Gln Ser Phe Gly Ala	
	50
	55
	60

<210> 3671
 <211> 445
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 59..445

<400> 3671
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 atg gcg gtg gcg cgc gtg gac gcg gct ttg cct ccc gga gaa gga tca 106
 Met Ala Val Ala Arg Val Asp Ala Ala Leu Pro Pro Gly Glu Gly Ser
 1 5 10 15
 gtg gtc aat tgg tca gga cag gga cta cag aaa tta ggt cca aat tta 154
 Val Val Asn Trp Ser Gly Gln Gly Leu Gln Lys Leu Gly Pro Asn Leu
 20 25 30
 ccc tgt gaa gct gat att cac act ttg att ctg gat aaa aat cag att 202
 Pro Cys Glu Ala Asp Ile His Thr Leu Ile Leu Asp Lys Asn Gln Ile
 35 40 45
 att aaa ttg gaa aat ctg gag aaa tgc aaa cga tta ata cag tta tca 250
 Ile Lys Leu Glu Asn Leu Glu Lys Cys Lys Arg Leu Ile Gln Leu Ser
 50 55 60
 gta gct aat aat cgg ctg gtt cgg atg atg ggt gtg gcc aag ctg acg 298
 Val Ala Asn Asn Arg Leu Val Arg Met Met Gly Val Ala Lys Leu Thr
 65 70 75 80
 ttg ctt cgt gta tta aat ttg cct cat aat agc att ggc tgt gtg gaa 346
 Leu Leu Arg Val Leu Asn Leu Pro His Asn Ser Ile Gly Cys Val Glu
 85 90 95
 ggg cta aag gaa cta gta srt ctg gaa tgg ctg aat ttg gca gga aat 394
 Gly Leu Lys Glu Leu Val Xaa Leu Glu Trp Leu Asn Leu Ala Gly Asn
 100 105 110
 aat ctt aag gcc atg gva cag atc aat agc tgc aca gct cta cag cat 442
 Asn Leu Lys Ala Met Xaa Gln Ile Asn Ser Cys Thr Ala Leu Gln His
 115 120 125
 ctc 445
 Leu

<210> 3672
 <211> 343
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 47..343

<400> 3672
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 Met Val Val
 1
 tcc sam gtg gac atc gca aaa vct gat cca gct gct gca tcc cac cct 103
 Ser Xaa Val Asp Ile Ala Lys Xaa Asp Pro Ala Ala Ala Ser His Pro
 5 10 15
 cta tya ctg amt ggm gat gct act gts gcc cag ama aat cca ggc tcg 151
 Leu Xaa Leu Xaa Gly Asp Ala Thr Val Ala Gln Xaa Asn Pro Gly Ser
 20 25 30 35
 gtg gct gac aac aac ctg tgc agc cag tat gag gag aag gtg cgc ccc 199
 Val Ala Asp Asn Asn Leu Cys Ser Gln Tyr Glu Glu Lys Val Arg Pro
 40 45 50

tgc atc gac ctc att gac tcc ctg csg gct cta ggt gtg gag cag gac	247
Cys Ile Asp Leu Ile Asp Ser Leu Xaa Ala Leu Gly Val Glu Gln Asp	
55 60 65	
ctg gcc ctg cca gcc atc gcc gtc atc ggg gac cag agc tcg ggc aag	295
Leu Ala Leu Pro Ala Ile Ala Val Ile Gly Asp Gln Ser Ser Gly Lys	
70 75 80	
asc tcc gtg ttg gag gca ctg tca gga gtt gcc ctt ccc aga ggc agc	343
Xaa Ser Val Leu Glu Ala Leu Ser Gly Val Ala Leu Pro Arg Gly Ser	
85 90 95	

<210> 3673
 <211> 313
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 74..313

<400> 3673	
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ttaaactgaa agc atg ttt ctt gca aag gct cta ttg gaa gga gca gat	109
Met Phe Leu Ala Lys Ala Leu Leu Glu Gly Ala Asp	
1 5 10	
cga ggt ctt gga gaa gct ctt gga ggc ctc ttt gga gga ggt ggt cag	157
Arg Gly Leu Gly Glu Ala Leu Gly Gly Leu Phe Gly Gly Gly Gly Gln	
15 20 25	
aga aga gaa gga gga gga aga aat att gga ggg ata gtt gga gga att	205
Arg Arg Glu Gly Gly Gly Arg Asn Ile Gly Gly Ile Val Gly Gly Ile	
30 35 40	
gtg aat ttt atc agt gag gct gca gca gct cag tat act cca gaa ccg	253
Val Asn Phe Ile Ser Glu Ala Ala Ala Ala Gln Tyr Thr Pro Glu Pro	
45 50 55 60	
cct ccc act cag cag cat ttc acc agt gtg gag gcc tca gaa agt gag	301
Pro Pro Thr Gln Gln His Phe Thr Ser Val Glu Ala Ser Glu Ser Glu	
65 70 75	
gaa gtt agg cta	313
Glu Val Arg Leu	
80	

<210> 3674
 <211> 196
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 43..195

<400> 3674	
cacttgaaag aaaaactatt caaataatta ccaaggcatc ac atg agc atg aag	54
Met Ser Met Lys	

1
 ata aaa gtc ctg aaa cag ttt tgc agt cgg cca att aag ttg gaa tat 102
 Ile Lys Val Leu Lys Gln Phe Cys Ser Arg Pro Ile Lys Leu Glu Tyr
 5 10 15 20
 gca agg ttg gtt aag ttg gcc caa gaa gac acc cca cca gaa acc gat 150
 Ala Arg Leu Val Lys Leu Ala Gln Glu Asp Thr Pro Pro Glu Thr Asp
 25 30 35
 tat cgt tta cat cat gta gtg gtc tac ttt atc cag aac cag cca c 196
 Tyr Arg Leu His His Val Val Val Tyr Phe Ile Gln Asn Gln Pro
 40 45 50

<210> 3675
 <211> 309
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 81..308

<400> 3675
 ttcaagacct ggaacgaaaa cttcgcttca aggaggacct cctgaacaat ggccagccga 60
 gggttaacata cgaagaaaga atg gct cgt cga ctg cta ggt gct gac agt gca 113
 Met Ala Arg Arg Leu Leu Gly Ala Asp Ser Ala
 1 5 10
 act gtc ttt aat att cag gag cca gaa gag gaa aca gct aat cag gaa 161
 Thr Val Phe Asn Ile Gln Glu Pro Glu Glu Glu Thr Ala Asn Gln Glu
 15 20 25
 tac aaa gtc tcc agc tgt gaa cag aga ctc atc agt gaa ata gag tac 209
 Tyr Lys Val Ser Ser Cys Glu Gln Arg Leu Ile Ser Glu Ile Glu Tyr
 30 35 40
 agg cta gaa agg tct cct gtg gat gaa tca ggt gat gaa gtt cag tat 257
 Arg Leu Glu Arg Ser Pro Val Asp Glu Ser Gly Asp Glu Val Gln Tyr
 45 50 55
 gga gat gtg cct gtg gaa aat gga atg gca cca dtc ttt gag atg aag 305
 Gly Asp Val Pro Val Glu Asn Gly Met Ala Pro Xaa Phe Glu Met Lys
 60 65 70 75
 ccg a 309
 Pro

<210> 3676
 <211> 373
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 7..372

<400> 3676
 gtagcc atg cag cga gcc gat tcc gag cag ccc tcc aag cgt ccc cgt 48
 Met Gln Arg Ala Asp Ser Glu Gln Pro Ser Lys Arg Pro Arg

1	5	10	
tgc gat gac agc ccg aga acc ccc tca aac acc cct tcc gca gag gca			96
Cys Asp Asp Ser Pro Arg Thr Pro Ser Asn Thr Pro Ser Ala Glu Ala			
15	20	25	30
gac tgg tcc ccg ggc ctg gaa ctc cat ccc gac tac aag aca tgg ggt			144
Asp Trp Ser Pro Gly Leu Glu Leu His Pro Asp Tyr Lys Thr Trp Gly			
35	40	45	
ccg gag cag gtg tgc tcc ttc ctc agg cgc ggt ggc ttt gaa gag ccg			192
Pro Glu Gln Val Cys Ser Phe Leu Arg Arg Gly Gly Phe Glu Glu Pro			
50	55	60	
gtg ctg ctg aag aac atc cga gaa aat gaa atc aca ggc gca tta ctg			240
Val Leu Leu Lys Asn Ile Arg Glu Asn Glu Ile Thr Gly Ala Leu Leu			
65	70	75	
cct tgt ctt gat gag tct cgt ttt gaa aat ctt gga gta agt tcc ttg			288
Pro Cys Leu Asp Glu Ser Arg Phe Glu Asn Leu Gly Val Ser Ser Leu			
80	85	90	
ggg gag agg aag aag ctg ctt agt tat atc cag cga ttg gtt caa atc			336
Gly Glu Arg Lys Lys Leu Leu Ser Tyr Ile Gln Arg Leu Val Gln Ile			
95	100	105	110
cac gtt gat aca atg aag gta att aat gat cct atc c			373
His Val Asp Thr Met Lys Val Ile Asn Asp Pro Ile			
115	120		

<210> 3677
 <211> 321
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 49..321

<400> 3677			
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	Met Ser Glu		
	1		
gcc ggc att ttg tac tcg cga ctc agc cac atg gct grt gcc ggc cgc	105		
Ala Gly Ile Leu Tyr Ser Arg Leu Ser His Met Ala Xaa Ala Gly Arg			
5	10	15	
sck cck acc ccr rsa gca cca ggg ctt tgg aag tgg tcc cct cgc tcc	153		
Xaa Pro Thr Pro Xaa Ala Pro Gly Leu Trp Lys Trp Ser Pro Arg Ser			
20	25	30	35
cac aga atg ccc gky cac ccc aar aac acc tcc cga aac gcc gca cct	201		
His Arg Met Pro Xaa His Pro Lys Asn Thr Ser Arg Asn Ala Ala Pro			
40	45	50	
aac aga tgt tcc ttc gtc tgc ctc gar gcg tcc cgc ttt cat ccg cac	249		
Asn Arg Cys Ser Phe Val Cys Leu Glu Ala Ser Arg Phe His Pro His			
55	60	65	
aat acg ctc cct ctc aac tcc rwc aac agc tac car atg gca gcc gcc	297		
Asn Thr Leu Pro Leu Asn Ser Xaa Asn Ser Tyr Gln Met Ala Ala Ala			
70	75	80	
ccg aca gct ccc caa tcc cca sca	321		
Pro Thr Ala Pro Gln Ser Pro Xaa			

85

90

<210> 3678
 <211> 361
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 145..360

<400> 3678
 ctggcaaacc gaatccagca gcacatcaaa aagcttatcc accatgatca agtgggcttc 60
 atccatgggr tgcaaggctg gttcaacacr cgaraatcaa taraagkaat ccatcatata 120
 aacagaacca aagacaaaac ccac atg att atc tca ata gat gca gaa aag 171
 Met Ile Ile Ser Ile Asp Ala Glu Lys
 1 5
 gcc ttc aac aaa att caa caa tgc ttc atg cta aaa act ctc aat aat 219
 Ala Phe Asn Lys Ile Gln Gln Cys Phe Met Leu Lys Thr Leu Asn Asn
 10 15 20 25
 tta ggt att gat ggg acg aat ctc aaa ata ata aga gct att tat gac 267
 Leu Gly Ile Asp Gly Thr Asn Leu Lys Ile Ile Arg Ala Ile Tyr Asp
 30 35 40
 aaa ccc aca gcc aat atc ata ctg aat ggg caa aaa ctg gaa gca ttc 315
 Lys Pro Thr Ala Asn Ile Ile Leu Asn Gly Gln Lys Leu Glu Ala Phe
 45 50 55
 cct ttg aaa act ggc ata aga caa gga tgc cat ctc tca cca ctc c 361
 Pro Leu Lys Thr Gly Ile Arg Gln Gly Cys His Leu Ser Pro Leu
 60 65 70

<210> 3679
 <211> 320
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 49..318

<400> 3679
 ttacaagaat taggagctta tgttgatgaa gaacttcctg attacatt atg gtg atg 57
 Met Val Met
 1
 gtg gcc aac aag aaa agt cag gac caa atg aca gag gat ctg tcc ctg 105
 Val Ala Asn Lys Lys Ser Gln Asp Gln Met Thr Glu Asp Leu Ser Leu
 5 10 15
 ttt cta ggg aac aac aca att cga ttc acc gta tgg ctt cat ggt gta 153
 Phe Leu Gly Asn Asn Thr Ile Arg Phe Thr Val Trp Leu His Gly Val
 20 25 30 35
 tta gat aaa ctt cgc tct gtt aca act gaa ccc tct agt ctg aag tct 201
 Leu Asp Lys Leu Arg Ser Val Thr Thr Glu Pro Ser Ser Leu Lys Ser
 40 45 50

tct gat acc aac atc ttt gat agt aac gtg cct tca aac aag agc aat	249
Ser Asp Thr Asn Ile Phe Asp Ser Asn Val Pro Ser Asn Lys Ser Asn	
55 60 65	
ttc agt cgg gga gat gag agg agg cat gaa gct gca gtg cca cca ctt	297
Phe Ser Arg Gly Asp Glu Arg Arg His Glu Ala Ala Val Pro Pro Leu	
70 75 80	
gcc ann cct agc gcg aga ccg tc	320
Ala Xaa Pro Ser Ala Arg Pro	
85 90	

<210> 3680
 <211> 349
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 163..348

<400> 3680	
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gctgctgcgc tcctgcccc mgccttgggc ccttgaaggg ctctgcgagt gacccggcgg	120
gcgagctccg tgctgsatgr aaamsctgm agaaggchca ar atg gmc aat cag	174
Met Xaa Asn Gln	
1	
gtg ctg ggc tac aag gac ctg gct gcc atc ccc aag gac aag gcc atc	222
Val Leu Gly Tyr Lys Asp Leu Ala Ala Ile Pro Lys Asp Lys Ala Ile	
5 10 15 20	
ctg gac atc gag cgg ccc gac ctc atg atc tac gag cct cac ttc act	270
Leu Asp Ile Glu Arg Pro Asp Leu Met Ile Tyr Glu Pro His Phe Thr	
25 30 35	
tat wmc ctc ctg gaa cac gtg gag ctg cct cgc agc cgc gag cgc tcg	318
Tyr Xaa Leu Leu Glu His Val Glu Leu Pro Arg Ser Arg Glu Arg Ser	
40 45 50	
ctg tca ccc aaa tcc aca tcc ccc cct aca c	349
Leu Ser Pro Lys Ser Thr Ser Pro Pro Thr	
55 60	

<210> 3681
 <211> 286
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 14..286

<400> 3681	
tcgagatgtg agg atg att tct gac aga aat tca aga cgt tcc aaa gga	49
Met Ile Ser Asp Arg Asn Ser Arg Arg Ser Lys Gly	
1 5 10	
att gct tat gtg gag ttc gtc gat gtt agc tca gtg cct cta gca ata	97

Ile	Ala	Tyr	Val	Glu	Phe	Val	Asp	Val	Ser	Ser	Val	Pro	Leu	Ala	Ile		
	15						20				25						
gga	tta	act	ggc	cad	cga	gtt	tta	ggc	gtg	cca	atc	ata	gta	cag	gca		145
Gly	Leu	Thr	Gly	Xaa	Arg	Val	Leu	Gly	Val	Pro	Ile	Ile	Val	Gln	Ala		
	30						35				40						
tca	cag	gta	att	ttt	ttg	ttg	gtt	aag	agt	ttg	att	att	ggt	ggt	gtt		193
Ser	Gln	Val	Ile	Phe	Leu	Leu	Val	Lys	Ser	Leu	Ile	Ile	Gly	Gly	Val		
	45				50					55					60		
gaa	agc	ctc	ctg	ttg	cat	ggg	ata	gtg	ctg	ttg	tgt	tct	gtg	act	gct		241
Glu	Ser	Leu	Leu	Leu	His	Gly	Ile	Val	Leu	Leu	Cys	Ser	Val	Thr	Ala		
				65					70					75			
gct	cat	tac	gtt	gag	tcg	gat	gtt	ttc	agg	act	ttt	ttt	ttt	ttt			286
Ala	His	Tyr	Val	Glu	Ser	Asp	Val	Phe	Arg	Thr	Phe	Phe	Phe	Phe			
			80					85					90				

<210> 3682
 <211> 443
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 214..441

<400>	3682																	
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agagcaagct	ggactgttgc	atctgggtag	tgagcttctc	ctcctccttc	ttcctcargc												120	
ctgccctatg	gtgtggcagt	gggkgtcgcc	ttctccgtcc	tggtcgtggt	cttccagact												180	
cagtttcgaa	atggctatgc	actggcccag	gtc atg	gac act	gac att	tat gtg											234	
			Met	Asp	Thr	Asp	Ile	Tyr	Val									
			1				5											
aat ccc aag acc tat aat agg gcc cag gat atc cag ggg att aar atc																	282	
Asn Pro Lys Thr Tyr Asn Arg Ala Gln Asp Ile Gln Gly Ile Lys Ile																		
	10					15				20								
atc acg tac tgc tcc cct ctc tac ttt gcc aac tca gag atc ttc agg																	330	
Ile Thr Tyr Cys Ser Pro Leu Tyr Phe Ala Asn Ser Glu Ile Phe Arg																		
	25				30				35									
caa aag gtc atc gcc aag aca ggm atg gds ccc cag aaa gta tta cwa																	378	
Gln Lys Val Ile Ala Lys Thr Gly Met Xaa Pro Gln Lys Val Leu Xaa																		
	40			45			50			55								
gcc aag caa aaa ata cct caa gaa gca gga gaa gcg gag aat gag gcc																	426	
Ala Lys Gln Lys Ile Pro Gln Glu Ala Gly Glu Ala Glu Asn Glu Ala																		
		60				65				70								
cac aca aca gag gag gt																	443	
His Thr Thr Glu Glu																		
		75																

<210> 3683
 <211> 337
 <212> DNA
 <213> Homo sapiens

<220>

<221> CDS
<222> 3..335

<400> 3683

at atg gga aag atc ctc ccc gaa tac ctc agc aac tgg acc atg gga	47
Met Gly Lys Ile Leu Pro Glu Tyr Leu Ser Asn Trp Thr Met Gly	
1 5 10 15	
aaa gtc aga cga gag ggg gtt aag gtg atg ccc aat gct att gtg caa	95
Lys Val Arg Arg Glu Gly Val Lys Val Met Pro Asn Ala Ile Val Gln	
20 25 30	
tcc gtt gga gtc agc agt ggc aag tta ctt atc aag ctg aaa gac ggc	143
Ser Val Gly Val Ser Ser Gly Lys Leu Ile Lys Leu Lys Asp Gly	
35 40 45	
agg aag gta gaa act gac cac ata gtg gca gct gtg ggc ctg gag ccc	191
Arg Lys Val Glu Thr Asp His Ile Val Ala Ala Val Gly Leu Glu Pro	
50 55 60	
aat gtt gag ttg gcc aag act ggt ggc ctg gaa ata gac tca gat ttt	239
Asn Val Glu Leu Ala Lys Thr Gly Gly Leu Glu Ile Asp Ser Asp Phe	
65 70 75	
ggg ggc ttc cgg gta aat gca gag cta caa gca cgc tct aac atc tgg	287
Gly Gly Phe Arg Val Asn Ala Glu Leu Gln Ala Arg Ser Asn Ile Trp	
80 85 90 95	
gtg gca gga gat gct gca tgc ttc tac gat ata aag ttg gga agg arg	335
Val Ala Gly Asp Ala Ala Cys Phe Tyr Asp Ile Lys Leu Gly Arg Xaa	
100 105 110	
ac	337

<210> 3684
<211> 378
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 216..377

<400> 3684

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aggcaccaaa atttaaaaag caaccaaaac ttcttcaaat tactttctct acttaaagag	120
gaggcttcaa ttaaaattat tcctcattca gtgtgtccat ttaktttgaa aaggcaaaaa	180
ggaaagcggt taccttatgt ttcgctgaat gctgg atg agc tct gta att aac	233
Met Ser Ser Val Ile Asn	
1 5	
act ttg tcc tgt tgc aac ctt cgc ttc ata agc ttg gag cag ttg ata	281
Thr Leu Ser Cys Cys Asn Leu Arg Phe Ile Ser Leu Glu Gln Leu Ile	
10 15 20	
tta atg gct tcc aaa atg tgg gat gta ttg tat tcc aca aat ggc cgg	329
Leu Met Ala Ser Lys Met Trp Asp Val Leu Tyr Ser Thr Asn Gly Arg	
25 30 35	
cta tca att agc agc act ttt tcc gtt cca ctt tcc agc aga gcc acc a	378
Leu Ser Ile Ser Ser Thr Phe Ser Val Pro Leu Ser Ser Arg Ala Thr	
40 45 50	

<210> 3687
 <211> 398
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 151..396

<400> 3687
 aaagctacat taatsraaac agtgtatgac tagcataaaa acagacgtct agacaaatgg 60
 aacagaatag agagctcaga aataaaccca caatgatgaa aatatagtct cttcaataaa 120
 tagtgttgga aaaattggat agccacatga atg aaa ctg gac tct tat gtt ata 174
 Met Lys Leu Asp Ser Tyr Val Ile
 1 5
 cta cat gca aac att aac tca aaa tgg att aaa gtc tta aac ata aaa 222
 Leu His Ala Asn Ile Asn Ser Lys Trp Ile Lys Val Leu Asn Ile Lys
 10 15 20
 cct gaa gca ata aaa cgt tta gac aaa aac atg ggg gaa aat att cta 270
 Pro Glu Ala Ile Lys Arg Leu Asp Lys Asn Met Gly Glu Asn Ile Leu
 25 30 35 40
 gac att gtg ctg gcc aat gat tta ttg gat atg aca cca aag tgg gat 318
 Asp Ile Val Leu Ala Asn Asp Leu Leu Asp Met Thr Pro Lys Trp Asp
 45 50 55
 tat acc aag tgg gat tac atc aaa cta aaa acc tcc tgc act ggc cgg 366
 Tyr Thr Lys Trp Asp Tyr Ile Lys Leu Lys Thr Ser Cys Thr Gly Arg
 60 65 70
 gtg cgg tgg ctc acg cct gta gtc cca gca ca 398
 Val Arg Trp Leu Thr Pro Val Val Pro Ala
 75 80

<210> 3688
 <211> 262
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 64..261

<400> 3688
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 ggb atg ctt tcc ccg gga agg agg cgc gcg ggg gct ctg ccg cac gtg 108
 Met Leu Ser Pro Gly Arg Arg Arg Ala Gly Ala Leu Pro His Val
 1 5 10 15
 agg ggc akg gcc gca ggt caa agc cta gag ccg gtt tct gtt agc agc 156
 Arg Gly Xaa Ala Ala Gly Gln Ser Leu Glu Pro Val Ser Val Ser Ser
 20 25 30
 ggt gtt tgg ctg ttt krt cag gca ttt cca gca gtg aag gag aca gcc 204
 Gly Val Trp Leu Phe Xaa Gln Ala Phe Pro Ala Val Lys Glu Thr Ala
 35 40 45

aga agc aag ctt kdg gag ctg aag gaa cct kwg aca gaa gct agt ccc 252
Arg Ser Lys Leu Xaa Glu Leu Lys Glu Pro Xaa Thr Glu Ala Ser Pro
50 55 60

tcc tct gaa t 262
Ser Ser Glu
65

<210> 3689
<211> 230
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 38..229

<400> 3689
taacgtatgc acagaagctg tttttttatt attggga atg ctc cgc agc atg ctg 55
Met Leu Arg Ser Met Leu
1 5
act tca cct tgg caa tca gaa gaa gag gga tct tgg ctc cga gaa tat 103
Thr Ser Pro Trp Gln Ser Glu Glu Glu Gly Ser Trp Leu Arg Glu Tyr
10 15 20
cct gtg acc ctg atg cag ttc ttc aga tat ntg tat cac aac gtg cca 151
Pro Val Thr Leu Met Gln Phe Phe Arg Tyr Xaa Tyr His Asn Val Pro
25 30 35
gac ctt gcc tcc atg tgg atg agc cct gac ttc ctg tgt gca tta gca 199
Asp Leu Ala Ser Met Trp Met Ser Pro Asp Phe Leu Cys Ala Leu Ala
40 45 50
gcc acc gtc ttc ccc ttc aat att cgc cca t 230
Ala Thr Val Phe Pro Phe Asn Ile Arg Pro
55 60

<210> 3690
<211> 411
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 120..410

<400> 3690
actcacgtgg cccttgcttc atccagcaca gctctcaggt gggcactgca gggacactgg 60
tgtcttccat gtagegtccc agctttgggc tctgtgaaca gacctctttt tggttatgg 119
atg gct cac aaa ata ggg ccc cca atg cta ttt ttt ttt tta agt ttg 167
Met Ala His Lys Ile Gly Pro Pro Met Leu Phe Phe Phe Leu Ser Leu
1 5 10 15
ttt aat tat ttg tta aga ttg tct aag gcc aaa ggc aat tgc gaa atc 215
Phe Asn Tyr Leu Leu Arg Leu Ser Lys Ala Lys Gly Asn Cys Glu Ile
20 25 30
aag tct gtc aag tac aat aac att ttt aaa aga aaa tgg atc cca ctg 263

Lys	Ser	Val	Lys	Tyr	Asn	Asn	Ile	Phe	Lys	Arg	Lys	Trp	Ile	Pro	Leu	
		35					40					45				
ttc	ctc	ttt	gcc	aca	gag	aaa	gca	ccc	aga	cgc	cam	agg	ctc	tgt	cgc	311
Phe	Leu	Phe	Ala	Thr	Glu	Lys	Ala	Pro	Arg	Arg	Xaa	Arg	Leu	Cys	Arg	
		50				55					60					
att	tca	aaa	caa	acc	atg	atg	gak	tgg	cgg	cma	gtc	cag	cct	ttt	aaa	359
Ile	Ser	Lys	Gln	Thr	Met	Met	Xaa	Trp	Arg	Xaa	Val	Gln	Pro	Phe	Lys	
65					70				75					80		
gaa	cgt	mag	gtg	aag	cag	cca	ggt	gaa	agg	cct	ggc	ggg	gag	gaa	agt	407
Glu	Arg	Xaa	Val	Lys	Gln	Pro	Gly	Glu	Arg	Pro	Gly	Gly	Glu	Glu	Ser	
				85					90					95		
gaa	a															411
Glu																

<210> 3691
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 <212> DNA
 <213> Homo sapiens

<220>
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 <222> 152..352

<400> 3691																								
cag	agt	ccct	tg	gaa	gat	g	ctt	gag	ctt	gt	ctc	agg	tc	cct	aaa	act	ta	gaa	agt	cc	ta	60		
ttc	ttt	ttc	ccc	caa	att	ct	ga	cat	gt	gct	gg	at	cag	agt	gt	tct	catt	tc	aat	agg	cc	ag	120	
tct	gcc	at	cc	at	cag	ga	ag	aac	tgc	gg	ca	c	at	g	g	ct	gat	gg	t	g	ct	aga	gag	172
													Met	Ala	Asp	Gly	Ala	Arg	Glu					
													1											
gta	gga	aat	at	g	act	gga	acc	act	gag	at	c	aac	tca	gat	caa	ggc	cta						220	
Val	Gly	Asn	Met	Thr	Gly	Thr	Thr	Glu	Ile	Asn	Ser	Asp	Gln	Gly	Leu									
		10				15						20												
gaa	aaa	gac	aac	tca	gag	t	g	ggg	agt	gaa	act	c	g	tac	cca	ctg	cta						268	
Glu	Lys	Asp	Asn	Ser	Glu	Leu	Gly	Ser	Glu	Thr	Arg	Tyr	Pro	Leu	Leu									
		25				30					35													
ttg	cct	aag	ggt	gta	gtc	ctg	aaa	ctg	aag	cca	gtt	gcc	gac	cgt	ttc								316	
Leu	Pro	Lys	Gly	Val	Val	Leu	Lys	Leu	Lys	Pro	Val	Ala	Asp	Arg	Phe									
		40			45				50					55										
ccc	aag	aag	gct	tgg	aga	cag	aag	cgt	tca	tca	gtc	ct											354	
Pro	Lys	Lys	Ala	Trp	Arg	Gln	Lys	Arg	Ser	Ser	Val													
				60					65															

<210> 3692
 <211> 208
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 40..207

<400> 3692

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ccctttcatc atgatcaact ggatcgata tttagtgtc atg ggg ttt cct gca      54
                                Met Gly Phe Pro Ala
                                1                    5
gat aaa gac tgg gaa gat att aga aag mtg cca gaa tat ccc aca ctt      102
Asp Lys Asp Trp Glu Asp Ile Arg Lys Xaa Pro Glu Tyr Pro Thr Leu
                                10                    15                    20
caa aaa gac ttt aga aga aca acg tat gcc aac agt agc ctc ata aag      150
Gln Lys Asp Phe Arg Arg Thr Thr Tyr Ala Asn Ser Ser Leu Ile Lys
                                25                    30                    35
tac atg gag aaa cac aag gtc aag cct gac agc aaa gtg ttc ctc ttg      198
Tyr Met Glu Lys His Lys Val Lys Pro Asp Ser Lys Val Phe Leu Leu
                                40                    45                    50
ctt cag aaa c                                                              208
Leu Gln Lys
                                55

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<210> 3693
 <211> 251
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 45..251

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<400> 3693
ttaggacggg cgggtgcaat cctcgaaggg gagtctcagc gacc atg ggg gac acc      56
                                Met Gly Asp Thr
                                1
atc cac tgt aag aka aca acg gca ggg ggc gtc agt ata gga tgg aam      104
Ile His Cys Lys Xaa Thr Thr Ala Gly Gly Val Ser Ile Gly Trp Xaa
5                                10                    15                    20
kcg cgg ggg gtg tgc agg ggg ggc tgg gct ggc ccg cgc tgg gcc cta      152
Xaa Arg Gly Val Cys Arg Gly Ala Trp Ala Ala Pro Arg Trp Ala Leu
                                25                    30                    35
ccg tcg gaa gtc tgc gag cgg gga acc aga atg tac cag gtc gag aag      200
Pro Ser Glu Val Cys Glu Arg Gly Thr Arg Met Tyr Gln Val Glu Lys
                                40                    45                    50
cac tgg gct gaa cca caa gaa gcc aat agg agg ggg gaa tcg gga cgt      248
His Trp Ala Glu Pro Gln Glu Ala Asn Arg Arg Gly Glu Ser Gly Arg
                                55                    60                    65
cca                                                              251
Pro

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<210> 3694
 <211> 260
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 77..259

<400> 3694
 tgggttgacc aggtgtgtca ttacataac gtgcgaagaa gatggctacc ccaccctaataat 60
 cttttattat gcagat atg tgc cat att gcc tgt ttc ttt act gta cac gtk 112
 Met Cys His Ile Ala Cys Phe Phe Thr Val His Val
 1 5 10
 rtg aca aag aaa agg gaa gat gga gcc tcc atg ctg aac atg cct ggt 160
 Xaa Thr Lys Lys Arg Glu Asp Gly Ala Ser Met Leu Asn Met Pro Gly
 15 20 25
 ccc cag gta gcc ttt tcc tat tgg cat agc tgc cag cat tca tcc atg 208
 Pro Gln Val Ala Phe Ser Tyr Trp His Ser Cys Gln His Ser Ser Met
 30 35 40
 caa gct tcc agt ttg ctt atc tat gtt tgc agc tca act ttt cag gcc 256
 Gln Ala Ser Ser Leu Leu Ile Tyr Val Cys Ser Ser Thr Phe Gln Ala
 45 50 55 60
 acc g 260
 Thr

<210> 3695
 <211> 318
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 34..318

<400> 3695
 acagcagcgg cgcgkwagac tgcggggcgg gcc atg gcg gcg aac ctg agc cgg 54
 Met Ala Ala Asn Leu Ser Arg
 1 5
 aac ggg cca gcg ctg caa gag gcc tac gtg cgg gtg gtc acc gag aag 102
 Asn Gly Pro Ala Leu Gln Glu Ala Tyr Val Arg Val Val Thr Glu Lys
 10 15 20
 tcc ccg acc gac tgg gct ctc ttt acc tat gaa ggc aac agc aat gac 150
 Ser Pro Thr Asp Trp Ala Leu Phe Thr Tyr Glu Gly Asn Ser Asn Asp
 25 30 35
 atc cgc gtg gct ggc aca ggg gag ggt ggc ctg gag gag atg gtg gag 198
 Ile Arg Val Ala Gly Thr Gly Glu Gly Gly Leu Glu Glu Met Val Glu
 40 45 50 55
 gag ctc aac agc ggg aag gtg atg tac gcc ttc tgc aga gtg aag gac 246
 Glu Leu Asn Ser Gly Lys Val Met Tyr Ala Phe Cys Arg Val Lys Asp
 60 65 70
 ccc aac tct gga ctg ccc aaa ttt gtc ctc atc aac tgg aca ggc gag 294
 Pro Asn Ser Gly Leu Pro Lys Phe Val Leu Ile Asn Trp Thr Gly Glu
 75 80 85
 ggc gtg aac gat gtg cgg aca ggg 318
 Gly Val Asn Asp Val Arg Thr Gly
 90 95

<210> 3696
 <211> 433
 <212> DNA

004320" 666E7560

<213> Homo sapiens

<220>

<221> CDS

<222> 226..432

<400> 3696

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gcgctttgtt caagatgtgg gtctggcgct ttcgtgactc aagaccctct taggaacttc      60
ttcactgaac tcaaggagga gatcaggcaa gatctgtgct gtgcagatcc tttggattga      120
ggctgctgtg cacaggavta tggatggata ctctccaagc tgtaagggaag aagtcaagga      180
ttaaggagac ctggactgga gaggagcctt tttcaaaaaa caaca atg aca aga gaa      237
                                   Met Thr Arg Glu
                                   1
aat gta gcc cac aat gct ctg aga caa gag ggc ctt gtg aag ggg aag      285
Asn Val Ala His Asn Ala Leu Arg Gln Glu Gly Leu Val Lys Gly Lys
5                               10                               15                               20
gat gat acc tgg aaa tgg gga acc agc ttc caa gga agt agc tcc tct      333
Asp Asp Thr Trp Lys Trp Gly Thr Ser Phe Gln Gly Ser Ser Ser Ser
25                               30                               35
gtt tgg gag acc tcc cac cta cac ttt aga caa tta cgt tac cat gag      381
Val Trp Glu Thr Ser His Leu His Phe Arg Gln Leu Arg Tyr His Glu
40                               45                               50
aca tct gga ccc cag gaa gcc ctg agc cgg ctc agg gaa ctc tgt cgc      429
Thr Ser Gly Pro Gln Glu Ala Leu Ser Arg Leu Arg Glu Leu Cys Arg
55                               60                               65
cgg t
Arg
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<210> 3697

<211> 356

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 195..356

<400> 3697

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ctaaaaatttc aactttttcag ggetgcccc a ttttccctgt ggatggcccg taattttattt      60
aaccagtgcc ccttgttgat gtatttaggt tatttttagtt ctgatgaact aaaaattatt      120
cctttctcct atttaaagga aaaaggctag ccctgtggac tccatgagct ttttgcacca      180
ttgggtacat ccat atg gtg gaa cgt cat gcg ggt tta aaa agc agc gta      230
                                   Met Val Glu Arg His Ala Gly Leu Lys Ser Ser Val
                                   1                               5                               10
tgt gag gaa ttt gag att gga gca gga tgg tgt gct aca gta gga aat      278
Cys Glu Glu Phe Glu Ile Gly Ala Gly Trp Cys Ala Thr Val Gly Asn
15                               20                               25
gga aga ggt aga gtg tgt gct gtg atc aca gcc tta ttt cct ctg act      326
Gly Arg Gly Arg Val Cys Ala Val Ile Thr Ala Leu Phe Pro Leu Thr
30                               35                               40
tct aat tta gag agc ana ata aag ata tat      356
Ser Asn Leu Glu Ser Xaa Ile Lys Ile Tyr
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50

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<220>  
<221> CDS  
<222> 24..248
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<210> 3699
<211> 461
<212> DNA
<213> Homo sapiens
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<220>  
<221> CDS  
<222> 302..460
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<400>	3699
tgatacttag cttcagcgac ttgacaacag taacctttag tcttttaata cttacctgac	60
agtatttgtg cattactgta aataactaat gagacttata ttttataaac taaatatatt	120
tttacatagc tatcaaacia aaaaatccct tcgggtgtga ttocatagtg tatcctctgg	180
tgaattactt ttaaaaaatt tttctttttt tatagagaaa aggtctcaact atgttgctca	240
ggctggctctt aacctctgg cctcaaacac tctccagct ttggettccc aaagtgcctgg	300
g atg aca gat ctg agc crc cat gcc tgg cct gtg aat tac ttt tat aaa	349
Met Thr Asp Leu Ser Xaa His Ala Trp Pro Val Asn Tyr Phe Tyr Lys	
1 5 10 15	
gtg gaa atg tct ttc ttt tgt gtg naw tat ctt agt tgt ttc ttc aga	397
Val Glu Met Ser Phe Phe Cys Val Xaa Tyr Leu Ser Cys Phe Phe Arg	
20 25 30	

tat aaa ata ctg tgt gta tgt atg caw gtg tgt gta cac acc aca cac	445
Tyr Lys Ile Leu Cys Val Cys Met Xaa Val Cys Val His Thr Thr His	
35 40 45	

ata tta agt gca agc a	461
Ile Leu Ser Ala Ser	
50	

<210> 3700
 <211> 385
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 144..383

<400> 3700	
gatttttcta gcgatttcca gtgtgcatgc tcaagagtta ttttaaagta gacgcaagtg	60
tttctcatgc cacagacatt ttgttaaaaa cctaacttga aatatacaag tgagttcacc	120
aaactcataa aaatgtcctt aaa atg ata aaa tgg aga act ttg ggg tcc caa	173
Met Ile Lys Trp Arg Thr Leu Gly Ser Gln	
1 5 10	
caa aga gga att aag gcc tgg atc atg att acc tct gtt ttc cat gtg	221
Gln Arg Gly Ile Lys Ala Trp Ile Met Ile Thr Ser Val Phe His Val	
15 20 25	
act ttg aaa gca gca ggg ctg gag cca agt tgg ccc tgc tcc ctc cta	269
Thr Leu Lys Ala Ala Gly Leu Glu Pro Ser Trp Pro Cys Ser Leu Leu	
30 35 40	
ggg aca gca ggg ttg atg tcc acc tcc att nbc att tgc ttc tgt bca	317
Gly Thr Ala Gly Leu Met Ser Thr Ser Ile Xaa Ile Cys Phe Cys Xaa	
45 50 55	
gcc ggc agg cct tgg cgg ccc ctc ctg gct ctg gag ctt tac ata ctt	365
Ala Gly Arg Pro Trp Arg Pro Leu Leu Ala Leu Glu Leu Tyr Ile Leu	
60 65 70	
tct tat tct atc cgc atc ca	385
Ser Tyr Ser Ile Arg Ile	
75 80	

<210> 3701
 <211> 307
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 62..307

<400> 3701	
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c atg cta tgg tgt tta tgg agg atg tak tct gca gca gga agt gtg atg	109
Met Leu Trp Cys Leu Trp Arg Met Xaa Ser Ala Ala Gly Ser Val Met	
1 5 10 15	

ggc act gac gsy gca gra aga ctc ctg kbg tcc acc tcg gga gct gac	157
Gly Thr Asp Xaa Ala Xaa Arg Leu Leu Xaa Ser Thr Ser Gly Ala Asp	
20 25 30	
acg ata aat gcg ggt aaa tct caa tcc ttt aat atc ttt atg act tct	205
Thr Ile Asn Ala Gly Lys Ser Gln Ser Phe Asn Ile Phe Met Thr Ser	
35 40 45	
ktc tct ttc gck tca att tct att ttc tca tgt tca agg ctg aca ttc	253
Xaa Ser Phe Ala Ser Ile Ser Ile Phe Ser Cys Ser Arg Leu Thr Phe	
50 55 60	
aaa act aaa cac ctt tct cta aca tgt tgc ttt aat tat tta agc att	301
Lys Thr Lys His Leu Ser Leu Thr Cys Cys Phe Asn Tyr Leu Ser Ile	
65 70 75 80	
ctg cct	307
Leu Pro	

<210> 3702
 <211> 297
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 112..297

<400> 3702	
gaggtgagtc tggagawgag agtttccacg ttgtcatcat aggatctgga ctcaagtac	60
caaaaccttg cttggatttt tacctgatga agtttgtctt gaaaagtga a atg gtt	117
Met Val	
1	
cca wtt cca ttt tcc chg dte ttm aag ggt aat tca gct ttc ttt gtg	165
Pro Xaa Pro Phe Ser Xaa Xaa Xaa Lys Gly Asn Ser Ala Phe Phe Val	
5 10 15	
tgt gag tgt gtg agt gtg tgc aag tgt gtg tgc gtg cag tct ccc cag	213
Cys Glu Cys Val Ser Val Cys Lys Cys Val Cys Val Gln Ser Pro Gln	
20 25 30	
cat aga aca ccc aca cat gca ccc acc cac atg cag aca cgc aca tac	261
His Arg Thr Pro Thr His Ala Pro Thr His Met Gln Thr Arg Thr Tyr	
35 40 45 50	
tca tgc atg gat tct tgt tca cga agt acc cac cgc	297
Ser Cys Met Asp Ser Cys Ser Arg Ser Thr His Arg	
55 60	

<210> 3703
 <211> 363
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 208..363

<400> 3703

004220" 666E7560

taaaggacta agagtaaaaa caaaaccagc aaggaaactg gaagaaaata gaggttttta 60
 aaagtaattt gagagaatga gtaaaacagt gggatctttc ttacccccta ataaaatgaa 120
 aaagtgaggg aatttaagaa attagttttt tgttggtatc atctgtttta cagattattg 180
 tggatatttg caatggtagg ctgaata atg tac ccc tcc aaa gat act cat gtt 234

Met Tyr Pro Ser Lys Asp Thr His Val

1 5
 tta atc cct aaa acc tgt gca tat gtt gcg tta gat ggt aaa ttg gat 282
 Leu Ile Pro Lys Thr Cys Ala Tyr Val Ala Leu Asp Gly Lys Leu Asp

10 15 20 25
 ttt gca aat ttg att aag gat ctt gca atg ggg agg ctg tcc tgg ata 330
 Phe Ala Asn Leu Ile Lys Asp Leu Ala Met Gly Arg Leu Ser Trp Ile

30 35 40
 act gga ttg gcc cag tgt gat cac aaa ggt tcc 363
 Thr Gly Leu Ala Gln Cys Asp His Lys Gly Ser
 45 50

<210> 3704

<211> 206

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 2..205

<400> 3704

a atg gtg gcg ggt cgn cgg agc tct gat cgc cgg gaa mcc ttg ccg ctg 49
 Met Val Ala Gly Arg Arg Ser Ser Asp Arg Arg Glu Xaa Leu Pro Leu

1 5 10 15
 ctg tcc tgc gac ccc aag caa ggt ata gac acg tgt ggc cgt tta cgc 97
 Leu Ser Cys Asp Pro Lys Gln Gly Ile Asp Thr Cys Gly Arg Leu Arg

20 25 30
 tgt agg atc ctc att ccc act ggc ttt gaa cat ttt ggg gac tta caa 145
 Cys Arg Ile Leu Ile Pro Thr Gly Phe Glu His Phe Gly Asp Leu Gln
 35 40 45

tgc cgc cac ccg scg gac atc gtc aag gtg gcc ata gan tgg ccg ggc 193
 Cys Arg His Pro Xaa Asp Ile Val Lys Val Ala Ile Xaa Trp Pro Gly
 50 55 60

gcc tac ccc aaa c 206
 Ala Tyr Pro Lys
 65

<210> 3705

<211> 247

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 68..247

<400> 3705

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catttgcctt ttgattttgt ttaatttctt tatggactt attttactaa ctgaggtttg      60
aatgtaa atg gta tac ata acc atc ttt tcc tct gtg gtt tct tcc att      109
      Met Val Tyr Ile Thr Ile Phe Ser Ser Val Val Ser Ser Ile
      1          5          10
acc tkk atg ctt aga aat tct tgc cta tct gag atc aga tat tca cca      157
Thr Xaa Met Leu Arg Asn Ser Cys Leu Ser Glu Ile Arg Tyr Ser Pro
15          20          25          30
gta ttt tct ttt gga att tgt ttg ttt att tac tat ttg tct ttt ccc      205
Val Phe Ser Phe Gly Ile Cys Leu Phe Ile Tyr Tyr Leu Ser Phe Pro
      35          40          45
ctc agg gtt agc aga cta agt cta tgg ggc aaa tct ggc cac      247
Leu Arg Val Ser Arg Leu Ser Leu Trp Gly Lys Ser Gly His
      50          55          60

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<210> 3706
 <211> 235
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 75..233

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<400> 3706
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ttgaggactc agca atg acc aga ggg tgc tgg gaa ggg cga gca cta ctt      110
      Met Thr Arg Gly Cys Trp Glu Gly Arg Ala Leu Leu
      1          5          10
cgc arg cac ggg aty cty mag cac cag ggg aac acr gta gtt cca gga      158
Arg Xaa His Gly Ile Leu Xaa His Gln Gly Asn Thr Val Val Pro Gly
15          20          25
agt tct ggg tgt tcc tgg gga gag agc ggc ttg tca ttt cgg agg cca      206
Ser Ser Gly Cys Ser Trp Gly Glu Ser Gly Leu Ser Phe Arg Arg Pro
30          35          40
ggg aaa ggg gcc tcc tgc cac cgc ctg cc      235
Gly Lys Gly Ala Ser Cys His Arg Leu
45          50

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<210> 3707
 <211> 259
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 11..259

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<400> 3707
aatactttta atg ctt ata gta tat att gtg atg ggc ctt gct ggg gga      49
      Met Leu Ile Val Tyr Ile Val Met Gly Leu Ala Gly Gly
      1          5          10
tac tgg act aaa cag ccc ctc ccc ccc ttt ttt ttt ctg agg cgg agt      97

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Tyr	Trp	Thr	Lys	Gln	Pro	Leu	Pro	Pro	Phe	Phe	Phe	Leu	Arg	Arg	Ser		
15						20				25							
ctc	agt	ctg	tcc	agg	ctg	gag	tgc	att	ggc	gca	aty	tct	tct	cac	tgc	145	
Leu	Ser	Leu	Ser	Arg	Leu	Glu	Cys	Ile	Gly	Ala	Ile	Ser	Ser	His	Cys		
30					35				40					45			
aac	ctc	tgc	cgc	cca	ggg	tca	agc	gat	ttt	ctt	gcc	tca	gcc	tcc	caa	193	
Asn	Leu	Cys	Arg	Pro	Gly	Ser	Ser	Asp	Phe	Leu	Ala	Ser	Ala	Ser	Gln		
				50					55					60			
gta	gct	ggg	att	aca	ggc	gcc	tgc	cac	tgt	gcc	cgg	cta	att	ttt	gta	241	
Val	Ala	Gly	Ile	Thr	Gly	Ala	Cys	His	Cys	Ala	Arg	Leu	Ile	Phe	Val		
			65					70						75			
ttt	tta	gta	gag	acg	gga											259	
Phe	Leu	Val	Glu	Thr	Gly												
			80														

<210> 3708
 <211> 440
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 180..440

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ttttcaattt	tcaactcctt	catgatgggtg	atcttcttgg	tgggcttagt	ttcaatgatt	120											
ttaatgagaa	cattaagaaa	agaattaatg	mctcsggtac	aktaaagagg	aagaaatgg	179											
atg	ang	atg	gat	aga	gac	cta	gga	gat	gaa	tat	gga	tgg	aaa	cag	gtg	227	
Met	Xaa	Met	Asp	Arg	Asp	Leu	Gly	Asp	Glu	Tyr	Gly	Trp	Lys	Gln	Val		
1			5					10					15				
cat	gga	gat	gta	ttt	aga	cca	tca	agt	cac	cca	ctg	ata	ttt	tcc	tct	275	
His	Gly	Asp	Val	Phe	Arg	Pro	Ser	Ser	His	Pro	Leu	Ile	Phe	Ser	Ser		
			20					25					30				
ctg	att	ggg	tct	gga	tgt	cag	ata	ttt	gct	gtg	tct	ctc	atc	gtt	atw	323	
Leu	Ile	Gly	Ser	Gly	Cys	Gln	Ile	Phe	Ala	Val	Ser	Leu	Ile	Val	Ile		
		35				40					45						
att	gtt	gca	atg	ata	gaa	gnt	tta	tat	act	gag	agg	gga	tca	atg	ctc	371	
Ile	Val	Ala	Met	Ile	Glu	Xaa	Leu	Tyr	Thr	Glu	Arg	Gly	Ser	Met	Leu		
		50				55				60							
agt	aca	gcc	ata	ttt	gtc	tat	gct	gmt	amg	tct	ccc	agt	gaa	tgg	tta	419	
Ser	Thr	Ala	Ile	Phe	Val	Tyr	Ala	Xaa	Xaa	Ser	Pro	Ser	Glu	Trp	Leu		
		65				70				75				80			
ttt	tgg	agg	aag	tct	gta	tgc										440	
Phe	Trp	Arg	Lys	Ser	Val	Cys											
					85												

<210> 3709
 <211> 277
 <212> DNA
 <213> Homo sapiens

<220>

<221> CDS
<222> 112..276

<400> 3709

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ctgattttct ttgacagttt ttattgccca tgtatttttt tcagctttgt tgaggtataa      60
ttgataaatc caaaatatat atttaaggta tgcaatgtga tgctttgatg t atg tat      117
                                     Met Tyr
                                     1
gga ttg tgd mat gat tac cac agt gaa gct aat caa tat gtt cgt cag      165
Gly Leu Xaa Xaa Asp Tyr His Ser Glu Ala Asn Gln Tyr Val Arg Gln
      5                                10                                15
ctc acc tca gta ccc gtt ttt ttg tgt gtg ttt gtg tgt gtg gtg aga      213
Leu Thr Ser Val Pro Val Phe Leu Cys Val Phe Val Cys Val Val Arg
      20                                25                                30
aaa cct gtg att tac tct cag cag att tca agt aca caa tct att gtc      261
Lys Pro Val Ile Tyr Ser Gln Gln Ile Ser Ser Thr Gln Ser Ile Val
      35                                40                                45                                50
att aac tac cgt ccc c
Ile Asn Tyr Arg Pro
                                     55

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<210> 3710
<211> 335
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 100..333

<400> 3710

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ttacggmatg gcggccacct gcatataaaa atawaactta gtggagagat cactataaat      60
actgatgawa ttgatttggc tgggtgatatc atccagtca atg gca tca ttt ktt      114
                                     Met Ala Ser Phe Xaa
                                     1                                5
gct att gaa gac ctt caa gta gaa gcg gat ttt cct gtc tat ttt gag      162
Ala Ile Glu Asp Leu Gln Val Glu Ala Asp Phe Pro Val Tyr Phe Glu
      10                                15                                20
gaa tta cga aag gtg cta gtt aag gtg gat gaa tat cat tca gtg cat      210
Glu Leu Arg Lys Val Leu Val Lys Val Asp Glu Tyr His Ser Val His
      25                                30                                35
cag aag ctc agt gct gat atg gct gat cat tct aat ttg atc cga agt      258
Gln Lys Leu Ser Ala Asp Met Ala Asp His Ser Asn Leu Ile Arg Ser
      40                                45                                50
tng ctg gtc gga gct gag grt gct cgt ctg atg agg gwc atg aaa aca      306
Xaa Leu Val Gly Ala Glu Xaa Ala Arg Leu Met Arg Xaa Met Lys Thr
      55                                60                                65
atg aag agt cgt nat atg gaa ctc tat ga
Met Lys Ser Arg Xaa Met Glu Leu Tyr
      70                                75

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<210> 3711

<211> 375
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 121..375

<400> 3711
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 gcttcctgat caaagggttc tgatgttatt agcagcataa ggcaattatc taaagcggcc 120
 atg aaa gan gga kgc maa mcc chg gca aad ata aat gwk hac gcc ttt 168
 Met Lys Xaa Gly Xaa Xaa Xaa Xaa Ala Xaa Ile Asn Xaa Xaa Ala Phe
 1 5 10 15
 tac aac tct cag aag ttc gaa gtc ctg tac tgt gga aag gtg acc gtg 216
 Tyr Asn Ser Gln Lys Phe Glu Val Leu Tyr Cys Gly Lys Val Thr Val
 20 25 30
 acc cac aag aag gcc ccc tca agc ctc atc gmt gac tgc atg gag aag 264
 Thr His Lys Lys Ala Pro Ser Ser Leu Ile Xaa Asp Cys Met Glu Lys
 35 40 45
 ttc agc ctg cac gaa cag cag cgc ctg aag atc caa ggc gag cag cgc 312
 Phe Ser Leu His Glu Gln Gln Arg Leu Lys Ile Gln Gly Glu Gln Arg
 50 55 60
 ggt ccg gam cma gga gag gac mwg gct gac wtg gag gtg gtg gtg ccc 360
 Gly Pro Xaa Xaa Gly Glu Asp Xaa Ala Asp Xaa Glu Val Val Val Pro
 65 70 75 80
 ggg tcc ccc gga aga 375
 Gly Ser Pro Gly Arg
 85

<210> 3712
 <211> 401
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 119..400

<400> 3712
 cccttctttt tctccctcc cctccaaccg cgccccccct cccggatggg gaaaaaaaaa 60
 gatgtcagct cctccgctgt agtattgtc cttaaaaacc cctctctctg aaaatgac 118
 atg ccc tcg caa kgt aac tcc gaa ctc gta cgc gga scc ttg gct gcg 166
 Met Pro Ser Gln Xaa Asn Ser Glu Leu Val Arg Gly Xaa Leu Ala Ala
 1 5 10 15
 ccc ggc gga gga gag cgc tat agc cgg agc gca ggc atg tat atg cag 214
 Pro Gly Gly Gly Glu Arg Tyr Ser Arg Ser Ala Gly Met Tyr Met Gln
 20 25 30
 tct ggg agt gac ttc aat tgc ggg gtg atg agg ggc tgc ggg ctc gcg 262
 Ser Gly Ser Asp Phe Asn Cys Gly Val Met Arg Gly Cys Gly Leu Ala
 35 40 45
 ccc tcg ctc tcc aag agg gac gag ggc agc agc ccc agc ytc gcc ctc 310

aga acc tct tct tct cca aag gaa mgc agc tcc tca cca gca gcg gaa	158
Arg Thr Ser Ser Ser Pro Lys Glu Xaa Ser Ser Ser Pro Ala Ala Glu	
20 25 30	
caa agc tgg atg gag aat gac ttt gat gag ttg aga gaa gaa ggc ttc	206
Gln Ser Trp Met Glu Asn Asp Phe Asp Glu Leu Arg Glu Glu Gly Phe	
35 40 45	
aga cga tca aac ttc tcc gag cta aag gag gag	239
Arg Arg Ser Asn Phe Ser Glu Leu Lys Glu Glu	
50 55	

<210> 3715
 <211> 207
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 7..207

<400> 3715	
ttttcc atg acc ata ggt cac tgt cta cac tgg gta cac ttt gta cca	48
Met Thr Ile Gly His Cys Leu His Trp Val His Phe Val Pro	
1 5 10	
gtg tcg gcc tcc act gat gct ggt gct cag gca cct ctg tcc aag gac	96
Val Ser Ala Ser Thr Asp Ala Gly Ala Gln Ala Pro Leu Ser Lys Asp	
15 20 25 30	
aat ccc ttt cac aaa caa acc agc tgc ctt tgt atc ttg tac ctt ttc	144
Asn Pro Phe His Lys Gln Thr Ser Cys Leu Cys Ile Leu Tyr Leu Phe	
35 40 45	
aga gaa agg gag gta tcc ctg tgc caa agg ctc cag gcc tct ccc stg	192
Arg Glu Arg Glu Val Ser Leu Cys Gln Arg Leu Gln Ala Ser Pro Xaa	
50 55 60	
caa ctc agg acc cca	207
Gln Leu Arg Thr Pro	
65	

<210> 3716
 <211> 457
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 15..455

<400> 3716	
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Met Ser Ser Asn Arg Pro Val Glu Ile Val Glu Asp	
1 5 10	
ccc cgg gtc gtc ggg atc tgg acc aaa aac aag gag ctg gag ctg tcg	98
Pro Arg Val Val Gly Ile Trp Thr Lys Asn Lys Glu Leu Glu Leu Ser	
15 20 25	

gtg ccc aaa ttc aag atc gat gag ttc tam gtg ggc ccg rtg cct mcg	146
Val Pro Lys Phe Lys Ile Asp Glu Phe Xaa Val Gly Pro Xaa Pro Xaa	
30 35 40	
aag cds gtg aca htt gcc aag ctk hat gat aac atc cgt gaa aac ttc	194
Lys Xaa Val Thr Xaa Ala Lys Leu Xaa Asp Asn Ile Arg Glu Asn Phe	
45 50 55 60	
ctg agg gac atg tgc aag aag tat ggk vag gtg gag gag gtg gag att	242
Leu Arg Asp Met Cys Lys Lys Tyr Gly Xaa Val Glu Glu Val Glu Ile	
65 70 75	
ttg tac aac ccc aag acc aag aag cac ctg ggc att gcc aag gtg gtc	290
Leu Tyr Asn Pro Lys Thr Lys Lys His Leu Gly Ile Ala Lys Val Val	
80 85 90	
ttt gcc acg gtc cgg gga gcc aag gat gcc gtt cag cac ttg cac agc	338
Phe Ala Thr Val Arg Gly Ala Lys Asp Ala Val Gln His Leu His Ser	
95 100 105	
act tcc gtc atg ggc aac att atc cac gtg gag ctg gac acc aaa ggg	386
Thr Ser Val Met Gly Asn Ile Ile His Val Glu Leu Asp Thr Lys Gly	
110 115 120	
gaa acc cga atg cgg ttc tat gaa ctg ttg gtc act ggc cga tac acc	434
Glu Thr Arg Met Arg Phe Tyr Glu Leu Leu Val Thr Gly Arg Tyr Thr	
125 130 135 140	
ccc car acc ctc cca gtg ggc ga	457
Pro Gln Thr Leu Pro Val Gly	
145	

<210> 3717
 <211> 244
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 56..244

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Met	
1	
gtg ttt agt ggc atg atc tgc gct cac tgc aac ata ccc ctc ctg ggt	106
Val Phe Ser Gly Met Ile Ser Ala His Cys Asn Ile Pro Leu Leu Gly	
5 10 15	
tca agt gat tct tct gnn tca gcc tcc caa gta gct ggg att aca ggt	154
Ser Ser Asp Ser Ser Xaa Ser Ala Ser Gln Val Ala Gly Ile Thr Gly	
20 25 30	
gtg cac cac cac acc tgg cta att ttw gta ttt tta gta gag atg ggc	202
Val His His His Thr Trp Leu Ile Xaa Val Phe Leu Val Glu Met Gly	
35 40 45	
ttt cgc cat gtt ggc cag gct ggt ctc aaa ctc cgg acc tca	244
Phe Arg His Val Gly Gln Ala Gly Leu Lys Leu Arg Thr Ser	
50 55 60	

<210> 3718
 <211> 257

<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 92..256

<400> 3718
aactgaatgg cggtgaaacc ctgccgggga cctcgtggca ttccatgaaa cgacctcatc 60
acaggggaat gaactttatc ttgaaggcta g atg aga atc tgt cta tgt tgc 112
Met Arg Ile Cys Leu Cys Cys
1 5
cca ggc tgg tct cca act cct gac ttc aag caa tcc tcc tgc ctc agc 160
Pro Gly Trp Ser Pro Thr Pro Asp Phe Lys Gln Ser Ser Cys Leu Ser
10 15 20
ctc cca aag tgc tgg gat tac agg cat gag cca bag tgc cca gcc cca 208
Leu Pro Lys Cys Trp Asp Tyr Arg His Glu Pro Xaa Cys Pro Ala Pro
25 30 35
ctc cca ttt tct gaa tct ttc aga att tca gat tgc ctt aaa ctg ccc a 257
Leu Pro Phe Ser Glu Ser Phe Arg Ile Ser Asp Cys Leu Lys Leu Pro
40 45 50 55

<210> 3719
<211> 244
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 80..244

<400> 3719
agaaaacacc actaaagccc cagcacagga gagaaccacc cagcccagaa gttccagggga 60
aggaactctc cgggtccacc atg gag tac ctc tca gct ctg aac ccc agt gac 112
Met Glu Tyr Leu Ser Ala Leu Asn Pro Ser Asp
1 5 10
tta ctc agg tca gta tct aat ata agc tcg gag ttt gga cgg agg gtc 160
Leu Leu Arg Ser Val Ser Asn Ile Ser Ser Glu Phe Gly Arg Arg Val
15 20 25
tgg acc tca gct cca cca ccc cag cga cct ttc cgt gtc tgt gat cac 208
Trp Thr Ser Ala Pro Pro Pro Gln Arg Pro Phe Arg Val Cys Asp His
30 35 40
aag cgg acc atc cgg aaa ggc ctg aca gct gcc ttc 244
Lys Arg Thr Ile Arg Lys Gly Leu Thr Ala Ala Phe
45 50 55

<210> 3720
<211> 404
<212> DNA
<213> Homo sapiens

<220>

<221> CDS
<222> 160..402

<400> 3720
aacaaagaca gaaaggatgg ctatgtgctg agactcaacc gagtgaacga cgcccaggaa 60
tacagacggg gtggcctggg atctctgttc tatcttacac tggatgtgct agagactgac 120
tgccatgtgc tcagaaagaa ggcatggcaa gactgtgga atg agg ata ttt ttt 174
Met Arg Ile Phe Phe
1 5
gaa tca gtt tat ggt caa tgc aaa gca ata ttt tat atg aac aac cca 222
Glu Ser Val Tyr Gly Gln Cys Lys Ala Ile Phe Tyr Met Asn Asn Pro
10 15 20
agt aga gtt ctc tat kna gct gct tat aac tgt act ctt cgc cca gtt 270
Ser Arg Val Leu Tyr Xaa Ala Ala Tyr Asn Cys Thr Leu Arg Pro Val
25 30 35
tca aaa aaa aag att tac atg acg tgc cct gac tgc cca agc tcc ata 318
Ser Lys Lys Lys Ile Tyr Met Thr Cys Pro Asp Cys Pro Ser Ser Ile
40 45 50
ccc act gac tct tcc aat cac caa gtg ctg gag gct gcc acc gag tct 366
Pro Thr Asp Ser Ser Asn His Gln Val Leu Glu Ala Ala Thr Glu Ser
55 60 65
cwn gcg aaa tac aac aat gag aac aca tcc aag cag ta 404
Xaa Ala Lys Tyr Asn Asn Glu Asn Thr Ser Lys Gln
70 75 80

<210> 3721
<211> 526
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 132..464

<221> sig_peptide
<222> 132..176
<223> score 9.3
seq ALVLLLCIGALLG/HS

<400> 3721
aatctgaagc ctgctggacg ctggattaga aggcagcaaa aaaagctctg tgctggctgg 60
agccccctca gtgtgcaggc ttagagggac taggctgggt gtggagctgc agcgtatcca 120
caggccccag g atg cag gcc ctg gtg cta ctc ctc tgc att gga gcc ctc 170
Met Gln Ala Leu Val Leu Leu Leu Cys Ile Gly Ala Leu
-15 -10 -5
ctc ggg cac agc agc tgc cag aac cct gcc agc ccc ccg gag gag ggc 218
Leu Gly His Ser Ser Cys Gln Asn Pro Ala Ser Pro Pro Glu Glu Gly
1 5 10
tcc cca gac ccc gac agc aca ggg gcg ctg gtg gag gag gag gat cct 266
Ser Pro Asp Pro Asp Ser Thr Gly Ala Leu Val Glu Glu Glu Asp Pro
15 20 25 30
ttc ttc aaa gtc ccc gtg aac aag ctg gca gcg gct gtc tcc aac ttc 314

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Phe Phe Lys Val Pro Val Asn Lys Leu Ala Ala Ala Val Ser Asn Phe
      35              40              45
ggc tat gac ctg tac cgg gtg cga tcc wgc acg agc ccc acg acc aac      362
Gly Tyr Asp Leu Tyr Arg Val Arg Ser Xaa Thr Ser Pro Thr Thr Asn
      50              55              60
gtg ctc ctg tct cct ctc agt gtg gcc acg gcc ctc tcg gcc ctc tcg      410
Val Leu Leu Ser Pro Leu Ser Val Ala Thr Ala Leu Ser Ala Leu Ser
      65              70              75
ctg gga gcg gas agc gaa cag aat cca tca ttc acc ggg ctc tct act      458
Leu Gly Ala Xaa Ser Glu Gln Asn Pro Ser Phe Thr Gly Leu Ser Thr
      80              85              90
atg act tgatcagcag cccagacatc catggtacct ataaggagct ccttgacacg      514
Met Thr
95
gtcaccgccc cc      526

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<210> 3722

<211> 660

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 244..588

<221> sig_peptide

<222> 244..297

<223> score 5.1

seq VFLLFLCFHLRFC/KV

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<400> 3722
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gtttcagtta cggtaaattc ctctggattt cagccaaatt ctttcagagt tcaaaagtac      120
aaagctcttt aggaggtttg ttcttttgaa acattttttc agagggtaaa aattaaattt      180
caaaagaata cctggagtgg aaaagagttc tcagcagaga caaagacccc gaacacctcc      240
aac atg aag ctt ctt cat gtt ttc ctg tta ttt ctg tgc ttc cac tta      288
Met Lys Leu Leu His Val Phe Leu Leu Phe Leu Cys Phe His Leu
      -15              -10              -5
agg ttt tgc aag gtc act tat aca tct caa gag gat ctg gtg gag aaa      336
Arg Phe Cys Lys Val Thr Tyr Thr Ser Gln Glu Asp Leu Val Glu Lys
      1              5              10
aag tgc tta gca aaa aaa tat act cac ctc tcc tgc gat aaa gtc ttc      384
Lys Cys Leu Ala Lys Lys Tyr Thr His Leu Ser Cys Asp Lys Val Phe
      15              20              25
tgc cag cca tgg cag aga tgc att gag ggc acc tgt gtt tgt aaa cta      432
Cys Gln Pro Trp Gln Arg Cys Ile Glu Gly Thr Cys Val Cys Lys Leu
      30              35              40              45
ccg tat cag tgc cca aag aat ggc act gca gtg tgt gca act aac agg      480
Pro Tyr Gln Cys Pro Lys Asn Gly Thr Ala Val Cys Ala Thr Asn Arg
      50              55              60
aga agc ttc cca aca tac tgt caa caa aag agt ttg gaa tgt ctt cat      528
Arg Ser Phe Pro Thr Tyr Cys Gln Gln Lys Ser Leu Glu Cys Leu His
      65              70              75

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<220>  
<221> CDS  
<222> 43..477
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2291

<210> 3724
 <211> 442
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 58..423

<221> sig_peptide
 <222> 58..114
 <223> score 10.8
 seq ILFLVAAATGAHS/QV

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 atg gac tgg acc tgg agc atc ctt ttc ttg gtg gca gca gca aca ggt 105
 Met Asp Trp Thr Trp Ser Ile Leu Phe Leu Val Ala Ala Ala Thr Gly
 -15 -10 -5
 gcc cac tcc cag gtt cag ytg gtg cag tct gga gct gag gtg aag aag 153
 Ala His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
 1 5 10
 cct ggg gcc tca gtg aag gtc tcc tgc aag rct tct ggt tac acc ttt 201
 Pro Gly Ala Ser Val Lys Val Ser Cys Lys Xaa Ser Gly Tyr Thr Phe
 15 20 25
 acc agc tat ggt atc anc tgg gtg cga cag gcc cct gga caa ggg ctt 249
 Thr Ser Tyr Gly Ile Xaa Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
 30 35 40 45
 gag tgg atg gga tgg atc agc gst tac aat ggt aac aca rac tat gca 297
 Glu Trp Met Gly Trp Ile Ser Xaa Tyr Asn Gly Asn Thr Xaa Tyr Ala
 50 55 60
 cag rag ytc cag ggc aga gtc acc atg acn aca gac aca tcc acg aac 345
 Gln Xaa Xaa Gln Gly Arg Val Thr Met Thr Thr Asp Thr Ser Thr Asn
 65 70 75
 aca gcc tac wtg gan ctg agg agn ctg aga yct gac gac acg gcc gtg 393
 Thr Ala Tyr Xaa Xaa Leu Arg Xaa Leu Arg Xaa Asp Asp Thr Ala Val
 80 85 90
 tat tac tgt gcg aga ccg atg gga tta ctt tgagagtcgt ggtagatga 442
 Tyr Tyr Cys Ala Arg Pro Met Gly Leu Leu
 95 100

<210> 3725
 <211> 458
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 83..442

<221> sig_peptide
 <222> 83..139

004220" 00666666

<223> score 11.9
seq LSLVLAVLQGVFA/EV

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aaaccagggt cccccctcca cagtgaagtct ccytcacyrc ccagctggga tctcagkgct 60
tymttttctg tctcctccca gg atg ggg tca acc gtc atc ctt tcc ctc gtc 112
Met Gly Ser Thr Val Ile Leu Ser Leu Val
-15 -10
ctg gct gtt ctc caa ggt gtc ttt gcc gag gtg cag ctg ttg cag tct 160
Leu Ala Val Leu Gln Gly Val Phe Ala Glu Val Gln Leu Leu Gln Ser
-5 1 5
gca gca gag gtg aaa aga ccc ggg gag tct ctg agg atc tcc tgt aag 208
Ala Ala Glu Val Lys Arg Pro Gly Glu Ser Leu Arg Ile Ser Cys Lys
10 15 20
act tct gga tac agc ttt acc agc tac tgg atc cac tgg gtg cgc cag 256
Thr Ser Gly Tyr Ser Phe Thr Ser Tyr Trp Ile His Trp Val Arg Gln
25 30 35
atg ccc ggg aaa gaa ctg gag tgg atg ggg agc atc tat cct ggg aac 304
Met Pro Gly Lys Glu Leu Glu Trp Met Gly Ser Ile Tyr Pro Gly Asn
40 45 50 55
tct gat acc aga tac agc cca tcc ttc caa ggc cac gtc acc atc tca 352
Ser Asp Thr Arg Tyr Ser Pro Ser Phe Gln Gly His Val Thr Ile Ser
60 65 70
gcc gac agc tcc agc agc acc gcc tac ctg cag tgg agc agc ctg aag 400
Ala Asp Ser Ser Ser Ser Thr Ala Tyr Leu Gln Trp Ser Ser Leu Lys
75 80 85
gcc tcg gac gcc gcc atg tat tat tgt gtg aga ngg acc atc 442
Ala Ser Asp Ala Ala Met Tyr Tyr Cys Val Arg Xaa Thr Ile
90 95 100
taaaaccttc cgcggt 458

<210> 3726
<211> 438
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 62..379

<221> sig_peptide
<222> 62..118
<223> score 9.9
seq FLFVVAATGVQS/QV

<400> 3726
agcatcacat aacaaccaca ttcctcctct aaagaagccc ctgggagcac agctcatcac 60
c atg gac tgg acc tgg agg ttc ctc ttt gtg gtg gca gca gct aca ggt 109
Met Asp Trp Thr Trp Arg Phe Leu Phe Val Val Ala Ala Ala Thr Gly
-15 -10 -5
gtc cag tcc cag gtg cag ctg gtg cag tct ggg gct gag gtg aag aag 157
Val Gln Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys

	1		5		10		
cct ggg tcc tgc gtg aag gtc tcc tgc aag rct tct gga ggc acc ttc							205
Pro Gly Ser Ser Val Lys Val Ser Cys Lys Xaa Ser Gly Gly Thr Phe							
15		20		25			
agc agc tmt gct atc agc tgg gtg cga cag gcc cct gga caa ggg ctt							253
Ser Ser Xaa Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu							
30		35		40		45	
gag tgg atg gga ggg atc ayn ccw ntc wtt aca gca rac tac gca cag							301
Glu Trp Met Gly Gly Ile Xaa Pro Xaa Xaa Thr Ala Xaa Tyr Ala Gln							
	50		55		60		
aas ttc cag ggc aga gts tcc gat tac cgc gga cga atc cac gag cac							349
Xaa Phe Gln Gly Arg Val Ser Asp Tyr Arg Gly Arg Ile His Glu His							
	65		70		75		
aac cta cat gga att gag cag cct gag atc tgaggacacg gccgtctatt							399
Asn Leu His Gly Ile Glu Gln Pro Glu Ile							
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actgtgcgag agaggcgcgg gaatggcagt ggctggtgt							438

<210> 3727

<211> 470

<212> DNA

<213> Homo sapiens

<220>

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<222> 62..382

<221> sig_peptide

<222> 62..118

<223> score 9.9

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Met Asp Trp Thr Trp Arg Phe Leu Phe Val Val Ala Ala Ala Thr Gly	

-15

-10

-5

gtc cag tcc cag gtg car ctg gtg cag tct ggg gct gag gtg aag aag	157
Val Gln Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys	

cct ggg tcc tgc gtg aag gtc tcc tgc aag gct tct gga ggc acc ttc	205	
Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe		
15	20	25

agc anc tat gck atc arc tgg gtg cga cag gcc cct gga caa ggg ctt	253		
Ser Xaa Tyr Ala Ile Xaa Trp Val Arg Gln Ala Pro Gly Gln Gly Leu			
30	35	40	45

gag tgg atg gga ggg atm ayc ccw wtc ttt ggn aca sca aac tac gca	301		
Glu Trp Met Gly Gly Ile Xaa Pro Xaa Phe Gly Thr Xaa Asn Tyr Ala			
	50	55	60

cmg aag ttc cag grc aga gtc acs att acc gcg gac gaa tcc acg aac	349		
Xaa Lys Phe Gln Xaa Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Asn			
	65	70	75

acc nnn nta tat ggg act gac cag cct gac atc tgaggacacg gmcatttact	402
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Thr Xaa Xaa Tyr Gly Thr Asp Gln Pro Asp Ile

80

85

actgtgag angycggcg ccttcrgtga ctacatcgc tccttanrnt tactactacg
gtatggac

462

470

<210> 3728

<211> 378

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 50..370

<221> sig_peptide

<222> 50..106

<223> score 9.9

seq FLFVVAATGVQS/QV

<400> 3728

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Met Asp Trp

58

acc tgg agg ttc ctc ttt gtg gtg gca gca gct aca ggt gtc cag tcc
Thr Trp Arg Phe Leu Phe Val Val Ala Ala Ala Thr Gly Val Gln Ser

106

-15 -10 -5

cag gtg mag ctg gwa cag tct ggg ama ggg ntn asg aag cct ggg tcc
Gln Val Xaa Leu Xaa Gln Ser Gly Xaa Gly Xaa Xaa Lys Pro Gly Ser

154

1 5 10 15
tca gtg aag atc tcc tgc aag gtt tct gga gac tcc ttc gcc aac tat
Ser Val Lys Ile Ser Cys Lys Val Ser Gly Asp Ser Phe Ala Asn Tyr

202

20 25 30
ggg atc cac tgg gtg cga cag gcc cct gga maa ggg ctg gag tgg atg
Gly Ile His Trp Val Arg Gln Ala Pro Gly Xaa Gly Leu Glu Trp Met

250

35 40 45
gga ggc atc gtc cct ctc ttt ggt aca gca gac aac gca cag agg ttc
Gly Gly Ile Val Pro Leu Phe Gly Thr Ala Asp Asn Ala Gln Arg Phe

298

50 55 60
cag agc aaa gtc acg att acc gmn nac aga tcc acg acc aya gtc ttc
Gln Ser Lys Val Thr Ile Thr Xaa Xaa Arg Ser Thr Thr Xaa Val Phe

346

65 70 75 80
atg gag gtg aag cag cct gag atc tgacgaca

378

Met Glu Val Lys Gln Pro Glu Ile

85

<210> 3729

<211> 495

<212> DNA

<213> Homo sapiens

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<222> 1..453

<221> sig_peptide
 <222> 1..75
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 Met Pro Arg Lys Arg Lys Cys Asp Leu Arg Ala Val Arg Val Gly Leu
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 tta ctc ggt ggt ggc gga gtc tac gga agc cgt ttt cgc ttc act ttt 96
 Leu Leu Gly Gly Gly Val Tyr Gly Ser Arg Phe Arg Phe Thr Phe
 -5 1 5
 cct ggc tgt aga gcg ctt tcc ccc tgg cgg gtg aga gtg cag aga cga 144
 Pro Gly Cys Arg Ala Leu Ser Pro Trp Arg Val Arg Val Gln Arg Arg
 10 15 20
 agg tgc gag atg agc act atg ttc gcg gac act ctc ctc atc gtt ttt 192
 Arg Cys Glu Met Ser Thr Met Phe Ala Asp Thr Leu Leu Ile Val Phe
 25 30 35
 atc tct gtg tgc acg gct ctg ctc gca gag ggc ata acc tgg gtc ctg 240
 Ile Ser Val Cys Thr Ala Leu Leu Ala Glu Gly Ile Thr Trp Val Leu
 40 45 50 55
 gtt tac agg aca gac aag tac aag aga ctg aag gca gaa gtg gaa aaa 288
 Val Tyr Arg Thr Asp Lys Tyr Lys Arg Leu Lys Ala Glu Val Glu Lys
 60 65 70
 cag agt aaa aaa ttg gaa aag aag aag gaa aca ata aca gag tca gct 336
 Gln Ser Lys Lys Leu Glu Lys Lys Lys Glu Thr Ile Thr Glu Ser Ala
 75 80 85
 ggt cga caa cag aaa aag anm ata gag aga caa gaa gag aaa ctg rag 384
 Gly Arg Gln Gln Lys Lys Xaa Ile Glu Arg Gln Glu Glu Lys Leu Xaa
 90 95 100
 aat aac aac aga gat cta tca atg gtt cga atg aaa tcc atg ttt gct 432
 Asn Asn Asn Arg Asp Leu Ser Met Val Arg Met Lys Ser Met Phe Ala
 105 110 115
 att ggc ttt tgt ttt act gcc taatgggrat gttcaattcc atatttgatg 483
 Ile Gly Phe Cys Phe Thr Ala
 120 125
 gtagagtggg gg 495

<210> 3730
 <211> 462
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 34..375

<221> sig_peptide
 <222> 34..93
 <223> score 9
 seq VVIFATFVTLCA/SC

Questions **A**nswers

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<211> 435
<212> DNA
<213> Homo sapiens
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<221> CDS
<222> 30..338

<221> sig_peptide
<222> 30..128
<223> score 5
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2297

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		10					15				20						
aga	tta	ttt	gcc	agg	gtt	tca	ctg	gca	aac	agg	gca	cct	ttc	aca	gcc	245	
Arg	Leu	Phe	Ala	Arg	Val	Ser	Leu	Ala	Asn	Arg	Ala	Pro	Phe	Thr	Ala		
		25					30				35						
agc	agg	cat	tgg	aat	atg	gca	cca	aac	tcg	ttg	gag	gaa	cca	ctc	cag	293	
Ser	Arg	His	Trp	Asn	Met	Ala	Pro	Asn	Ser	Leu	Glu	Glu	Pro	Leu	Gln		
		40				45				50					55		
gga	aag	gag	gcc	aga	cac	atc	tgg	gct	tac	ctg	tct	tta	ata	ctg		338	
Gly	Lys	Glu	Ala	Arg	His	Ile	Trp	Ala	Tyr	Leu	Ser	Leu	Ile	Leu			
			60						65					70			
tgaaggaggc	caaagaacag	acaggagcaa	cggttntgt	catttatggt	cctccgcctt											398	
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<210> 3732

<211> 444

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

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<223> score 7

seq ITFLQLAIRNTTA/AE

<400> 3732

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gctcctggga	aacctgctca	gccccgaca	atg tgg tcc	gga aac agg	cag agg		113
			Met Trp Ser	Gly Asn Arg	Gln Arg		
			-30		-25		
aaa cct atg	aga ata ntc	cca ggc	cag tca aag	atc aca ttc	ctc tta		161
Lys Pro Met	Arg Ile Xaa	Pro Gly	Gln Ser Lys	Ile Thr Phe	Leu Leu		
	-20		-15		-10		
caa gcc atc	aga aat aca	aca gct	gct gaa gag	gct aga caa	atg gcc		209
Gln Ala Ile	Arg Asn Thr	Thr Ala	Ala Glu Glu	Ala Arg Gln	Met Ala		
	-5		1		5		
gcc gtt ctc	cta aga cgt	ctc ttg	tcc tct gca	ttt gat gaa	gtc tat		257
Ala Val Leu	Leu Arg Arg	Leu Leu	Ser Ser Ala	Phe Asp Glu	Val Tyr		
	10		15		20		
cca gca ctt	ccc tct gat	gtt cag	act gcc atc	aag agt gag	cta ctc		305
Pro Ala Leu	Pro Ser Asp	Val Gln Thr	Ala Ile Lys	Ser Glu Leu	Leu Leu		
	25		30		35		40
atg att att	cag atg gaa	aca caa	tct agc atg	agg aaa	aaa gtt	tgt	353
Met Ile Ile	Gln Met Glu	Thr Gln Ser	Ser Met Arg	Lys Lys Val	Cys		
	45		50		55		
gat att gcg	gsa gaa ctg	gcc agg	aat tta ata	gat gag gat	ggc aat		401
Asp Ile Ala	Xaa Glu Leu	Ala Arg Asn	Leu Ile Asp	Glu Asp Gly	Asn		
	60		65		70		
aac cag tgg	ccc gaa gtt	tgaagttcct	ttttgattca	gtcag			444
Asn Gln Trp	Pro Glu Val						

<210> 3733
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 <212> DNA
 <213> Homo sapiens

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 <222> 240..641

<221> sig_peptide
 <222> 240..278
 <223> score 5.3
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 gcgttacttg actcttctcg cgataatttt kkttttaaaaa tctcccaagg aaagttgaag 120
 gaagagtaca aaattttcat ctgcgagac ttgtgagcgg ccattcttgg tctgccctga 180
 cagattctcc tatcggggtc acagggacgc taagattgct acctggactt tcgttgacc 239
 atg ctg tcc cgg gtg gta ctt tcc gcc gcc gcc aca gcg gcc ccc tct 287
 Met Leu Ser Arg Val Val Leu Ser Ala Ala Ala Thr Ala Ala Pro Ser
 -10 -5 1
 ctg aag aat gca gcc ttc cta ggt cca ggg gta ttg cag gca aca agg 335
 Leu Lys Asn Ala Ala Phe Leu Gly Pro Gly Val Leu Gln Ala Thr Arg
 5 10 15
 acc ttt cat aca ggg cag cca cac ctt gtc cct gta cca cct ctt cct 383
 Thr Phe His Thr Gly Gln Pro His Leu Val Pro Val Pro Pro Leu Pro
 20 25 30 35
 gaa tac gga gga aaa gtt cgt tat gga ctg atc cct gag gaa ttc ttc 431
 Glu Tyr Gly Gly Lys Val Arg Tyr Gly Leu Ile Pro Glu Glu Phe Phe
 40 45 50
 cag ttt ctt tat cct aaa act ggt gta aca gga ccc tat gta ctc gga 479
 Gln Phe Leu Tyr Pro Lys Thr Gly Val Thr Gly Pro Tyr Val Leu Gly
 55 60 65
 act ggg ctt atc ttg tac gct tta tcc aaa gaa ata tat gtg att agc 527
 Thr Gly Leu Ile Leu Tyr Ala Leu Ser Lys Glu Ile Tyr Val Ile Ser
 70 75 80
 gca gag acc ttc act gcc cta tca gta cta ggt gta atg gtc tat gga 575
 Ala Glu Thr Phe Thr Ala Leu Ser Val Leu Gly Val Met Val Tyr Gly
 85 90 95
 att aaa aaa tat ggt ccc ttt gtt gca gac ttt gct gat aac tca atg 623
 Ile Lys Lys Tyr Gly Pro Phe Val Ala Asp Phe Ala Asp Asn Ser Met
 100 105 110 115
 agc aaa aac ttg ccc aac tagaagaggc grasaggctt ccatccaamc 671
 Ser Lys Asn Leu Pro Asn
 120
 atccagaatg caattgatac ggagragtcr caacaggcac tg 713

<210> 3734
 <211> 516
 <212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 43..408

<221> sig_peptide

<222> 43..87

<223> score 9.4

seq LLTGLVFCSLVLX/VS

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                                   Met Lys Leu Leu
                                   -15
acg ggc ctg gtt ttc tgc tcc ttg gtc ctg rgt gtc agc agc cga agc      102
Thr Gly Leu Val Phe Cys Ser Leu Val Leu Xaa Val Ser Ser Arg Ser
   -10                               -5                               1                               5
ttc ttt tcg ttc ctt ggc gag gct ttt gat ggg gct cgg gac atg tgg      150
Phe Phe Ser Phe Leu Gly Glu Ala Phe Asp Gly Ala Arg Asp Met Trp
                   10                   15                   20
aga gcc tac tct gac atg aga gaa gcc aat tac atc ggc tca gac aaa      198
Arg Ala Tyr Ser Asp Met Arg Glu Ala Asn Tyr Ile Gly Ser Asp Lys
                   25                   30                   35
tac ttc cat gct cgg ggg aac tat gat gct gcc aaa agg gga cct ggg      246
Tyr Phe His Ala Arg Gly Asn Tyr Asp Ala Ala Lys Arg Gly Pro Gly
                   40                   45                   50
ggt gtc tgg gct gca gaa gcg atc agc gat gcc aga gag aat atc cag      294
Gly Val Trp Ala Ala Glu Ala Ile Ser Asp Ala Arg Glu Asn Ile Gln
   55                   60                   65
aga ttc ttt ggc cat ggt gcg gag gac tcg ctg gct gat cag gct gcc      342
Arg Phe Phe Gly His Gly Ala Glu Asp Ser Leu Ala Asp Gln Ala Ala
   70                   75                   80                   85
aat gaa tgg ggc agg agt ggc aaa gac ccc aat cac ttc cga cct gct      390
Asn Glu Trp Gly Arg Ser Gly Lys Asp Pro Asn His Phe Arg Pro Ala
                   90                   95                   100
ggc ctg cct gag aaa tac tgagcttcct ctctactctg ctctcaggag      438
Gly Leu Pro Glu Lys Tyr
                   105
atctggctgt gaggcctca gggcagggat acaaagcggg gagaggggtac acaatgggta      498
tctaataaat acttaaga                                         516
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<211> 583

<212> DNA

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<222> 124..576

<221> sig_peptide

<222> 124..180

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gtttgtcttg tgaccgcggg cgcccgctgc ttctttcccg agcttggaac ttcgttatcc 120
gcg atg cgt ttc ctg gca gct aca ttc ctg ctc ctg gcg ctc agc acc 168
Met Arg Phe Leu Ala Ala Thr Phe Leu Leu Leu Ala Leu Ser Thr
-15 -10 -5
gct gcc cag gcc gaa ccg gtg cag ttc aag gac tgc ggt tct gtg gat 216
Ala Ala Gln Ala Glu Pro Val Gln Phe Lys Asp Cys Gly Ser Val Asp
1 5 10
gga gtt ata aag gaa gtg aat gtg agc cca tgc ccc acc caa ccc tgc 264
Gly Val Ile Lys Glu Val Asn Val Ser Pro Cys Pro Thr Gln Pro Cys
15 20 25
cag ctg agc aaa gga cag tct tac agc gtc aat gtc acc ttc acc agc 312
Gln Leu Ser Lys Gly Gln Ser Tyr Ser Val Asn Val Thr Phe Thr Ser
30 35 40
aat att cag tct aaa agc agc aag gcc gtg gtg cat ggc atc ctg atg 360
Asn Ile Gln Ser Lys Ser Ser Lys Ala Val Val His Gly Ile Leu Met
45 50 55 60
ggc gtc cca gtt ccc ttt ccc att cct gag cct gat ggt tgt aag agt 408
Gly Val Pro Val Pro Phe Pro Ile Pro Glu Pro Asp Gly Cys Lys Ser
65 70 75
gga att aac tgc cct atc caa aaa gac aag acc tat agc tac ctg aat 456
Gly Ile Asn Cys Pro Ile Gln Lys Asp Lys Thr Tyr Ser Tyr Leu Asn
80 85 90
aaa cta cca gtg aaa agc gaa tat ccc tct ata aaa ctg gtg gtg gag 504
Lys Leu Pro Val Lys Ser Glu Tyr Pro Ser Ile Lys Leu Val Val Glu
95 100 105
tgg caa ctt cag gat gac aaa aac caa agt ctc ttc tgc tgg gaa atc 552
Trp Gln Leu Gln Asp Asp Lys Asn Gln Ser Leu Phe Cys Trp Glu Ile
110 115 120
cca gta cag atc gtt tct cat ctc taagtgc 583
Pro Val Gln Ile Val Ser His Leu
125 130

<210> 3736
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<212> DNA
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<222> 603..1433

<221> sig_peptide
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<223> score 4.2
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<400> 3736

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gactagccag	ccggctacaa	ttggagtcag	agtcccaaaag	acatgggctt	gttagagtg	180
tgtgcaagat	gtctggtagg	ggcccccttt	gcttccctgg	tggccactgg	attgtgtttc	240
tttggggwgg	cnnngttctt	nggctgtgga	catgaagccc	tacttggcac	agaaaaagcta	300
attgagacct	atttctccaa	aaaaaaaccc	cccntacca	agactatgag	tatctcatca	360
atgtgatcca	tgccttccag	taatgtcatc	tatggaactg	cctctttctt	cttccttttt	420
akgggggttg	tgkcaatsag	aaagcccttt	tcattgcagg	agaagaggac	aaagatactc	480
agagagaaaa	agtaaaagac	cgaagaagga	ggctggagag	accaggatcc	ttccagctga	540
acaaagtcag	ccacaaagca	gactagccag	ccggctacaa	ttggagtcag	agtcccaaaag	600
ac atg ggc ttg tta gag tgc tgt gca aga tgt ctg gta ggg gcc ccc						647
Met Gly Leu Leu Glu Cys Cys Ala Arg Cys Leu Val Gly Ala Pro						
-35	-30	-25				
ttt gct tcc ctg gtg gcc act gga ttg tgt ttc	ttt ggg gtg gca ctg					695
Phe Ala Ser Leu Val Ala Thr Gly Leu Cys Phe	Phe Gly Val Ala Leu					
-20	-15	-10				
ttc tgt ggc tgt gga cat gaa gcc ctc act ggc	aca gaa aag cta att					743
Phe Cys Gly Cys Gly His Glu Ala Leu Thr Gly Thr	Glu Lys Leu Ile					
-5	1	5	10			
gag acc tat ttc tcc aaa aac tac caa gac tat	gag tat ctc atc aat					791
Glu Thr Tyr Phe Ser Lys Asn Tyr Gln Asp Tyr	Glu Tyr Leu Ile Asn					
15	20	25				
gtg atc cat gcc ttc cag tat gtc atc tat gga	act gcc tct ttc ttc					839
Val Ile His Ala Phe Gln Tyr Val Ile Tyr Gly Thr	Ala Ser Phe Phe					
30	35	40				
ttc ctt tat ggg gcc ctc ctg ctg gct gag ggc	ttc tac acc acc ggc					887
Phe Leu Tyr Gly Ala Leu Leu Leu Ala Glu Gly	Phe Tyr Thr Thr Gly					
45	50	55				
gca gtc agg cag atc ttt ggc gac tac aag acc	acc atc tgc ggc aag					935
Ala Val Arg Gln Ile Phe Gly Asp Tyr Lys Thr	Thr Ile Cys Gly Lys					
60	65	70	75			
ggc ctg agc gca acg gta aca ggg ggc cag aag	ggg agg ggt tcc aga					983
Gly Leu Ser Ala Thr Val Thr Gly Gly Gln Lys	Gly Arg Gly Ser Arg					
80	85	90				
ggc caa cat caa gct cat tct ttg gag cgg gtg	tgt cat tgt ttg gga					1031
Gly Gln His Gln Ala His Ser Leu Arg Val Cys	His Cys Leu Gly					
95	100	105				
aaa tgg cta gga cat ccc gac aag ttt gtg ggc	atc acc tat gcc ctg					1079
Lys Trp Leu Gly His Pro Asp Lys Phe Val Gly	Ile Thr Tyr Ala Leu					
110	115	120				
acc gtt gtg tgg ctc ctg gtg ttt gcc tgc tct	gct gtg cct gtg tac					1127
Thr Val Val Trp Leu Leu Val Phe Ala Cys Ser	Ala Val Pro Val Tyr					
125	130	135				
att tac ttc aac acc tgg acc acc tgc cag tct	att gcc ttc ccc agc					1175
Ile Tyr Phe Asn Thr Trp Thr Thr Cys Gln Ser	Ile Ala Phe Pro Ser					
140	145	150	155			
aag acc tct gcc agt ata ggc agt ctc tgt gct	gat gcc aga atg tat					1223
Lys Thr Ser Ala Ser Ile Gly Ser Leu Cys Ala	Asp Ala Arg Met Tyr					
160	165	170				
ggg gtt ctc cca tgg aat gct ttc cct ggc aag	gtt tgt ggc tcc aac					1271
Gly Val Leu Pro Trp Asn Ala Phe Pro Gly Lys	Val Cys Gly Ser Asn					
175	180	185				
ctt ctg tcc atc tgc aaa aca gct gag ttc caa	atg acc ttc cac ctg					1319
Leu Leu Ser Ile Cys Lys Thr Ala Glu Phe Gln	Met Thr Phe His Leu					

190	195	200	
ttt att gct gca ttt gtg ggg gct gca gct aca ctg gtt tcc ctg ctc			1367
Phe Ile Ala Ala Phe Val Gly Ala Ala Ala Thr Leu Val Ser Leu Leu			
205	210	215	
acc ttc atg att gct gcc act tac aac ttt gcc gtc ctt aaa ctc atg			1415
Thr Phe Met Ile Ala Ala Thr Tyr Asn Phe Ala Val Leu Lys Leu Met			
220	225	230	235
ggc cga ggc acc aag ttc tgatcccccg			1443
Gly Arg Gly Thr Lys Phe			
240			

<210> 3737
 <211> 521
 <212> DNA
 <213> Homo sapiens

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 <222> 85..396
 <221> sig_peptide
 <222> 85..132
 <223> score 6
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Met Val Arg Ser Arg Leu Thr Ala Val	
-15	-10
tcc gcc tct tgg gtt cag gct cat cca cct gca gac atg ggg cgc aga	159
Ser Ala Ser Trp Val Gln Ala His Pro Pro Ala Asp Met Gly Arg Arg	
-5	1
aag tca aaa cga aag ccg cct ccc aag aag aag atg aca ggc acc ctc	207
Lys Ser Lys Arg Lys Pro Pro Lys Lys Met Thr Gly Thr Leu	
10	15
gag acc cag ttc acc tgc ccc ttc tgc aac cac gag aaa tcc tgt gat	255
Glu Thr Gln Phe Thr Cys Pro Phe Cys Asn His Glu Lys Ser Cys Asp	
30	35
gtg aaa atg gac cgt gcc cgc aac acc gga gtc atc tct tgt acc gtg	303
Val Lys Met Asp Arg Ala Arg Asn Thr Gly Val Ile Ser Cys Thr Val	
45	50
tgc cta gag gaa ttc cag acg ccc ata acg tat ctg tca gaa ccy gtg	351
Cys Leu Glu Glu Phe Gln Thr Pro Ile Thr Tyr Leu Ser Glu Pro Val	
60	65
gat gtg tac agt gat tgg ata gac gcc tgc gag gcg gcc aat cag	396
Asp Val Tyr Ser Asp Trp Ile Asp Ala Cys Glu Ala Ala Asn Gln	
75	80
tagcgacaca gaggaccgc cccctgagca gccccgcgta ctgtggatcc agctgttcgg	456
ttctggtcca gagacattcc aggggtccag ggtgtgggtc ctgggctgtm cagccgtgtg	516
tgtgt	521

<210> 3738

<211> 1066
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> 43..744

<221> sig_peptide
 <222> 43..93
 <223> score 9.2
 seq VVFLTLSVTWIGA/AP

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 Met Trp Val Pro
 -15
 gtt gtc ttc ctc acc ctg tcc gtg acg tgg att ggt gct gca ccc ctc 102
 Val Val Phe Leu Thr Leu Ser Val Thr Trp Ile Gly Ala Ala Pro Leu
 -10 -5 1
 atc ctg tct cgg att gtg gga ggc tgg gag tgc gag aag cat tcc caa 150
 Ile Leu Ser Arg Ile Val Gly Gly Trp Glu Cys Glu Lys His Ser Gln
 5 10 15
 ccc tgg cag gtg ctt gtg gcc tct cgt ggc agg gca gtc tgc ggc ggt 198
 Pro Trp Gln Val Leu Val Ala Ser Arg Gly Arg Ala Val Cys Gly Gly
 20 25 30 35
 gtt ctg gtg cac ccc cag tgg gtc ctc aca gct gcc cac tgc atc agg 246
 Val Leu Val His Pro Gln Trp Val Leu Thr Ala Ala His Cys Ile Arg
 40 45 50
 aag cca ggt gat gac tcc agc cac gac ctc atg ctg ctc cgc ctg tca 294
 Lys Pro Gly Asp Asp Ser Ser His Asp Leu Met Leu Leu Arg Leu Ser
 55 60 65
 gag cct gcc gag mtc acg gat gct gtg aag gtc atg gac ctg ccc amc 342
 Glu Pro Ala Glu Xaa Thr Asp Ala Val Lys Val Met Asp Leu Pro Xaa
 70 75 80
 cag gag cca gca ctg ggg acc acc tgc tac gcc tca ggc tgg ggc agc 390
 Gln Glu Pro Ala Leu Gly Thr Thr Cys Tyr Ala Ser Gly Trp Gly Ser
 85 90 95
 att gaa cca gag gag ttc ttg acc cca aag aaa ctt cag tgt gtg gac 438
 Ile Glu Pro Glu Glu Phe Leu Thr Pro Lys Lys Leu Gln Cys Val Asp
 100 105 110 115
 ctc cat gtt att tcc aat gac gtg tgt gcg caa gtt cac cct cag aag 486
 Leu His Val Ile Ser Asn Asp Val Cys Ala Gln Val His Pro Gln Lys
 120 125 130
 gtg acc aag ttc atg ctg tgt gct gga cgc tgg aca ggg ggc aaa agc 534
 Val Thr Lys Phe Met Leu Cys Ala Gly Arg Trp Thr Gly Gly Lys Ser
 135 140 145
 acc tgc tcg ggt gat ctg ggg gcc cac ttg tct gta atg gtg tgc ttc 582
 Thr Cys Ser Gly Asp Leu Gly Ala His Leu Ser Val Met Val Cys Phe
 150 155 160
 aag gta tca cgt cat ggg gca gtg aac cat gtg ccc tgc ccg aaa ggc 630
 Lys Val Ser Arg His Gly Ala Val Asn His Val Pro Cys Pro Lys Gly
 165 170 175

004220" 666ET560

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ctt ccc tgt aca cca agg tgg tgc att acc gga agt gga tca agg aca      678
Leu Pro Cys Thr Pro Arg Trp Cys Ile Thr Gly Ser Gly Ser Arg Thr
180                      185                      190                      195
cca tcg tgg cca acc cct gag cac ccc tat caa ctc cct att gta gta      726
Pro Ser Trp Pro Thr Pro Glu His Pro Tyr Gln Leu Pro Ile Val Val
                      200                      205                      210
aac ttg gaa cct tgg aaa tgaccaggcc aagactcaag cctccccagt      774
Asn Leu Glu Pro Trp Lys
                      215
tctactgacc tttgtcctta ggtgtgaggt ccagggttgc taggaaaaga aatcagcaga      834
cacagggtgta gaccagagtgt tttcttaaat ggtgtaattt tgtcctctct gtgtcctggg      894
gaataactggc catgcctgga gacatatcac tcaatttctc tgaggacaca gataggatgg      954
ggtgtctgtg ttatttgtgg ggtacagaga tgaaagaggg gtgggatcca cactgagaga     1014
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<210> 3739
<211> 528
<212> DNA
<213> Homo sapiens

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<221> sig_peptide
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<223> score 7.8
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tga atg cat acg caa gac tcg gag gta gtt ccg gtt ccg gcg tgg cca      108
      Met His Thr Gln Asp Ser Glu Val Val Pro Val Pro Ala Trp Pro
                      -25                      -20                      -15
ttt tcg ttg gtg gtg ttc agt tgt ggc ggt tgc tgg tca gta aca gcc      156
Phe Ser Leu Val Val Phe Ser Cys Gly Gly Cys Trp Ser Val Thr Ala
                      -10                      -5                      1
aag atg ctg cgg aat ctg ctg gct ctt cgt cag att ggg cag agg acg      204
Lys Met Leu Arg Asn Leu Leu Ala Leu Arg Gln Ile Gly Gln Arg Thr
      5                      10                      15
ata agc act gct tcc cgc agg cat ttt aaa aat aaa gtt ccg gag aag      252
Ile Ser Thr Ala Ser Arg Arg His Phe Lys Asn Lys Val Pro Glu Lys
      20                      25                      30                      35
caa aaa ctg ttc cag gag gat gat gaa att cca ctg tat cta aag ggt      300
Gln Lys Leu Phe Gln Glu Asp Asp Glu Ile Pro Leu Tyr Leu Lys Gly
                      40                      45                      50
ggg gta gct gat gcc ctc ctg tat aga gcc acc atg att ctt aca gtt      348
Gly Val Ala Asp Ala Leu Leu Tyr Arg Ala Thr Met Ile Leu Thr Val
                      55                      60                      65
ggt gga aca gca tat gcc ata tat gag ctg gct gtg gct tca ttt ccc      396
Gly Gly Thr Ala Tyr Ala Ile Tyr Glu Leu Ala Val Ala Ser Phe Pro
      70                      75                      80
aag aag cag gag tgacttcagt catcccagca atcgcttggt tcagtttcat      448

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Lys Lys Gln Glu

85

tcagctctct atggaccagt aatctgataa ataaccgagc tcttctttgg ggatcaatat 508
ttattgactt gtagtaactg 528

<210> 3740

<211> 661

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 306..629

<221> sig_peptide

<222> 306..353

<223> score 3.9

seq CAKLACTPSLIRA/GS

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ggrtccgaac ccaggggtgg ggggtggagg cggctcctgc gatcgaagag gacttgagac 120
tcaccggccg cagccatga gggccctgtg ggtgctgggc ctctgctgcg tctgtgagt 180
ccactcctt cgacctctgc tgcagcccgt gccgccgccg cctcctggga agagaggaag 240
cgggagagga gccacgtcg cctgtcacc aatatctcca gccgcgcagt cccgaagagt 300
gtaag atg ttc gcc tgc gcc aag ctg gcc tgc acc ccc tct ctg atc cga 350
Met Phe Ala Cys Ala Lys Leu Ala Cys Thr Pro Ser Leu Ile Arg
-15 -10 -5
gct gga tcc aga gtt gca tac aga cca att tct gca tca gtg tta tct 398
Ala Gly Ser Arg Val Ala Tyr Arg Pro Ile Ser Ala Ser Val Leu Ser
1 5 10 15
cga cca gag gct agt agg act gga gag gcc tct acg gta ttt aat ggg 446
Arg Pro Glu Ala Ser Arg Thr Gly Glu Gly Ser Thr Val Phe Asn Gly
20 25 30
gcc cag aat ggt gtg tct cag cta atc caa agg gag ttt cag acc agt 494
Ala Gln Asn Gly Val Ser Gln Leu Ile Gln Arg Glu Phe Gln Thr Ser
35 40 45
gca atc agc aga gac att gat act gct gcc aaa ttt att ggt gca ggt 542
Ala Ile Ser Arg Asp Ile Asp Thr Ala Ala Lys Phe Ile Gly Ala Gly
50 55 60
gct gca aca gta gga gtg gct ggt tct ggt gct ggt att gga aca gtc 590
Ala Ala Thr Val Gly Val Ala Gly Ser Gly Ala Gly Ile Gly Thr Val
65 70 75
ttt ggc agc tta tca ttg gtt atg cca gaa ant nnt cgc tgaagcagca 639
Phe Gly Ser Leu Ser Leu Val Met Pro Glu Xaa Xaa Arg
80 85 90
gctgttctca tatgctatcc tg 661

<210> 3741

<211> 525

<212> DNA

<213> Homo sapiens

<220>
 <221> CDS
 <222> 191..511

 <221> sig_peptide
 <222> 191..292
 <223> score 5.1
 seq ASLLNFWNPPTTA/QV

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 gaagtgtccc tgccccggga agaggctcag cacagaagga ggaaggacag cacagctgac 120
 agccgtrctc aggaagytte tggatcctag gctyatctcc acagaggaga acacacaagc 180
 agcagagacc atg ggg ccc ctc tca gcc cct ccc tgc aca cas ckc atc 229
 Met Gly Pro Leu Ser Ala Pro Pro Cys Thr Xaa Xaa Ile
 -30 -25
 act tgg aag ggg stc ctg ctc aca gca tca ctt tta aac ttc tgg aay 277
 Thr Trp Lys Gly Xaa Leu Leu Thr Ala Ser Leu Leu Asn Phe Trp Asn
 -20 -15 -10
 ccg ccc acm act gcc caa gtc acg att gaa gcc cag cca ccc aaa gtt 325
 Pro Pro Thr Thr Ala Gln Val Thr Ile Glu Ala Gln Pro Pro Lys Val
 -5 1 5 10
 tcy gag ggg aag gat gtt ctt cta ctt gtc cac aat ttg ccc cag aat 373
 Ser Glu Gly Lys Asp Val Leu Leu Leu Val His Asn Leu Pro Gln Asn
 15 20 25
 ctt gct ggc tac att tgg tac aaa ggg caa atg aca tac ctc tac cat 421
 Leu Ala Gly Tyr Ile Trp Tyr Lys Gly Gln Met Thr Tyr Leu Tyr His
 30 35 40
 tac att aca tca tat gta gta gac ggt caa aga att ata tat ggg cct 469
 Tyr Ile Thr Ser Tyr Val Val Asp Gly Gln Arg Ile Ile Tyr Gly Pro
 45 50 55
 gca tac agt gga aga gaa aga gta tat tcc aat gca tcc tgc 511
 Ala Tyr Ser Gly Arg Glu Arg Val Tyr Ser Asn Ala Ser Cys
 60 65 70
 tgatccagaa tgtc 525

<210> 3742
 <211> 575
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> 73..546

 <221> sig_peptide
 <222> 73..141
 <223> score 8.6
 seq LVLALALILVLES/SV

<400> 3742
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actaagttgg tc atg atg cag aag cta ctc aaa tgc agt cgg ctt gtc ctg      111
      Met Met Gln Lys Leu Leu Lys Cys Ser Arg Leu Val Leu
      -20                               -15

gct ctt gcc ctc atc ctg gtt ctg gaa tcc tca gtt caa ggt tat cct      159
Ala Leu Ala Leu Ile Leu Val Leu Glu Ser Ser Val Gln Gly Tyr Pro
-10                               -5                               1                               5

acg crg aga gcc agg tac caa tgg gtg cgc tgc aat cca gac agt aat      207
Thr Xaa Arg Ala Arg Tyr Gln Trp Val Arg Cys Asn Pro Asp Ser Asn
      10                               15                               20

tct gca aac tgc ctt gaa gaa aaa gga cca atg ttc gaa cta ctt cca      255
Ser Ala Asn Cys Leu Glu Glu Lys Gly Pro Met Phe Glu Leu Leu Pro
      25                               30                               35

ggg gaa tcc aac aag atc ccc cgt ctg agg act gac ctt ttt cca aag      303
Gly Glu Ser Asn Lys Ile Pro Arg Leu Arg Thr Asp Leu Phe Pro Lys
      40                               45                               50

acg aga atc cag gac ttg aat cgt atc ttc cca ctt tct gag gac tac      351
Thr Arg Ile Gln Asp Leu Asn Arg Ile Phe Pro Leu Ser Glu Asp Tyr
      55                               60                               65                               70

tct gga tca ggc ttc ggc tcc ggc tcc ggc tct gga tca gga tct ggg      399
Ser Gly Ser Gly Phe Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly
      75                               80                               85

agt ggc ttc cta acg gaa atg gaa cag gat tac caa cta gta gac gaa      447
Ser Gly Phe Leu Thr Glu Met Glu Gln Asp Tyr Gln Leu Val Asp Glu
      90                               95                               100

agt gat gct ttc cat gac aac ctt agg tct ctt gac agg aat ctg ccc      495
Ser Asp Ala Phe His Asp Asn Leu Arg Ser Leu Asp Arg Asn Leu Pro
      105                               110                               115

tca gac agc cag gac ttg ggt caa cat gga tta gaa gag gat ttt atg      543
Ser Asp Ser Gln Asp Leu Gly Gln His Gly Leu Glu Glu Asp Phe Met
      120                               125                               130

tta taaaagagga ttttcccacc ttgacacca      575
Leu
135

<210> 3743
<211> 860
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 139..741

<221> sig_peptide
<222> 139..192
<223> score 10.5
      seq VLTVLSLLPLLEA/QI

<400> 3743
aagtgtctggc asgattgtgt cacagacaca gagtaaactt ttgctgggct ccaagtgacc      60
gcccatagtt tattataaag gtgactgcac cctgcagcca ccagcactgc ctggctccac      120
gtgcctcctg gtctcagt atg gcg ctg tcc tgg gtt ctt aca gtc ctg agc      171
      Met Ala Leu Ser Trp Val Leu Thr Val Leu Ser

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								-15						-10					
ctc	cta	cct	ctg	ctg	gaa	gcc	cag	atc	cca	ttg	tgt	gcc	aac	cta	gta				219
Leu	Leu	Pro	Leu	Leu	Glu	Ala	Gln	Ile	Pro	Leu	Cys	Ala	Asn	Leu	Val				
		-5					1				5								
ccg	gtg	ccc	atc	acc	aac	gcc	acc	ctg	gac	cag	atc	act	ggc	aag	tgg				267
Pro	Val	Pro	Ile	Thr	Asn	Ala	Thr	Leu	Asp	Gln	Ile	Thr	Gly	Lys	Trp				
10					15					20				25					
ttt	tat	atc	gca	tcg	gcc	ttt	cga	aac	gag	gag	tac	aat	aag	tcg	gtt				315
Phe	Tyr	Ile	Ala	Ser	Ala	Phe	Arg	Asn	Glu	Glu	Tyr	Asn	Lys	Ser	Val				
			30						35				40						
cag	gag	atc	caa	gca	acc	ttc	ttt	tac	ttc	acc	ccc	aac	aag	aca	gag				363
Gln	Glu	Ile	Gln	Ala	Thr	Phe	Phe	Tyr	Phe	Thr	Pro	Asn	Lys	Thr	Glu				
			45					50				55							
gac	acg	atc	ttt	ctc	aga	gag	tac	cag	acc	cga	cag	gac	cag	tgc	atc				411
Asp	Thr	Ile	Phe	Leu	Arg	Glu	Tyr	Gln	Thr	Arg	Gln	Asp	Gln	Cys	Ile				
		60					65				70								
tat	aac	acc	acc	tac	ctg	aat	gtc	cag	cgg	gaa	aat	ggg	acc	atc	tcc				459
Tyr	Asn	Thr	Thr	Tyr	Leu	Asn	Val	Gln	Arg	Glu	Asn	Gly	Thr	Ile	Ser				
	75					80					85								
aga	tac	gtg	gga	ggc	caa	gag	cat	ttc	gct	cac	ttg	ctg	atc	ctc	agg				507
Arg	Tyr	Val	Gly	Gly	Gln	Glu	His	Phe	Ala	His	Leu	Leu	Ile	Leu	Arg				
	90				95				100					105					
gac	acc	aag	acc	tac	atg	ctt	gct	ttt	gac	gtg	aac	gat	gag	aag	aac				555
Asp	Thr	Lys	Thr	Tyr	Met	Leu	Ala	Phe	Asp	Val	Asn	Asp	Glu	Lys	Asn				
			110					115				120							
tgg	ggg	ctg	tct	gtc	tat	gct	gac	aag	cca	gag	acg	acc	aag	gag	caa				603
Trp	Gly	Leu	Ser	Val	Tyr	Ala	Asp	Lys	Pro	Glu	Thr	Thr	Lys	Glu	Gln				
			125				130					135							
ctg	gga	gag	ttc	tac	gaa	gct	ctc	gac	tgc	ttg	cgc	att	ccc	aag	tca				651
Leu	Gly	Glu	Phe	Tyr	Glu	Ala	Leu	Asp	Cys	Leu	Arg	Ile	Pro	Lys	Ser				
	140					145					150								
gat	gtc	gtg	tac	acc	gat	tgg	aaa	aag	gat	aag	tgt	gag	cca	ctg	gag				699
Asp	Val	Val	Tyr	Thr	Asp	Trp	Lys	Lys	Asp	Lys	Cys	Glu	Pro	Leu	Glu				
	155					160					165								
aag	cag	cac	gag	aag	gag	agg	aaa	cag	gag	gag	ggg	gaa	tcc						741
Lys	Gln	His	Glu	Lys	Arg	Lys	Gln	Glu	Glu	Gly	Glu	Ser							
	170				175				180										
tagcaggaca	cagccttgga	tcaggacaga	gacttggggg	ccatcctgcc	cctccaaccc														801
gacatgtgta	cctcagcttt	ttccctcact	tgcatcaata	aagcttctgt	gtttggaac														860

<210> 3744

<211> 562

<212> DNA

<213> Homo sapiens

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<222> 132..536

<221> sig_peptide

<222> 132..203

<223> score 10.9

seq LAGLCCLVPVSLA/ED

<400> 3744

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gctaattgtga gacgaatttt tgagctcctc agcttcaggc accaccactg acctgggaca      120
gtgaatcgac a atg ccg tct tct gtc tcg tgg ggc atc ctc ctg ctg gca      170
          Met Pro Ser Ser Val Ser Trp Gly Ile Leu Leu Leu Ala
                    -20                                -15
ggc ctg tgc tgc ctg gtc cct gtc tcc ctg gct gag gat ccc cag gga      218
Gly Leu Cys Cys Leu Val Pro Val Ser Leu Ala Glu Asp Pro Gln Gly
      -10                                -5                                1                                5
gat gct gcc cag aag aca gat aca tcc cac cat gat cag gat cac cca      266
Asp Ala Ala Gln Lys Thr Asp Thr Ser His His Asp Gln Asp His Pro
                    10                                15                                20
acc ttc aac aag atc acc ccc aac ctg gct gag ttc gcc ttc agc cta      314
Thr Phe Asn Lys Ile Thr Pro Asn Leu Ala Glu Phe Ala Phe Ser Leu
                    25                                30                                35
tac cgc cag ctg gca cac cag tcc aac agc acc aat atc ttc ttc tcc      362
Tyr Arg Gln Leu Ala His Gln Ser Asn Ser Thr Asn Ile Phe Phe Ser
                    40                                45                                50
cca gtg agc atc gct aca gcc ttt gca atg ctc tcc ctg ggg acc aag      410
Pro Val Ser Ile Ala Thr Ala Phe Ala Met Leu Ser Leu Gly Thr Lys
                    55                                60                                65
gct gac act cac gat gaa atc ctg gag ggc ctg aat ttc aac ctc acg      458
Ala Asp Thr His Asp Glu Ile Leu Glu Gly Leu Asn Phe Asn Leu Thr
      70                                75                                80                                85
gag att ccg gag gct cag atc cat gaa ggc ttc cag gaa ctc ctc gta      506
Glu Ile Pro Glu Ala Gln Ile His Glu Gly Phe Gln Glu Leu Leu Val
                    90                                95                                100
ccc tca acc agc cag aca gcc agc tcc agc tgaccaccgg caatggcctg      556
Pro Ser Thr Ser Gln Thr Ala Ser Ser Ser
                    105                                110
ttcctc      562

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<210> 3745

<211> 474

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 48..413

<221> sig_peptide

<222> 48..116

<223> score 6.2

seq ILYFYALLFLSST/CV

<400> 3745

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gacagtgctg acactacaag gctcggagct ccgggcactc agacatc atg agt tgg      56
                                Met Ser Trp
tcc ttg cac ccc cgg aat tta att ctc tac ttc tat gct ctt tta ttt      104
Ser Leu His Pro Arg Asn Leu Ile Leu Tyr Phe Tyr Ala Leu Leu Phe
      -20                                -15                                -10                                -5

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ctc tct tca aca tgt gta gca tat gtt gct acc aga gac aac tgc tgc      152
Leu Ser Ser Thr Cys Val Ala Tyr Val Ala Thr Arg Asp Asn Cys Cys
      1              5              10
atc tta gat gaa aga ttc ggt agt tat tgt cca act acc tgt ggc att      200
Ile Leu Asp Glu Arg Phe Gly Ser Tyr Cys Pro Thr Thr Cys Gly Ile
      15              20              25
gca gat ttc ctg tct act tat caa acc aaa gta gac aag gat cta cag      248
Ala Asp Phe Leu Ser Thr Tyr Gln Thr Lys Val Asp Lys Asp Leu Gln
      30              35              40
tct ttg gaa gac atc tta cat caa gtt gaa aac aaa aca tca gaa gtc      296
Ser Leu Glu Asp Ile Leu His Gln Val Glu Asn Lys Thr Ser Glu Val
      45              50              55              60
aaa cag ctg ata aaa gca atc caa ctc act tat aat cct gat gaa tca      344
Lys Gln Leu Ile Lys Ala Ile Gln Leu Thr Tyr Asn Pro Asp Glu Ser
      65              70              75
tca aaa cca aat atg ata gac gct gct act ttg aag tcc agg aaa atg      392
Ser Lys Pro Asn Met Ile Asp Ala Ala Thr Leu Lys Ser Arg Lys Met
      80              85              90
tta gaa gaa att att gaa ata tgaagcatcg atttttaaca catgactcaa      443
Leu Glu Glu Ile Ile Glu Ile
      95
gtawtcgatw tttgcaggga atatataatt c      474

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<210> 3746
 <211> 489
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 126..455

<221> sig_peptide
 <222> 126..233
 <223> score 9.7
 seq LWTVLILFSCCCA/FX

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cacctctggg gctatggagg cccctgagcc gggagaagcc ctggagttga gcctggcggg      120
tgccc atg gcc atg gag tgc aca aga aaa aac aca aga agc acc tac tac      170
      Met Ala Met Glu Cys Thr Arg Lys Asn Thr Arg Ser Thr Tyr Tyr
      -35              -30              -25
tat gag ctc tgg tgg ttc tgg ctg ctc tgg act gtc ctc atc ctc ttt      218
Tyr Glu Leu Trp Trp Phe Trp Leu Leu Trp Thr Val Leu Ile Leu Phe
      -20              -15              -10
agc tgc tgt tgc gcc ttc ngc cac cga cga gct aaa ctc agg ctg caa      266
Ser Cys Cys Cys Ala Phe Xaa His Arg Arg Ala Lys Leu Arg Leu Gln
      -5              1              5              10
caa cag cag cgg cas gtg aaa tca act tgt tgg cct atc atg ggg cat      314
Gln Gln Gln Arg Xaa Val Lys Ser Thr Cys Trp Pro Ile Met Gly His
      15              20              25
gcc atg ggg ctg gtc ctt tcc cta ccg gtt cac tgc ttg acc ttc gst      362

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Ala Met Gly Leu Val Leu Ser Leu Pro Val His Cys Leu Thr Phe Xaa	
30 35 40	
tcc tca gca cct tca ngc ccc cag cct acg agg atg tgg ttc amc gcn	410
Ser Ser Ala Pro Ser Xaa Pro Gln Pro Thr Arg Met Trp Phe Xaa Ala	
45 50 55	
nag gca cac cam ccc ccc ctt ata ctg tgg ccc cag gcc gcc cct	455
Xaa Ala His Xaa Pro Pro Leu Ile Leu Trp Pro Gln Ala Ala Pro	
60 65 70	
tgactgcttc cagtgaacaa acctgctggt cctc	489

<210> 3747
 <211> 556
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 119..457

<221> sig_peptide
 <222> 119..241
 <223> score 4.6
 seq AYLLYILLTGALQ/FG

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gtggtcgacg ggtcctccaa gagtttgggg cgcggaccgg agtaccttgc gtgcagtt	118
atg tcg gcg tcg gta gtg tct gtc att tcg cgg ttc tta gaa gag tac	166
Met Ser Ala Ser Val Val Ser Val Ile Ser Arg Phe Leu Glu Glu Tyr	
-40 -35 -30	
ttg agc tcc act ccg cag cgt ctg aag ttg ctg gac gcg tac ctg ctg	214
Leu Ser Ser Thr Pro Gln Arg Leu Lys Leu Leu Asp Ala Tyr Leu Leu	
-25 -20 -15 -10	
tat ata ctg ctg acc ggg gcg ctg cag ttc ggt tac tgt ctc ctc gtg	262
Tyr Ile Leu Leu Thr Gly Ala Leu Gln Phe Gly Tyr Cys Leu Leu Val	
-5 1 5	
ggg acc ttc ccc ttc aac tct ttt ctc tcg ggc ttc atc tct tgt gtg	310
Gly Thr Phe Pro Phe Asn Ser Phe Leu Ser Gly Phe Ile Ser Cys Val	
10 15 20	
ggg agt ttc atc cta gcg gtt tgc ctg aga ata cag atc aac cca cag	358
Gly Ser Phe Ile Leu Ala Val Cys Leu Arg Ile Gln Ile Asn Pro Gln	
25 30 35	
aac aaa gcg gat ttc caa ggc atc tcc cca gag cga gcc ttt gct gat	406
Asn Lys Ala Asp Phe Gln Gly Ile Ser Pro Glu Arg Ala Phe Ala Asp	
40 45 50 55	
ttt ctc ttt gcc agc acc atc ctg cac ctt gtt gtc atg aac ttw rtt	454
Phe Leu Phe Ala Ser Thr Ile Leu His Leu Val Val Met Asn Xaa Xaa	
60 65 70	
ggc tgactcattc tcatttactt aattgaggag taggagacta aaagaatgtt	507
Gly	
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<211> 568
 <212> DNA
 <213> Homo sapiens

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 <222> 74..520

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 <222> 74..151
 <223> score 10.8
 seq MLPLLWLLPHSWA/VP

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 gtggcaagaa ggt atg ggt cat gaa cag aac caa gga gct gcg ctg cta 109
 Met Gly His Glu Gln Asn Gln Gly Ala Ala Leu Leu
 -25 -20 -15
 cag atg tta cca ctt ctg tgg ctg cta ccc cac tcc tgg gcc gtc cct 157
 Gln Met Leu Pro Leu Leu Trp Leu Leu Pro His Ser Trp Ala Val Pro
 -10 -5 1
 gaa gct cct act cca atg tgg cca gat gac ctg caa aac cac aca ttc 205
 Glu Ala Pro Thr Pro Met Trp Pro Asp Asp Leu Gln Asn His Thr Phe
 5 10 15
 ctg cac aca gtg tac tgc cag gat ggg agt ccc agt gtg gga ctc tct 253
 Leu His Thr Val Tyr Cys Gln Asp Gly Ser Pro Ser Val Gly Leu Ser
 20 25 30
 gag gcc tac gac gag gac cag ctt ttc ttc ttc gac ttt tcc cag aac 301
 Glu Ala Tyr Asp Glu Asp Gln Leu Phe Phe Phe Asp Phe Ser Gln Asn
 35 40 45 50
 act cgg gtg cct cgc ctg ccc gaa ttt gct gac tgg gct cag gaa cag 349
 Thr Arg Val Pro Arg Leu Pro Glu Phe Ala Asp Trp Ala Gln Glu Gln
 55 60 65
 gga gat gct cct gcc att tta ttt gac aaa gag ttc tgc gag tgg atg 397
 Gly Asp Ala Pro Ala Ile Leu Phe Asp Lys Glu Phe Cys Glu Trp Met
 70 75 80
 atc cag caa ata ggg cca aaa ctt gat ggg aaa atc ccg gtg tcc aga 445
 Ile Gln Gln Ile Gly Pro Lys Leu Asp Gly Lys Ile Pro Val Ser Arg
 85 90 95
 ggg ttt cct atc gct gaa gtg ttc acg ctg wag ccc tkg agt ttg gca 493
 Gly Phe Pro Ile Ala Glu Val Phe Thr Leu Xaa Pro Xaa Ser Leu Ala
 100 105 110
 agc caa cac ttt ggt ctg twt trw cag taatctcttc ccacccatgc 540
 Ser Gln His Phe Gly Leu Xaa Xaa Gln
 115 120
 tgacagtgaa mwggcagcat cattccgt 568

<210> 3749
 <211> 491
 <212> DNA
 <213> Homo sapiens

<220>

<221> CDS
<222> 108..455

<221> sig_peptide
<222> 108..161
<223> score 6.3
seq LLFVGLLLTWESG/QV

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acagggtgcc gctgaccgag gcgtgcaaag actccagaat tggaggc atg atg aag 116
Met Met Lys
act ctg ctg ctg ttt gtg ggg ctg ctg ctg acc tgg gag agt ggg cag 164
Thr Leu Leu Leu Phe Val Gly Leu Leu Leu Thr Trp Glu Ser Gly Gln
-15 -10 -5 1
gtc ctg ggg gac cag acg gtc tca gac aat gag ctc cag gaa atg tcc 212
Val Leu Gly Asp Gln Thr Val Ser Asp Asn Glu Leu Gln Glu Met Ser
5 10 15
aat cag gga agt aag tac gtc aat aag gaa att caa aat gct gtc aac 260
Asn Gln Gly Ser Lys Tyr Val Asn Lys Glu Ile Gln Asn Ala Val Asn
20 25 30
ggg gtg aaa cag ata aag act ctc ata gaa aaa aca aac gaa gag cgc 308
Gly Val Lys Gln Ile Lys Thr Leu Ile Glu Lys Thr Asn Glu Glu Arg
35 40 45
aag aca ctg ctc agc aac cta gaa gaa gcc aag aag aag aaa gag gat 356
Lys Thr Leu Leu Ser Asn Leu Glu Glu Ala Lys Lys Lys Lys Glu Asp
50 55 60 65
gcc cta aat gag acc agg gaa tca gag aca aag ctg aag gag ctc cca 404
Ala Leu Asn Glu Thr Arg Glu Ser Glu Thr Lys Leu Lys Glu Leu Pro
70 75 80
gga gtg tgc aat gag acc atg atg gcc ctc tgg gaa gag tgt agc cct 452
Gly Val Cys Asn Glu Thr Met Met Ala Leu Trp Glu Glu Cys Ser Pro
85 90 95
gcc tganacagac ctgcatgggt ttctacgcac gcgtct 491
Ala

<210> 3750
<211> 732
<212> DNA
<213> Homo sapiens

<220>
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<222> 124..690

<221> sig_peptide
<222> 124..207
<223> score 12.5
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acc atg gct ctg gag aag tct ctt gtc cgg ctc ctt ctg ctt gtc ctg 168
    Met Ala Leu Glu Lys Ser Leu Val Arg Leu Leu Leu Leu Val Leu
        -25                -20                -15
ata ctg ctg gtg ctg ggc tgg gtc cag cct tcc ctg ggc aag gaa tcc 216
Ile Leu Leu Val Leu Gly Trp Val Gln Pro Ser Leu Gly Lys Glu Ser
        -10                -5                1
cgg gcc aag aaa ttc cag cgg cag cat atg gac tca gac agt tcc ccc 264
Arg Ala Lys Lys Phe Gln Arg Gln His Met Asp Ser Asp Ser Ser Pro
    5                10                15
agc agc agc tcc acc tac tgt aac caa atg atg agg cgc cgg aat atg 312
Ser Ser Ser Ser Thr Tyr Cys Asn Gln Met Met Arg Arg Arg Asn Met
20                25                30                35
aca cag ggg cgg tgc aaa cca gtg aac acc ttt gtg cac gag ccc ctg 360
Thr Gln Gly Arg Cys Lys Pro Val Asn Thr Phe Val His Glu Pro Leu
        40                45                50
gta gat gtc cag aat gtc tgt ttc cag gaa aag gtc acc tgc aag aac 408
Val Asp Val Gln Asn Val Cys Phe Gln Glu Lys Val Thr Cys Lys Asn
        55                60                65
ggg cag ggc aac tgc tac aag agc aac tcc agc atg cac atc aca gac 456
Gly Gln Gly Asn Cys Tyr Lys Ser Asn Ser Ser Met His Ile Thr Asp
        70                75                80
tgc cgc ctg aca aac ggc tcc agt acc cca act gtg cat acc gga cca 504
Cys Arg Leu Thr Asn Gly Ser Ser Thr Pro Thr Val His Thr Gly Pro
        85                90                95
gcc cga agg aga gac aca tca ttg tgg cct gtg aag gga gcc cat atg 552
Ala Arg Arg Arg Asp Thr Ser Leu Trp Pro Val Lys Gly Ala His Met
100                105                110                115
tgc cag tcc act ttg atg ctt ctg tgg agg act cta cct aag gtc aga 600
Cys Gln Ser Thr Leu Met Leu Leu Trp Arg Thr Leu Pro Lys Val Arg
        120                125                130
sca gcg aga tac ccc acc tcc ctc aac ctc atc ctc tcc aca gct gcc 648
Xaa Ala Arg Tyr Pro Thr Ser Leu Asn Leu Ile Leu Ser Thr Ala Ala
        135                140                145
tct tcc ctc ttc ctt ccc tgc tgt gaa aga agt aac tac agt 690
Ser Ser Leu Phe Leu Pro Cys Glu Arg Ser Asn Tyr Ser
        150                155                160
tagggctcct attcacacac acatgcttcc ctttctgac tc 732

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<210> 3751

<211> 811

<212> DNA

<213> Homo sapiens

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<221> CDS

<222> 203..769

<221> sig_peptide

<222> 203..286

<223> score 12.5

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gggaggaaga cctcgctttg gagagtggga ataaaacgct cgtggaaaag ggtacacgct      180
tttctgggaa agtgaggcca cc atg gct ctg gag aag tct ctt gtc cgg ctc      232
                Met Ala Leu Glu Lys Ser Leu Val Arg Leu
                        -25                                -20

ctt ctg ctt gtc ctg ata ctg ctg gtg ctg ggc tgg gtc cag cct tcc      280
Leu Leu Leu Val Leu Ile Leu Leu Val Leu Gly Trp Val Gln Pro Ser
                        -15                                -10                                -5

ctg ggc aag gaa tcc cgg gcc aag aaa ttc cag cgg cag cat atg gac      328
Leu Gly Lys Glu Ser Arg Ala Lys Lys Phe Gln Arg Gln His Met Asp
                        1                                5                                10

tca gac agt tcc ccc agc agc agc tcc acc kac tgt aac caa atg atg      376
Ser Asp Ser Ser Pro Ser Ser Ser Ser Thr Xaa Cys Asn Gln Met Met
15                                20                                25                                30

agg cgc cgg aat atg aca cag ggg cgg tgc aaa cca gtg aac acc ttt      424
Arg Arg Arg Asn Met Thr Gln Gly Arg Cys Lys Pro Val Asn Thr Phe
                        35                                40                                45

gtg cac gag ccc ctg gta gat gtc cag aat gtc tgt ttc cag gaa aag      472
Val His Glu Pro Leu Val Asp Val Gln Asn Val Cys Phe Gln Glu Lys
                        50                                55                                60

gtc acc tgc aag aac ggg cag ggc aac tgc tac aag agc aac tcc agc      520
Val Thr Cys Lys Asn Gly Gln Gly Asn Cys Tyr Lys Ser Asn Ser Ser
65                                70                                75

atg cac atc aca gac tgc cgc ctg aca aac ggc tcc agt acc cca act      568
Met His Ile Thr Asp Cys Arg Leu Thr Asn Gly Ser Ser Thr Pro Thr
80                                85                                90

gtg cat acc gga cca gcc cga agg aga gac aca tca ttg tgg cct gtg      616
Val His Thr Gly Pro Ala Arg Arg Arg Asp Thr Ser Leu Trp Pro Val
95                                100                                105                                110

aag gga gcc cat atg tgc cag tcc act ttg atg ctt ctg tgg agg act      664
Lys Gly Ala His Met Cys Gln Ser Thr Leu Met Leu Leu Trp Arg Thr
                        115                                120                                125

cta cct aag gtc aga sca gcg aga tac ccc acc tcc ctc aac ctc atc      712
Leu Pro Lys Val Arg Xaa Ala Arg Tyr Pro Thr Ser Leu Asn Leu Ile
                        130                                135                                140

ctc tcc aca gct gcc tct tcc ctc ttc ctt ccc tgc tgt gaa aga agt      760
Leu Ser Thr Ala Ala Ser Ser Leu Phe Leu Pro Cys Cys Glu Arg Ser
145                                150                                155

aac tac agt tagggctcct attcacacac acatgcttcc ctttcttgac tc      811
Asn Tyr Ser
160

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<210> 3752
<211> 813
<212> DNA
<213> Homo sapiens

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<220>
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<222> 207..671

<221> sig_peptide

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<222> 207..290
 <223> score 12.5
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 agaggggagg aagacctcgc tttggagagt gggaataaaa cgctcgtgga aaagggtaca 180
 cgcttttctg ggaaagtgag gccacc atg gct ctg gag aag tct ctt gtc cgg 233
 Met Ala Leu Glu Lys Ser Leu Val Arg
 -25 -20
 ctc ctt ctg ctt gtc ctg ata ctg ctg gtg ctg ggc tgg gtc cag cct 281
 Leu Leu Leu Leu Val Leu Ile Leu Leu Val Leu Gly Trp Val Gln Pro
 -15 -10 -5
 tcc ctg ggc aag gaa tcc cgg gcc aag aaa ttc cag cgg cag cat atg 329
 Ser Leu Gly Lys Glu Ser Arg Ala Lys Lys Phe Gln Arg Gln His Met
 1 5 10
 gac tca gac agt tcc ccc agc agc agc tcc acc tac tgt aac caa atg 377
 Asp Ser Asp Ser Ser Pro Ser Ser Ser Ser Thr Tyr Cys Asn Gln Met
 15 20 25
 atg agg cgc cgg aat atg aca cag ggg cgg tgc aaa cca gtg aac acc 425
 Met Arg Arg Arg Asn Met Thr Gln Gly Arg Cys Lys Pro Val Asn Thr
 30 35 40 45
 ttt gtg cac gag ccc ctg gta gat gtc cag aat gtc tgt ttc cag gaa 473
 Phe Val His Glu Pro Leu Val Asp Val Gln Asn Val Cys Phe Gln Glu
 50 55 60
 aag gtc acc tgc aag aac ggg agn caa ctg cta caa gag cra ctc cag 521
 Lys Val Thr Cys Lys Asn Gly Xaa Gln Leu Leu Gln Glu Xaa Leu Gln
 65 70 75
 cat gca cat cac aga ctg ccg cct gac aaa cgg ctc cag tac ccc aac 569
 His Ala His His Arg Leu Pro Pro Asp Lys Arg Leu Gln Tyr Pro Asn
 80 85 90
 tgt gca tac cgg acc agc ccg aag gag aga cac atc att gtg gcc tgt 617
 Cys Ala Tyr Arg Thr Ser Pro Lys Glu Arg His Ile Ile Val Ala Cys
 95 100 105
 gaa ggg agc cca tat gtg cca gtc cac ttt gat gct tct gtg gag gac 665
 Glu Gly Ser Pro Tyr Val Pro Val His Phe Asp Ala Ser Val Glu Asp
 110 115 120 125
 tct acc taaggtcaga scagcgagat accccacctc cctcaacctc atcctctcca 721
 Ser Thr
 cagctgcctc ttcctctctc cttccctgct gtgaaagaag taactacagt tagggctcct 781
 attcacacac acatgcttcc ctttctgac tc 813

<210> 3753
 <211> 473
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 22..438
 <221> sig_peptide

seq ASLVLAFLGVCLG/IT

agt taacatggct gagggaccta caagatcatc ttgam 473

<213> Homo sapiens

<222> 168..548

seq LFWLCGILILALA/IW

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<400> 3754
agtttaataa cttttttattc ctccctctac ttctttgctt tctctttctg ctctgaagcc 60
gtggatacag aaatctctgc aggcaagttg ctccagagca tattgcagga caagcctgta 120

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004220"666E1560

40	45	50	
cag ctc gtt aga aag atg att ttg aga acc tct gag gaa acc att tct			404
Gln Leu Val Arg Lys Met Ile Leu Arg Thr Ser Glu Glu Thr Ile Ser			
55	60	65	
aca gtt caa gaa aag caa caa aat att tct ccc cta gtg aga gaa aga			452
Thr Val Gln Glu Lys Gln Gln Asn Ile Ser Pro Leu Val Arg Glu Arg			
70	75	80	85
ggt ctc aga gag tagcagctca ca			476
Gly Leu Arg Glu			

<210> 3757
 <211> 463
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 89..454

<221> sig_peptide
 <222> 89..223
 <223> score 7.2
 seq SFALCMFVAAAGA/YV

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tggagactgc tgcacggact ctggaacc atg aac ata ttt gat cga aag atc	112
Met Asn Ile Phe Asp Arg Lys Ile	
-45	-40
aac ttt gat gcg ctt tta aaa ttt tct cat ata acc ccg tcr acg cag	160
Asn Phe Asp Ala Leu Leu Lys Phe Ser His Ile Thr Pro Ser Thr Gln	
-35	-30
cag cac ctg aag aag gtc tat gca agt ttt gcc ctt tgt atg ttt gtg	208
Gln His Leu Lys Lys Val Tyr Ala Ser Phe Ala Leu Cys Met Phe Val	
-20	-15
gcg gct gca ggg gcc tat gtc cat atg gtc act cat ttc att cag gct	256
Ala Ala Ala Gly Ala Tyr Val His Met Val Thr His Phe Ile Gln Ala	
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ggc ctg ctg tct gcc ttg ggc tcc ctg ata ttg atg att tgg ctg atg	304
Gly Leu Leu Ser Ala Leu Gly Ser Leu Ile Leu Met Ile Trp Leu Met	
15	20
gca aca cct cat agc cat gaa act gaa cag aaa aga ctg gga ctt ctt	352
Ala Thr Pro His Ser His Glu Thr Glu Gln Lys Arg Leu Gly Leu Leu	
30	35
gct gga ttt gca ttc ctt aca gga gtt ggc ctg ggc cct gcc tgg agt	400
Ala Gly Phe Ala Phe Leu Thr Gly Val Gly Leu Gly Pro Ala Trp Ser	
45	50
ttt gta ttg ctg tca acc cca gca tcc ttc cca ctg ctt tca tgg gca	448
Phe Val Leu Leu Ser Thr Pro Ala Ser Phe Pro Leu Leu Ser Trp Ala	
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cag caa tgatcttta	463
Gln Gln	

<210> 3758
 <211> 509
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 106..492

<221> sig_peptide
 <222> 106..180
 <223> score 8.9
 seq IIAVLMSAQESWA/IK

<400> 3758
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 cactcccgag ctctactgac tcccaamaga gcgccaaga agaaa atg gcc ata agt 117
 Met Ala Ile Ser
 -25
 gga gtc cct gtg cta gga ttt ttc atc ata gct gtg ctg atg agc gct 165
 Gly Val Pro Val Leu Gly Phe Phe Ile Ile Ala Val Leu Met Ser Ala
 -20 -15 -10
 cag gaa tca tgg gct atc aaa gaa gaa cat gtg atc atc cag gcc gag 213
 Gln Glu Ser Trp Ala Ile Lys Glu Glu His Val Ile Ile Gln Ala Glu
 -5 1 5 10
 ttc tat ctg aat cct gac caa tca ggc gag ttt atg ttt gac ttt gat 261
 Phe Tyr Leu Asn Pro Asp Gln Ser Gly Glu Phe Met Phe Asp Phe Asp
 15 20 25
 ggt gat gag att ttc cat gtg gat atg gca aag aag gag acg gtc tgg 309
 Gly Asp Glu Ile Phe His Val Asp Met Ala Lys Lys Glu Thr Val Trp
 30 35 40
 cgg ctt gaa gaa ttt gga cga ttt gcc agc ttt gag gct caa ggt gca 357
 Arg Leu Glu Glu Phe Gly Arg Phe Ala Ser Phe Glu Ala Gln Gly Ala
 45 50 55
 ttg gcc aac ata gct gtg gac aaa gcc aac ctg gaa atc atg aca aag 405
 Leu Ala Asn Ile Ala Val Asp Lys Ala Asn Leu Glu Ile Met Thr Lys
 60 65 70 75
 cgc tcc aac tat act ccg atc acc aat gta cct cca gag gta act gtg 453
 Arg Ser Asn Tyr Thr Pro Ile Thr Asn Val Pro Pro Glu Val Thr Val
 80 85 90
 ctc acg aac agc cct gtg gaa ctg aga gag ccc tta ggc tgaggcagga 502
 Leu Thr Asn Ser Pro Val Glu Leu Arg Glu Pro Leu Gly
 95 100
 gaatggc 509

<210> 3759
 <211> 498
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 162..491

004220"0060150

<221> sig_peptide
 <222> 162..233
 <223> score 4.7
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<400> 3759
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 attaatttta gtgtatgatt actggccttt ttcatttatt tataattttac ctaagattac 120
 aaatcagaag tcatcttgct accagtattt agaagccaac t atg att att aac gat 176
 Met Ile Ile Asn Asp
 -20
 gtc cag gcg ccc tgg tgg ctc ttg atg atc agg tcc acg gcg gct gcc 224
 Val Gln Ala Pro Trp Trp Leu Leu Met Ile Arg Ser Thr Ala Ala Ala
 -15 -10 -5
 aca cgc tcc tct agg ccc ttc agc ggc agc agc gag ctt tca gag aat 272
 Thr Arg Ser Ser Arg Pro Phe Ser Gly Ser Ser Glu Leu Ser Glu Asn
 1 5 10
 cag caa cca gga gca cca aat gct cct act cat cct gct cct cca ggc 320
 Gln Gln Pro Gly Ala Pro Asn Ala Pro Thr His Pro Ala Pro Pro Gly
 15 20 25
 ctt cat cac cac cat aag cac aag ggt cag cat agg cag ggt cac cca 368
 Leu His His His His Lys His Lys Gly Gln His Arg Gln Gly His Pro
 30 35 40 45
 gag aac cga gat atg cca gca agt gaa gat tta caa gat tta caa aag 416
 Glu Asn Arg Asp Met Pro Ala Ser Glu Asp Leu Gln Asp Leu Gln Lys
 50 55 60
 aag ctc tgt cga aag aga tgt ata aat caa tta ctc tgt aaa ttg ccc 464
 Lys Leu Cys Arg Lys Arg Cys Ile Asn Gln Leu Leu Cys Lys Leu Pro
 65 70 75
 aca gat tca gag ttg gct cct agg agc tgatgct 498
 Thr Asp Ser Glu Leu Ala Pro Arg Ser
 80 85

<210> 3760
 <211> 500
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 70..378

<221> sig_peptide
 <222> 70..129
 <223> score 6.9
 seq AAFLSPLLPLLLG/FL

<400> 3760
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 cccggcgat atg gct gcc gct gtg ccc cgc gcc gca ttt ctc tcc ccg ctg 111
 Met Ala Ala Ala Val Pro Arg Ala Ala Phe Leu Ser Pro Leu

-20	-15	-10	
ctt ccc ctt ctc ctg ggc ttc ctg ctc ctc tcc gct ccg cat ggc ggc	159		
Leu Pro Leu Leu Leu Gly Phe Leu Leu Leu Ser Ala Pro His Gly Gly			
-5 1 5 10			
agc ggc ctg cac acc aag ggc gcc ctt ccc ctg gat acg gtc act ttc	207		
Ser Gly Leu His Thr Lys Gly Ala Leu Pro Leu Asp Thr Val Thr Phe			
15 20 25			
tac aag gtc att ccc aaa agc aag ttc gtc ttg gtg aag ttc gac acc	255		
Tyr Lys Val Ile Pro Lys Ser Lys Phe Val Leu Val Lys Phe Asp Thr			
30 35 40			
cag tac ccc tac ggt gag aag cag gat gag ttc aag cgt ctt gct gaa	303		
Gln Tyr Pro Tyr Gly Glu Lys Gln Asp Glu Phe Lys Arg Leu Ala Glu			
45 50 55			
aac tcg gct tcc agc gat gat ctc ttg gtg gca gag gtg ggg atc tca	351		
Asn Ser Ala Ser Ser Asp Asp Leu Leu Val Ala Glu Val Gly Ile Ser			
60 65 70			
gat tat ggt gac aag cga aca tgg agc tgagtgagaa atacaagctg	398		
Asp Tyr Gly Asp Lys Arg Thr Trp Ser			
75 80			
gacaaagaga gctacccagt cttctacctc ttccgggatg gggactttga gaaccagtcc	458		
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<210> 3761
 <211> 526
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 116..418

<221> sig_peptide
 <222> 116..166
 <223> score 10.4
 seq LLPALFLVLLVLG/FE

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tgtgcccgtc cggagctggt gaggacagcc tgccagagtc tggctctctgg acact atg	118
	Met
ggc aca cga ctc ctc cca gct ctg ttt ctt gtc ctc ctg gta ttg gga	166
Gly Thr Arg Leu Leu Pro Ala Leu Phe Leu Val Leu Leu Val Leu Gly	
-15 -10 -5	
ttt gag gtc cag ggg acc caa cag ccc cag caa gat gag atg cct agc	214
Phe Glu Val Gln Gly Thr Gln Gln Pro Gln Gln Asp Glu Met Pro Ser	
1 5 10 15	
ccg acc ttc ctc acc cag gtg aag gaa tct ctc tcc agt tac tgg gag	262
Pro Thr Phe Leu Thr Gln Val Lys Glu Ser Leu Ser Ser Tyr Trp Glu	
20 25 30	
tca gca aag aca gcc gcc cag aac ctg tac gag aag aca tac ctg ccc	310
Ser Ala Lys Thr Ala Ala Gln Asn Leu Tyr Glu Lys Thr Tyr Leu Pro	
35 40 45	
gct gta gat gag aaa ctc agg gac ttg tac agc aaa agc aca gca gcc	358

Ala Val Asp Glu Lys Leu Arg Asp Leu Tyr Ser Lys Ser Thr Ala Ala	
50 55 60	
atg agc act tac aca ggc att ttt act gac caa gtt ctt tct gtg ctg	406
Met Ser Thr Tyr Thr Gly Ile Phe Thr Asp Gln Val Leu Ser Val Leu	
65 70 75 80	
aag gga gag gag taacagccag annmccccat cagtggacaa ggggagagtc	458
Lys Gly Glu Glu	
ccctactccc ctgatccccc aggttcagac tgagctcccc cttcccagta gctcttgc	518
cctccccc	526

<210> 3762
 <211> 445
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 <213> Homo sapiens

<220>
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 <222> 74..385

<221> sig_peptide
 <222> 74..145
 <223> score 6.5
 seq LSICLSAVATATG/AE

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ggcgaggaga gac atg agg ctg agc tgg ttc cgg gtc ctg aca gta ctg	109
Met Arg Leu Ser Trp Phe Arg Val Leu Thr Val Leu	
-20 -15	
tcc atc tgc ctg agc gcc gtg gcc acg gcc acg ggg gcc gag ggc aaa	157
Ser Ile Cys Leu Ser Ala Val Ala Thr Ala Thr Gly Ala Glu Gly Lys	
-10 -5 1	
agg aag ctg cag atc ggg gtc aag aag cgg gtg gac cac tgt ccc atc	205
Arg Lys Leu Gln Ile Gly Val Lys Lys Arg Val Asp His Cys Pro Ile	
5 10 15 20	
aaa tcg cgc aaa ggg gat gtc ctg cac atg cac tac acg ggg aag ctg	253
Lys Ser Arg Lys Gly Asp Val Leu His Met His Tyr Thr Gly Lys Leu	
25 30 35	
gaa gat ggg aca gag ttt gac agc agc ctg ccc cag aac cag ccc ttt	301
Glu Asp Gly Thr Glu Phe Asp Ser Ser Leu Pro Gln Asn Gln Pro Phe	
40 45 50	
gtc ttc tcc ctt ggc aca ggc cag gtc atc aag ggc tgg gac cag gnn	349
Val Phe Ser Leu Gly Thr Gly Gln Val Ile Lys Gly Trp Asp Gln Xaa	
55 60 65	
ctg ctg ggg atg tgt gag ggg gaa aag cgc rrc tgg tgatcccatc	395
Leu Leu Gly Met Cys Glu Gly Glu Lys Arg Xaa Trp	
70 75 80	
cgagctaggg tatggagagc ggggastccc ccaaagattc caggcggtgc	445

<210> 3763
 <211> 651
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> 1..345

<221> sig_peptide
 <222> 1..51
 <223> score 4.4
 seq AWATALFSSNVFP/LP

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 Met Pro Leu Pro Ala Trp Ala Thr Ala Leu Phe Ser Ser Asn Val Phe
 -15 -10 -5
 cct cta cct ggg ttg gct gtt tct tca ttc ata ttt gag aag aat cac 96
 Pro Leu Pro Gly Leu Ala Val Ser Ser Phe Ile Phe Glu Lys Asn His
 1 5 10 15
 ctc cta att aaa tgt wgc aac ttc gct ctc tcc cta cat gaa ggc tgt 144
 Leu Leu Ile Lys Cys Xaa Asn Phe Ala Leu Ser Leu His Glu Gly Cys
 20 25 30
 ctt' ggt tac ccg act agg caa cgc gca ttg gta tca aat tac cga aag 192
 Leu Gly Tyr Pro Thr Arg Gln Arg Ala Leu Val Ser Asn Tyr Arg Lys
 35 40 45
 tct aca ccg gag cag tcc tca tat tta cat aca aat aac tca ggg gct 240
 Ser Thr Pro Glu Gln Ser Ser Tyr Leu His Thr Asn Asn Ser Gly Ala
 50 55 60
 tgc att tat gtc acc att ckg tcc tgc wag agg ctt gcc aga gga gtt 288
 Cys Ile Tyr Val Thr Ile Xaa Ser Cys Xaa Arg Leu Ala Arg Gly Val
 65 70 75
 ttt aat cca atc aga agg agc ttt aaa agg atg tct gcg aag tgg tca 336
 Phe Asn Pro Ile Arg Arg Ser Phe Lys Arg Met Ser Ala Lys Trp Ser
 80 85 90 95
 aaa gga tct taacctcaat taagtggggg tttttaaaaa gattttttgg 385
 Lys Gly Ser
 ggggcctgaa attttgaaaa tcttcgaact ctgagtgggg aaagatgtat aattcctcaa 445
 ttgcctacga ggatatcaag atgctgagag gaattcagcg gtggtgaaga gagggtgatac 505
 aaaccaggga ttggtttsmt tgagctgttt tggaggttga ttctaaatca ctgcttaagg 565
 aattcctgga aacatcagga aaacatttga tcatccaagc ctagtggaaa tggctttacc 625
 gcagagtgaa gatgcaatga ccgggc 651

<210> 3764
 <211> 584
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 84..434
 <221> sig_peptide
 <222> 84..164
 <223> score 3.6
 seq ACLLCSLVKTIDQ/FE

<400> 3764

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tggtgttctt cccatcggcg aag atg gcc ctg gag acg gtg ccg aag gac ctg      113
               Met Ala Leu Glu Thr Val Pro Lys Asp Leu
               -25                               -20

cgg cat ctg cgg gcc tgt ttg ctg tgt tcg ctg gtc aag act ata gac      161
Arg His Leu Arg Ala Cys Leu Leu Cys Ser Leu Val Lys Thr Ile Asp
               -15                               -10                               -5

cag ttt gaa tat gat ggt tgt gac aat tgt gat gca tat cta caa atg      209
Gln Phe Glu Tyr Asp Gly Cys Asp Asn Cys Asp Ala Tyr Leu Gln Met
               1                               5                               10                               15

aag ggt aac cga gag atg gta tat gac tgc act agc tct tcc ttt gat      257
Lys Gly Asn Arg Glu Met Val Tyr Asp Cys Thr Ser Ser Ser Phe Asp
               20                               25                               30

gga atc att gcg atg atg agt cca gag gac agc tgg gtc tcc aag tgg      305
Gly Ile Ile Ala Met Met Ser Pro Glu Asp Ser Trp Val Ser Lys Trp
               35                               40                               45

cag cga gtc agt aac ttt aag cca ggt gta tat gcg gtg tca gtc act      353
Gln Arg Val Ser Asn Phe Lys Pro Gly Val Tyr Ala Val Ser Val Thr
               50                               55                               60

ggt cgc ctg ccc caa gga atc gtg cgg gag ctg aaa agt cga gga gtg      401
Gly Arg Leu Pro Gln Gly Ile Val Arg Glu Leu Lys Ser Arg Gly Val
               65                               70                               75

gcc tac aaa tcc aga gac aca gct ata aag acc tagcaagatg caaggctgcc      454
Ala Tyr Lys Ser Arg Asp Thr Ala Ile Lys Thr
               80                               85                               90

agcatctttg ctctccamct cctgcctctg cttatttctt gttctggact aaatgnacag      514
amttcaaata cttcctaccc tccaattcag actcagctga ctgttragag agcagcmcat      574
cattttatca      584

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<210> 3765

<211> 448

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 94..426

<221> sig_peptide

<222> 94..219

<223> score 7.4

seq SLSVLVLLLTIIA/VT

<400> 3765

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gagatgtgca agtggcgaac ttgaccgaga gcaggctgga gcagccgccc aactcctggc      60
gcgggatctg ctgaggggtc acgatttttag gtg atg ggc aag tca gaa agt cag      114
               Met Gly Lys Ser Glu Ser Gln
               -40

atg gat ata act gat atc aac act cca aag cca aag aag aaa cag cga      162
Met Asp Ile Thr Asp Ile Asn Thr Pro Lys Pro Lys Lys Lys Gln Arg

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-35	-30	-25	-20	
tgg act cca ctg gag atc agc ctc tcg gtc ctt gtc ctg ctc ctc acc				210
Trp Thr Pro Leu Glu Ile Ser Leu Ser Val Leu Val Leu Leu Leu Thr				
	-15	-10	-5	
atc ata gct gtg aca atg atc gca ctc tat gca acc tac gat gat ggt				258
Ile Ile Ala Val Thr Met Ile Ala Leu Tyr Ala Thr Tyr Asp Asp Gly				
	1	5	10	
att tgc aag tca tca gac tgc ata aaa tca gct gct cga ctg atc caa				306
Ile Cys Lys Ser Ser Asp Cys Ile Lys Ser Ala Ala Arg Leu Ile Gln				
	15	20	25	
aac atg gat gcc amc act gag cct tgt aca gac ttt ttc aaa tat gct				354
Asn Met Asp Ala Xaa Thr Glu Pro Cys Thr Asp Phe Phe Lys Tyr Ala				
	30	35	40	45
tgc gga ggc tgg ttg aaa cgt aat gtc att ccc gag acc agc tcc cgt				402
Cys Gly Gly Trp Leu Lys Arg Asn Val Ile Pro Glu Thr Ser Ser Arg				
	50	55	60	
tac ggc ctt tgr cat ttt aag aga tgaactagaa gtcgttttga aa				448
Tyr Gly Leu Xaa His Phe Lys Arg				
	65			

<210> 3766
 <211> 447
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 69..398

<221> sig_peptide
 <222> 69..131
 <223> score 9.1
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atgcgggtc atg gcg ccc cga acc ctc mtc ctg ctg ctc tcg ggr gcc ctg	110
Met Ala Pro Arg Thr Leu Xaa Leu Leu Leu Ser Gly Ala Leu	
	-20 -15 -10
gcc ctg acc gag acc tgg gcc ggc tcc cac tcc atg agg tat ttc tac	158
Ala Leu Thr Glu Thr Trp Ala Gly Ser His Ser Met Arg Tyr Phe Tyr	
	-5 1 5
acm kcc gtg tcc cgg ccc ggc cgc ggr gag ccc cgc ttc atc kca gtg	206
Thr Xaa Val Ser Arg Pro Gly Arg Gly Glu Pro Arg Phe Ile Xaa Val	
	10 15 20 25
ggc tac gtg gac gac acg cag ttc gtg cgg ttc gac agc gac gcc gcg	254
Gly Tyr Val Asp Asp Thr Gln Phe Val Arg Phe Asp Ser Asp Ala Ala	
	30 35 40
agc caa gak gga gcc gcg ggm gcc gtg grt rga gca gga ggg gcc gga	302
Ser Gln Xaa Gly Ala Ala Gly Ala Val Xaa Xaa Ala Gly Gly Ala Gly	
	45 50 55
gta ttg gga ccr gga gac aca gaa gta caa gcg cca ggc aca ggc ggt	350
Val Leu Gly Pro Gly Asp Thr Glu Val Gln Ala Pro Gly Thr Gly Gly	

60	65	70	
ttg gac ccc acc act gtt gcc atg gtg acc aaa ctc tgg agt ccg agg	398		
Leu Asp Pro Thr Thr Val Ala Met Val Thr Lys Leu Trp Ser Pro Arg			
75	80	85	
taacagaaca cctgtccccc taggcttctc cgttgtccac aaggaaaag	447		

<210> 3767
 <211> 480
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 61..468

<221> sig_peptide
 <222> 61..132
 <223> score 9.4
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atg cgg gtc atg gcg ccc cga acc ctc mtc ctg ctg ctc tcg ggr gcc	108
Met Arg Val Met Ala Pro Arg Thr Leu Xaa Leu Leu Leu Ser Gly Ala	
-20 -15 -10	
ctg gcc ctg acc gag acc tgg gcc kgc tcc cac tcc atg agg tat ttc	156
Leu Ala Leu Thr Glu Thr Trp Ala Xaa Ser His Ser Met Arg Tyr Phe	
-5 1 5	
kac acc gcc gtg tcc cgg ccc ggc cgc ggr gag ccc cgc ttc atc kca	204
Xaa Thr Ala Val Ser Arg Pro Gly Arg Gly Glu Pro Arg Phe Ile Xaa	
10 15 20	
gtg ggc tac gtg gac gac acg cag ttc gtg cgg ttc gac agc gac gcc	252
Val Gly Tyr Val Asp Asp Thr Gln Phe Val Arg Phe Asp Ser Asp Ala	
25 30 35 40	
gcg agt ccg aga grg gag ccg cgg gcg ccg tgg rtr gag cag gag ggg	300
Ala Ser Pro Arg Xaa Glu Pro Arg Ala Pro Trp Xaa Glu Gln Glu Gly	
45 50 55	
ccg gar tat tgg gac cgg ras aca cag aag tac aag cca ctg agg aag	348
Pro Glu Tyr Trp Asp Arg Xaa Thr Gln Lys Tyr Lys Pro Leu Arg Lys	
60 65 70	
agt ggt ttt cct aag aag aca ttg ctg gag ttg act ttc ttc tgt cca	396
Ser Gly Phe Pro Lys Lys Thr Leu Leu Glu Leu Thr Phe Phe Cys Pro	
75 80 85	
ars aaa caa aca aaa act aaa cac aca cac aaa ccc cca gaa acc cac	444
Xaa Lys Gln Thr Lys Thr Lys His Thr His Lys Pro Pro Glu Thr His	
90 95 100	
aat atg tac acg cta agg aaa aac tagcaccctt ct	480
Asn Met Tyr Thr Leu Arg Lys Asn	
105 110	

<210> 3768
 <211> 492
 <212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 129..473

<221> sig_peptide

<222> 129..188

<223> score 10.4

seq VLFGLLLVLAVFC/HS

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gccagtcttt agcaccagtt ggtgtaggag ttgagaccta cttcacagta gttctgtgga 120
caatcaca atg gga atc caa gga ggg tct gtc ctg ttc ggg ctg ctg ctc 170
Met Gly Ile Gln Gly Gly Ser Val Leu Phe Gly Leu Leu Leu
-20 -15 -10
gtc ctg gct gtc ttc tgc cat tca ggt cat agc ctg cag tgc tac aac 218
Val Leu Ala Val Phe Cys His Ser Gly His Ser Leu Gln Cys Tyr Asn
-5 1 5 10
tgt cct aac cca act gct gac tgc aaa aca gcc gtc aat tgt tca tct 266
Cys Pro Asn Pro Thr Ala Asp Cys Lys Thr Ala Val Asn Cys Ser Ser
15 20 25
gat ttt gat gcg tgt ctc att acc aaa gct ggg tta caa gtg tat aac 314
Asp Phe Asp Ala Cys Leu Ile Thr Lys Ala Gly Leu Gln Val Tyr Asn
30 35 40
aag tgt tgg aag ttt gag cat tgc aat ttc aac gac gtc aca acc cgc 362
Lys Cys Trp Lys Phe Glu His Cys Asn Phe Asn Asp Val Thr Thr Arg
45 50 55
ttg agg gaa aat gag cta acg tac tac tgc tgc aag aag gac ctg tgt 410
Leu Arg Glu Asn Glu Leu Thr Tyr Tyr Cys Cys Lys Lys Asp Leu Cys
60 65 70
aac ttt aac gaa cag ctt gaa aat ggt ggg aca tcc tta tca gaa aaa 458
Asn Phe Asn Glu Gln Leu Glu Asn Gly Gly Thr Ser Leu Ser Glu Lys
75 80 85 90
cag ttc ttc tgc tgg tgactccatt tctggcagc 492
Gln Phe Phe Cys Trp
95

<210> 3769

<211> 418

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 55..399

<221> sig_peptide

<222> 55..114

<223> score 10.4

seq VLFGLLLVLAVFC/HS

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Met
-20
gga atc caa gga ggg tct gtc ctg ttc ggg ctg ctg ctc gtc ctg gct 105
Gly Ile Gln Gly Gly Ser Val Leu Phe Gly Leu Leu Leu Val Leu Ala
-15 -10 -5
gtc ttc tgc cat tca ggt cat agc ctg cag tgc tac aac tgt cct aac 153
Val Phe Cys His Ser Gly His Ser Leu Gln Cys Tyr Asn Cys Pro Asn
1 5 10
cca act gct gac tgc aaa aca gcc gtc aat tgt tca tct gat ttt gat 201
Pro Thr Ala Asp Cys Lys Thr Ala Val Asn Cys Ser Ser Asp Phe Asp
15 20 25
gcg tgt ctc att acc aaa gct ggg tta caa gtg tat aac aag tgt tgg 249
Ala Cys Leu Ile Thr Lys Ala Gly Leu Gln Val Tyr Asn Lys Cys Trp
30 35 40 45
aag ttt gag cat tgc aat ttc aac gac gtc aca acc cgc ttg agg gaa 297
Lys Phe Glu His Cys Asn Phe Asn Asp Val Thr Thr Arg Leu Arg Glu
50 55 60
aat gag cta acg tac tac tgc tgc aag aag gac ctg tgt aac ttt aac 345
Asn Glu Leu Thr Tyr Tyr Cys Cys Lys Lys Asp Leu Cys Asn Phe Asn
65 70 75
gaa cag ctt gaa aat ggt ggg aca tcc tta tca gaa aaa cag ttc ttc 393
Glu Gln Leu Glu Asn Gly Gly Thr Ser Leu Ser Glu Lys Gln Phe Phe
80 85 90
tgc tgg tgactccatt tctggcagc 418
Cys Trp
95

<210> 3770
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<212> DNA
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<222> 84..428

<221> sig_peptide
<222> 84..143
<223> score 10.4
seq VLFGLLLVLAVFC/HS

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gccaggttct gtggacaatc aca atg gga atc caa gga ggg tct gtc ctg ttc 113
Met Gly Ile Gln Gly Gly Ser Val Leu Phe
-20 -15
ggg ctg ctg ctc gtc ctg gct gtc ttc tgc cat tca ggt cat agc ctg 161
Gly Leu Leu Leu Val Leu Ala Val Phe Cys His Ser Gly His Ser Leu
-10 -5 1 5
cag tgc tac aac tgt cct aac cca act gct gac tgc aaa aca gcc gtc 209

Gln	Cys	Tyr	Asn	Cys	Pro	Asn	Pro	Thr	Ala	Asp	Cys	Lys	Thr	Ala	Val		
			10					15					20				
aat	tgt	tca	tct	gat	ttt	gat	gcg	tgt	ctc	att	acc	aaa	gct	ggg	tta	257	
Asn	Cys	Ser	Ser	Asp	Phe	Asp	Ala	Cys	Leu	Ile	Thr	Lys	Ala	Gly	Leu		
		25					30				35						
caa	gtg	tat	aac	aag	tgt	tgg	aag	ttt	gag	cat	tgc	aat	ttc	aac	gac	305	
Gln	Val	Tyr	Asn	Lys	Cys	Trp	Lys	Phe	Glu	His	Cys	Asn	Phe	Asn	Asp		
	40					45					50						
gtc	aca	acc	cgc	ttg	agg	gaa	aat	gag	cta	acg	tac	tac	tgc	tgc	aag	353	
Val	Thr	Thr	Arg	Leu	Arg	Glu	Asn	Glu	Leu	Thr	Tyr	Tyr	Cys	Cys	Lys		
	55				60				65						70		
aag	gac	ctg	tgt	aac	ttt	aac	gaa	cag	ctt	gar	aat	ggg	ggg	aca	tcc	401	
Lys	Asp	Leu	Cys	Asn	Phe	Asn	Glu	Gln	Leu	Glu	Asn	Gly	Gly	Thr	Ser		
			75					80						85			
tta	tca	gaa	aaa	cag	ttc	ttc	tgc	tgg	tgactccatt	tctggcagc						447	
Leu	Ser	Glu	Lys	Gln	Phe	Phe	Cys	Trp									
			90					95									

<210> 3771
 <211> 806
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> 115..708

<221> sig_peptide
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 <223> score 5.1
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gccaggtgga	gcaaccggcc	ggataccgcc	acagccctgg	caggcggcgc	tgtg atg											117	
					Met												
cct gag ctg atc ctg tat gtt gca atc act cta tcc gtg gct gag cga																165	
Pro Glu Leu Ile Leu Tyr Val Ala Ile Thr Leu Ser Val Ala Glu Arg																	
	-45				-40				-35								
ctc gtt ggc ccg ggt cac gca tgc gct gag cct tcc ttt cgc tct tcc																213	
Leu Val Gly Pro Gly His Ala Cys Ala Glu Pro Ser Phe Arg Ser Ser																	
	-30				-25				-20								
cgc tgc tcc gcc cct ctc tgt ctt ctc tgc agt ggg agc agc tct cct																261	
Arg Cys Ser Ala Pro Leu Cys Leu Leu Cys Ser Gly Ser Ser Ser Pro																	
	-15				-10				-5						1		
gcc aca gct cct cac ccc ctg aaa atg ttc gcc tgc tcc aag ttt gtc																309	
Ala Thr Ala Pro His Pro Leu Lys Met Phe Ala Cys Ser Lys Phe Val																	
	5							10				15					
tcc act ccc tcc ttg gtc aag agc acc tca cag ctg ctg agc cgt ccg																357	
Ser Thr Pro Ser Leu Val Lys Ser Thr Ser Gln Leu Leu Ser Arg Pro																	
	20						25					30					
cta tct gca gtg gtg ctg aaa cga ccg gag ata ctg aca gat gag agc																405	
Leu Ser Ala Val Val Leu Lys Arg Pro Glu Ile Leu Thr Asp Glu Ser																	

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      35              40              45
ctc agc agc ttg gca gtc tca tgt ccc ctt acc tca ctt gtc tct agc      453
Leu Ser Ser Leu Ala Val Ser Cys Pro Leu Thr Ser Leu Val Ser Ser
50              55              60              65
cgc agc ttc caa acc agc gcc att tca agg gac atc gac aca gca gcc      501
Arg Ser Phe Gln Thr Ser Ala Ile Ser Arg Asp Ile Asp Thr Ala Ala
      70              75              80
aag ttc att gga gct ggg gct gcc aca gtt ggg gtg gct ggt tct ggg      549
Lys Phe Ile Gly Ala Gly Ala Ala Thr Val Gly Val Ala Gly Ser Gly
      85              90              95
gct ggg att gga act gtg ttt ggg agc ctc atc att ggt tat gcc agg      597
Ala Gly Ile Gly Thr Val Phe Gly Ser Leu Ile Ile Gly Tyr Ala Arg
      100              105              110
aac cct tct ctg aag caa cag ctc ttc tcc tac gcc att ctg ggc ttt      645
Asn Pro Ser Leu Lys Gln Gln Leu Phe Ser Tyr Ala Ile Leu Gly Phe
      115              120              125
gcc ctc tcg gag gcc atg ggg ctc ttt tgt ctg atg gta gcc ttt ctc      693
Ala Leu Ser Glu Ala Met Gly Leu Phe Cys Leu Met Val Ala Phe Leu
130              135              140              145
atc ctc ttt gcc atg tgaaggagcc gtctccacct cccatagttc tcccgcgtct      748
Ile Leu Phe Ala Met
      150
ggttggcccc gtgtgttctt tttcctatac ctccccaggc agcctgggga acgtggtt      806

<210> 3772
<211> 509
<212> DNA
<213> Homo sapiens

<220>
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<222> 36..500

<221> sig_peptide
<222> 36..92
<223> score 3.5
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      Met Ala Ala Ala Val Gly
      -15
cgg ttg ctc cga gcg tcg gtt gcc cga cat gtg agt gcc att cct tgg      101
Arg Leu Leu Arg Ala Ser Val Ala Arg His Val Ser Ala Ile Pro Trp
      -10              -5              1
ggc att tct gcc act gca gcc ctc agg cct gct gca tgt gga aga acg      149
Gly Ile Ser Ala Thr Ala Ala Leu Arg Pro Ala Ala Cys Gly Arg Thr
      5              10              15
agc ttg aca aat tta ttg tgt tct ggt tcc agt caa gca aaa tta ttc      197
Ser Leu Thr Asn Leu Leu Cys Ser Gly Ser Ser Gln Ala Lys Leu Phe
20              25              30              35
agc acc agt tcc tca tgc cat gca cct gct gtc acc cag cat gca ccc      245
Ser Thr Ser Ser Ser Cys His Ala Pro Ala Val Thr Gln His Ala Pro

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tat ttt aag ggt	aca gcc gtt gtc	aat gga gag ttc	aaa gac cta agc		293	
Tyr Phe Lys Gly	Thr Ala Val Val	Asn Gly Glu Phe	Lys Asp Leu Ser			
	55		60		65	
ctt gat gac ttt	aag ggg aaa tat	ttg gtg ctt ttc	ttc tat cct ttg		341	
Leu Asp Asp Phe	Lys Gly Lys Tyr	Leu Val Leu Phe	Phe Tyr Pro Leu			
	70		75		80	
gat ttc acc ttt	gtg tgt cct aca	gaa att gtt gct	ttt agt gac aaa		389	
Asp Phe Thr Phe	Val Cys Pro Thr	Glu Ile Val Ala	Phe Ser Asp Lys			
	85		90		95	
gct aac gaa ttt	cac gat gtg aac	tgt gaa gtt gtc	gca gtc tca gtg		437	
Ala Asn Glu Phe	His Asp Val Asn	Cys Glu Val Val	Ala Val Ser Val			
100	105		110		115	
gat tcc cac ttt	agc cat ctt gcc	tgg ata aat aca	cca aga aag aat		485	
Asp Ser His Phe	Ser His Leu Ala	Trp Ile Asn Thr	Pro Arg Lys Asn			
	120		125		130	
ggg ggt ttg ggc	aca tgaacatcg				509	
Gly Gly Leu Gly	Thr					
	135					

<210> 3773
 <211> 398
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 75..377

 <221> sig_peptide
 <222> 75..155
 <223> score 10.9
 seq LFLGXLLLPLVVA/FA

<400> 3773	
attggccaca gagacccagc ccgagtttcc catcgcaactg agcactgaga tcctgctgga	60
agctctgccc cagc atg agc tcc gca gcc ggg ttc tgc gcy tca cgc ccc	110
Met Ser Ser Ala Ala Gly Phe Cys Ala Ser Arg Pro	
-25	-20
ggg ctg ctg ttc ctg ggg ktg ctg ctc ctg cca ctt gtg gtc gcc ttc	158
Gly Leu Leu Phe Leu Gly Xaa Leu Leu Leu Pro Leu Val Val Ala Phe	
-15	-10
gcc agc gct gaa gct gaa gaa gat ggg gac ctg cag tgc ctg tgt gtg	206
Ala Ser Ala Glu Ala Glu Glu Asp Gly Asp Leu Gln Cys Leu Cys Val	
5	10
aag acc acc tcc cag gtc cgt ccc agg cac atc acc agc ctg gag gtg	254
Lys Thr Thr Ser Gln Val Arg Pro Arg His Ile Thr Ser Leu Glu Val	
20	25
atc aag gcc gga ccc cac tgc ccc act gcc caa ctg ata gcc acg ctg	302
Ile Lys Ala Gly Pro His Cys Pro Thr Ala Gln Leu Ile Ala Thr Leu	
35	40
aag aat gga agg aaa att tgc ttg gac ctg caa gcc ccg ctg tac aag	350
Lys Asn Gly Arg Lys Ile Cys Leu Asp Leu Gln Ala Pro Leu Tyr Lys	

<221> sig_peptide
 <222> 92..148
 <223> score 5.1
 seq SLLWAATCLGVLC/VL

<400> 3775
 gtagtctcgg aggcggcgcc gcaggggatt gaggggttga ctgagcgttg cgagccttag 60
 ctttctcccc aacgccagcg ctgaggacac g atg tcg cgg ctc tcc cgc tca 112
 Met Ser Arg Leu Ser Arg Ser
 -15
 ctg ctt tgg gcc gcc acc tgc ctg ggc gtg ctc tgc gtg ctg tcc gcg 160
 Leu Leu Trp Ala Ala Thr Cys Leu Gly Val Leu Cys Val Leu Ser Ala
 -10 -5 1
 gac aag aac acg acc cag cac ccg aac gtg acg act tta gcg ccc atc 208
 Asp Lys Asn Thr Thr Gln His Pro Asn Val Thr Thr Leu Ala Pro Ile
 5 10 15 20
 tcc aac gta acc tgc gcg ccg gtg acg tcc ctc ccg ctg gtc acc act 256
 Ser Asn Val Thr Ser Ala Pro Val Thr Ser Leu Pro Leu Val Thr Thr
 25 30 35
 ccg gca cca gaa acc tgt gaa ggt cga aac agc tgc gtt tcc tgt ttt 304
 Pro Ala Pro Glu Thr Cys Glu Gly Arg Asn Ser Cys Val Ser Cys Phe
 40 45 50
 aat gtt agc gtt gtt aat act acc tgc ttt tgg ata gaa tgt aaa gat 352
 Asn Val Ser Val Val Asn Thr Thr Cys Phe Trp Ile Glu Cys Lys Asp
 55 60 65
 gag agc tat tgt tca cat aac tca aca gtt agt gat tgt caa gtg ggg 400
 Glu Ser Tyr Cys Ser His Asn Ser Thr Val Ser Asp Cys Gln Val Gly
 70 75 80
 aac acg aca gac ttc tgt tcc gtt tcc acg gcc act cca gtg cca aca 448
 Asn Thr Thr Asp Phe Cys Ser Val Ser Thr Ala Thr Pro Val Pro Thr
 85 90 95 100
 gcc aat tct aca gct aaa ccc aca gtt cag ccc tcc cct tct aca act 496
 Ala Asn Ser Thr Ala Lys Pro Thr Val Gln Pro Ser Pro Ser Thr Thr
 105 110 115
 tcc aag aca gtt act aca tca ggt aca aca aat aac act gtg act cca 544
 Ser Lys Thr Val Thr Thr Ser Gly Thr Thr Asn Asn Thr Val Thr Pro
 120 125 130
 acc tca caa cct gtg cga aag tct acc ttt gat gca gcc agt ttc att 592
 Thr Ser Gln Pro Val Arg Lys Ser Thr Phe Asp Ala Ala Ser Phe Ile
 135 140 145
 gga gga att gtc ctg gtc ttn ggt gtg can gct gta att ttc ttt ctt 640
 Gly Gly Ile Val Leu Val Xaa Gly Val Xaa Ala Val Ile Phe Phe Leu
 150 155 160
 tat aaa tnc tgc aaa tst aaa gaa cga aat tac cac act ctg taaac 687
 Tyr Lys Xaa Cys Lys Xaa Lys Glu Arg Asn Tyr His Thr Leu
 165 170 175

<210> 3776
 <211> 449
 <212> DNA
 <213> Homo sapiens

<220>

<221> CDS
 <222> 32..412

<221> sig_peptide
 <222> 32..109
 <223> score 10.4
 seq LCLCVLVLACIGA/CQ

<400> 3776
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 Met Ser Leu Leu Arg Asn Arg
 -25 -20
 ctc cag gcc ctg cct gcc ctg tgc ctc tgc gtg ctg gtc ctg gcc tgc 100
 Leu Gln Ala Leu Pro Ala Leu Cys Leu Cys Val Leu Val Leu Ala Cys
 -15 -10 -5
 att ggg gca tgc cag cca gag gcc cag gaa gga acc cyg agc ccc cca 148
 Ile Gly Ala Cys Gln Pro Glu Ala Gln Glu Gly Thr Xaa Ser Pro Pro
 1 5 10
 cca aag cta aag atg agt cgc tgg agc ctg gtg agg ggc agg atg aag 196
 Pro Lys Leu Lys Met Ser Arg Trp Ser Leu Val Arg Gly Arg Met Lys
 15 20 25
 gag ctg ctg gag aca gtg gtg aac agg acc aga gnn ggg tgg caa tgg 244
 Glu Leu Leu Glu Thr Val Val Asn Arg Thr Arg Xaa Gly Trp Gln Trp
 30 35 40 45
 ttc tgg agc ccg agc acc ttc cgg ggc ttc atg cag acc tac tat gac 292
 Phe Trp Ser Pro Ser Thr Phe Arg Gly Phe Met Gln Thr Tyr Tyr Asp
 50 55 60
 gac cac ctg agg gac ctg ggt ccg cgc acc aag gcc tgg ttc ctc gaa 340
 Asp His Leu Arg Asp Leu Gly Pro Arg Thr Lys Ala Trp Phe Leu Glu
 65 70 75
 tcc aaa gac agc ctc ttg aag aag acc cac agc ctg tgc ccc agg ctt 388
 Ser Lys Asp Ser Leu Leu Lys Lys Thr His Ser Leu Cys Pro Arg Leu
 80 85 90
 gtc tgt ggg gac aan gac cag ggt taaaatgttc ataaaagcca ggtgtggttg 442
 Val Cys Gly Asp Xaa Asp Gln Gly
 95 100
 tggcggg 449

<210> 3777
 <211> 577
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 73..474

<221> sig_peptide
 <222> 73..123
 <223> score 9.3
 seq LALSLLILVLAFG/IP

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<400> 3777
acacagaccc ccaacttgca gctgcccacc tcaccctcag ctctggcctc ttactcaccc      60
tctaccacag ac atg gct cag tca ctg gct ctg agc ctc ctt atc ctg gtt      111
      Met Ala Gln Ser Leu Ala Leu Ser Leu Leu Ile Leu Val
      -15 -10 -5
ctg gcc ttt ggc atc ccc agg acc caa ggc agt gat gga ggg gct cag      159
Leu Ala Phe Gly Ile Pro Arg Thr Gln Gly Ser Asp Gly Gly Ala Gln
      1 5 10
gac tgt tgc ctc aag tac agc caa agg aag att ccc gcc aag gtt gtc      207
Asp Cys Cys Leu Lys Tyr Ser Gln Arg Lys Ile Pro Ala Lys Val Val
      15 20 25
cgc agc tac cgg aag cag gaa cca agc tta ggc tgc tcc atc cca gct      255
Arg Ser Tyr Arg Lys Gln Glu Pro Ser Leu Gly Cys Ser Ile Pro Ala
      30 35 40
atc ctg ttc ttg ccc cgc aag cgc tct cag gca gag cta tgt gca gac      303
Ile Leu Phe Leu Pro Arg Lys Arg Ser Gln Ala Glu Leu Cys Ala Asp
      45 50 55 60
cca aag gag ctc tgg gtg cag cag ctg atg cag cat ctg gac aag aca      351
Pro Lys Glu Leu Trp Val Gln Gln Leu Met Gln His Leu Asp Lys Thr
      65 70 75
cca tcc cca cag aaa cca gcc cag ggc tgc agg aag gac agg ggg gcc      399
Pro Ser Pro Gln Lys Pro Ala Gln Gly Cys Arg Lys Asp Arg Gly Ala
      80 85 90
tcc aag act ggc aag aaa gga aag ggc tcc aaa ggc tgc aag agg act      447
Ser Lys Thr Gly Lys Lys Gly Lys Gly Ser Lys Gly Cys Lys Arg Thr
      95 100 105
aag cgg tca cag acc cct aaa ggg cca tagcccagtg agcagcctgg      494
Lys Arg Ser Gln Thr Pro Lys Gly Pro
      110 115
agccctggag accccaccag cctcaccagc gcttgaagcc tgaaccaag atgcaagaag      554
gaggctatgc tcagggggccc tgg      577

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<210> 3778
<211> 506
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> 133..480

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<221> sig_peptide
<222> 133..213
<223> score 8.6
      seq IVLALGCVTGAPS/DP

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<400> 3778
aaaaaacaga gggagacggt tgagagcaca caagccgctt taggagcgag gttcggagcc      60
atcgctgctg cctgctgata cgcgcctaga gtttgaccag ccactctcca gctcggcttt      120
cgcggcgccc ag atg ctg tcc tgc cgc ctc cag tgc gcg ctg gct gcg ctg      171
      Met Leu Ser Cys Arg Leu Gln Cys Ala Leu Ala Ala Leu
      -25 -20 -15
tcc atc gtc ctg gcc ctg ggc tgt gtc acc ggc gct ccc tcg gac ccc      219

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	60	65	70	
cat cgc cag cca gag gag cag ctc ccc tgt ggg cct tgc caa atg gtt				344
His Arg Gln Pro Glu Glu Gln Leu Pro Cys Gly Pro Cys Gln Met Val				
	75	80	85	
tgg ctc aga tgt gct aca gca acc cct gcc ctm cat gcc cgc caa agt				392
Trp Leu Arg Cys Ala Thr Ala Thr Pro Ala Leu His Ala Arg Gln Ser				
	90	95	100	
tat cag tgt aga tgaatnggaa taccgacagt gagsa				429
Tyr Gln Cys Arg				
105				

<210> 3780
 <211> 444
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 5..430
 <221> sig_peptide
 <222> 5..133
 <223> score 5.1
 seq PTLGAFWLAVLLA/DM

<400> 3780	
gaga atg aga agt cat cct gga gca cag ctc ttc cca cgc tcc ggg ccc	49
Met Arg Ser His Pro Gly Ala Gln Leu Phe Pro Arg Ser Gly Pro	
	-40 -35 -30
aca cac cca gcc tca ctc cat caa agg agc ccc gct gcc tgc cca ccc	97
Thr His Pro Ala Ser Leu His Gln Arg Ser Pro Ala Ala Cys Pro Pro	
	-25 -20 -15
acc ctg ggt gct ttc tgg ctt gca gtg ctc ttg gca gac atg agg caa	145
Thr Leu Gly Ala Phe Trp Leu Ala Val Leu Leu Ala Asp Met Arg Gln	
	-10 -5 1
cga ttg ctc ccg tcc gtc acc agc ctt ctc ctn gtg gcc ctg ctg ttt	193
Arg Leu Leu Pro Ser Val Thr Ser Leu Leu Leu Val Ala Leu Leu Phe	
5 10 15 20	
cca gga tcg tct caa gcc aga cat gtg aac cac tca gcc act gag gct	241
Pro Gly Ser Ser Gln Ala Arg His Val Asn His Ser Ala Thr Glu Ala	
	25 30 35
ctc gga gaa ctc agg gaa aga gcc cct ggg caa ggc aca aac ggg ttt	289
Leu Gly Glu Leu Arg Glu Arg Ala Pro Gly Gln Gly Thr Asn Gly Phe	
	40 45 50
cag ctg cta cgc cac gca gtn caa atg gga cct ctt acc acc gcg cac	337
Gln Leu Leu Arg His Ala Val Gln Met Gly Pro Leu Thr Thr Ala His	
	55 60 65
ccc acc tta cca agg gga tgt tcc act ggg aat gag aaa tac cat ctg	385
Pro Thr Leu Pro Arg Gly Cys Ser Thr Gly Asn Glu Lys Tyr His Leu	
	70 75 80
ccg tat gca gca agg gat ctg cag act ttt ttt ctg cca ttc tgg	430
Pro Tyr Ala Ala Arg Asp Leu Gln Thr Phe Phe Leu Pro Phe Trp	
85 90 95	

tgagaaaaag cgtg

444

<210> 3781

<211> 637

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 6..446

<221> sig_peptide

<222> 6..125

<223> score 4.6

seq ITGVILLAVGVWG/KL

<400> 3781

gtagt atg gca tgc agg aga atg gag acc aaa cct gtg ata acc tgt ctc 50

Met Ala Ser Arg Arg Met Glu Thr Lys Pro Val Ile Thr Cys Leu

-40 -35 -30

aaa acc ctc ctc atc atc tac tcc ttc gtc ttc tgg atc act ggg gtg 98

Lys Thr Leu Leu Ile Ile Tyr Ser Phe Val Phe Trp Ile Thr Gly Val

-25 -20 -15 -10

atc ctg ctg gct gtt gga gtc tgg ggc aaa ctt act ctg ggc acc tat 146

Ile Leu Leu Ala Val Gly Val Trp Gly Lys Leu Thr Leu Gly Thr Tyr

-5 1 5

atc tcc ctt att gcc gag aac tcc aca aat gct ccc tat gtg ctc atc 194

Ile Ser Leu Ile Ala Glu Asn Ser Thr Asn Ala Pro Tyr Val Leu Ile

10 15 20

gga act ggc acc act att gtt gtc ttt ggc ctg ttt gga tgc ttt gct 242

Gly Thr Gly Thr Thr Ile Val Val Phe Gly Leu Phe Gly Cys Phe Ala

25 30 35

aca tgt cgt ggt agc cca tgg atg ctg aaa ctg tat gcc atg ttt ctg 290

Thr Cys Arg Gly Ser Pro Trp Met Leu Lys Leu Tyr Ala Met Phe Leu

40 45 50 55

tcc ctg gtg ttc ctg gct gag ctc gta gct ggc att tca ggg ttt gtg 338

Ser Leu Val Phe Leu Ala Glu Leu Val Ala Gly Ile Ser Gly Phe Val

60 65 70

ttt cgt cat gag atc aag gac acc ttc ctg agg act tac acg gac gct 386

Phe Arg His Glu Ile Lys Asp Thr Phe Leu Arg Thr Tyr Thr Asp Ala

75 80 85

atg cag act tac aat ggc aat gat gag agg agc cgg gca gtg gac cat 434

Met Gln Thr Tyr Asn Gly Asn Asp Glu Arg Ser Arg Ala Val Asp His

90 95 100

gtg cag cgc asc tgagctgctg tgggtgtgcag aactacacca actggagcac 486

Val Gln Arg Xaa

105

cagcccctac ttcttgagc atggcatccc cccagctgc tgcataaacg aaactgattg 546

taatccccag gatctacaca atctgactgt ggccgccacc aaagttaacc agaaggggtg 606

ttatgatctg gtaactagtt tcatggagac t 637

<210> 3782

<211> 436

<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 16..369

<221> sig_peptide
<222> 16..78
<223> score 9.3
seq GLLAALAVCGSWG/LN

<400> 3782
agtcagaggg atggg atg gag ggg ccg gtg ctg aca ctg ggg ctg ctg gct 51
Met Glu Gly Pro Val Leu Thr Leu Gly Leu Leu Ala
-20 -15 -10
gcc ctg gcg gtg tgt ggc agc tgg ggg ctg aac gag gag gag cgg ctg 99
Ala Leu Ala Val Cys Gly Ser Trp Gly Leu Asn Glu Glu Glu Arg Leu
-5 1 5
atc cgg cac ctg ttt caa gag aag ggc tac aac aag gag ctc cgg ccc 147
Ile Arg His Leu Phe Gln Glu Lys Gly Tyr Asn Lys Glu Leu Arg Pro
10 15 20
gtg gca cac aaa gag gag agt gtg gac gtt gcc ctg gcc ctc aca ctc 195
Val Ala His Lys Glu Glu Ser Val Asp Val Ala Leu Ala Leu Thr Leu
25 30 35
tcc aac ctc atc tcc ctg aaa gaa gtt gag gag acc ctc act acc aat 243
Ser Asn Leu Ile Ser Leu Lys Glu Val Glu Glu Thr Leu Thr Thr Asn
40 45 50 55
gtg tgg ata gag cac ggc tgg aca gac aac cgg ctg aag tgg ant gct 291
Val Trp Ile Glu His Gly Trp Thr Asp Asn Arg Leu Lys Trp Xaa Ala
60 65 70
gaa gaa ttt gga aac atc agt gtc ywg cgc ctc ccc ccg gac atg gtg 339
Glu Glu Phe Gly Asn Ile Ser Val Xaa Arg Leu Pro Pro Asp Met Val
75 80 85
tgg ctc aga gat tgt gct gga gaa caa caa tgacggctcc ttccagatct 389
Trp Leu Arg Asp Cys Ala Gly Glu Gln Gln
90 95
cctactcctg caacgtgctt gtctaccact acggcttcgt gtactgg 436

<210> 3783
<211> 547
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 133..498

<221> sig_peptide
<222> 133..213
<223> score 5.7
seq LVSLFCSCFLADP/LN

<400> 3783

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accactaatt gagggagtga ggaagagagc agctcgcttc taactggact gcacgttggt      60
gacagcgtcc caagctgggtg acagaccac tctgtaactt tcagctagat tcagccacca      120
gatcccagaa ac atg acc ctt gct gcc tac aaa gag aag atg aag gag ctc      171
          Met Thr Leu Ala Ala Tyr Lys Glu Lys Met Lys Glu Leu
                    -25              -20              -15
ccg ctg gtg tcc ttg ttc tgc tcc tgc ttc ctg gcc gat ccc ctg aat      219
Pro Leu Val Ser Leu Phe Cys Ser Cys Phe Leu Ala Asp Pro Leu Asn
                    -10              -5              1
aag tcg tcc tac aaa tat gaa gca gac acg gtg gac ctg aat tgg tgc      267
Lys Ser Ser Tyr Lys Tyr Glu Ala Asp Thr Val Asp Leu Asn Trp Cys
                    5              10              15
gtc att tcc gac atg gaa gtc atc gag ctg aac aaa tgc acc tcg ggc      315
Val Ile Ser Asp Met Glu Val Ile Glu Leu Asn Lys Cys Thr Ser Gly
                    20              25              30
caa tcc ttt gaa gtc atc ctg aag cca ccc tcc ttt gat ggg gtt ccc      363
Gln Ser Phe Glu Val Ile Leu Lys Pro Pro Ser Phe Asp Gly Val Pro
                    35              40              45              50
gag ttc aac gcc tcc ctg cca agg cgg cga gac cca tcc ctg gaa gag      411
Glu Phe Asn Ala Ser Leu Pro Arg Arg Arg Asp Pro Ser Leu Glu Glu
                    55              60              65
atc cag aag aaa cta gaa gcg gct gaa gga gcg aag gaa gta cca gga      459
Ile Gln Lys Lys Leu Glu Ala Ala Glu Gly Ala Lys Glu Val Pro Gly
                    70              75              80
agc gga stc ctg aaa cac cta gca gag aaa acg gga aca tgagagagag      508
Ser Gly Xaa Leu Lys His Leu Ala Glu Lys Thr Gly Thr
                    85              90              95
gtgatccaaa aggccattga ggaaaacaac aacttcac      547

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<210> 3784

<211> 443

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 96..437

<221> sig_peptide

<222> 96..239

<223> score 4.6

seq VFSGSFLLLLFSLT/QF

<400> 3784

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cactgcgagc ccagccgcag cagccgggca ccaacgcttg agtgcacgct cggcgccccc      60
gaggagagcc acggcgagcc cccaaagccc gcacg atg cag gcc act gcc gat      113
          Met Gln Ala Thr Ala Asp
                    -45
tcc acc aag atg gac tgt gtg tgg agc aac tgg aaa agt cag gct att      161
Ser Thr Lys Met Asp Cys Val Trp Ser Asn Trp Lys Ser Gln Ala Ile
                    -40              -35              -30
gac ctg ttg tat tgg cgg gac atc aag cag acg ggc atc gtg ttt ggg      209

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Asp	Leu	Leu	Tyr	Trp	Arg	Asp	Ile	Lys	Gln	Thr	Gly	Ile	Val	Phe	Gly		
-25						-20					-15						
agt	ttc	ctg	ctg	ctg	ctc	ttc	tcc	ctg	acc	cag	ttc	agc	gtg	gtg	agc	257	
Ser	Phe	Leu	Leu	Leu	Leu	Phe	Ser	Leu	Thr	Gln	Phe	Ser	Val	Val	Ser		
-10					-5				1		5						
gtc	gtg	gcc	tac	ctg	gcc	ctg	gcc	gca	ctc	tca	gcc	acc	atc	agt	ttn	305	
Val	Val	Ala	Tyr	Leu	Ala	Leu	Ala	Ala	Leu	Ser	Ala	Thr	Ile	Ser	Xaa		
		10					15				20						
cgc	atc	tac	aag	tct	gtt	taa	caa	gca	gts	cag	ata	acc	gac	gaa	ggc	353	
Arg	Ile	Tyr	Lys	Ser	Val	Leu	Gln	Ala	Val	Gln	Ile	Thr	Asp	Glu	Gly		
	25					30					35						
cac	cgt	nga	agg	cct	act	tgg	agc	ttg	aga	tca	ccc	ttt	ctc	agg	agc	401	
His	Arg	Xaa	Arg	Pro	Thr	Trp	Ser	Leu	Arg	Ser	Pro	Phe	Leu	Arg	Ser		
	40				45					50							
aga	ttc	aga	agt	aca	cgg	act	gcc	tgc	agt	tct	acg	tgaaca				443	
Arg	Phe	Arg	Ser	Thr	Arg	Thr	Ala	Cys	Ser	Ser	Thr						
55					60					65							

<210> 3785
 <211> 528
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 55..510

<221> sig_peptide
 <222> 55..153
 <223> score 9.5
 seq LLLGLVMPLAIIA/QV

<400> 3785																	
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						Met											
ggg	acc	atg	aag	acc	caa	agg	gat	ggc	cac	tcc	ctg	ggg	cgg	tgg	tca	105	
Gly	Thr	Met	Lys	Thr	Gln	Arg	Asp	Gly	His	Ser	Leu	Gly	Arg	Trp	Ser		
	-30					-25					-20						
ctg	gtg	ctc	ctg	ctg	ctg	ggc	ctg	gtg	atg	cct	ctg	gcc	atc	att	gcc	153	
Leu	Val	Leu	Leu	Leu	Leu	Gly	Leu	Val	Met	Pro	Leu	Ala	Ile	Ile	Ala		
	-15					-10					-5						
cag	gtc	ctc	agc	tac	aag	gaa	gct	gtg	ctt	cgt	gct	ata	gat	ggc	atc	201	
Gln	Val	Leu	Ser	Tyr	Lys	Glu	Ala	Val	Leu	Arg	Ala	Ile	Asp	Gly	Ile		
1			5					10			15						
aac	cag	cgg	tcc	tgc	gat	gct	aac	ctc	tac	cgc	ctc	ctg	gac	ctg	gac	249	
Asn	Gln	Arg	Ser	Ser	Asp	Ala	Asn	Leu	Tyr	Arg	Leu	Leu	Asp	Leu	Asp		
	20					25					30						
ccc	agg	ccc	acg	atg	gat	ggg	gac	cca	gac	acg	cca	aag	cct	gtg	agc	297	
Pro	Arg	Pro	Thr	Met	Asp	Gly	Asp	Pro	Asp	Thr	Pro	Lys	Pro	Val	Ser		
	35					40					45						
ttc	aca	gtg	aag	gag	aca	gtg	tgc	ccc	agg	acg	aca	cag	cag	tca	cca	345	
Phe	Thr	Val	Lys	Glu	Thr	Val	Cys	Pro	Arg	Thr	Thr	Gln	Gln	Ser	Pro		
	50					55					60						

gag gat tgt gac ttc aag aag gac ggg ctg gtg aag cgg tgt atg ggg	393
Glu Asp Cys Asp Phe Lys Lys Asp Gly Leu Val Lys Arg Cys Met Gly	
65 70 75 80	
aca gtg acc ctc aac cag gcc agg ggc tcc ttt gac atc agt tgt gat	441
Thr Val Thr Leu Asn Gln Ala Arg Gly Ser Phe Asp Ile Ser Cys Asp	
85 90 95	
aag gat aac aag aga ttt gcc ctg ctg ggt gat ttc ttc cgg aaa tct	489
Lys Asp Asn Lys Arg Phe Ala Leu Leu Gly Asp Phe Phe Arg Lys Ser	
100 105 110	
aaa gag aag atg gca aag agt taaaagaatt gtccagag	528
Lys Glu Lys Met Ala Lys Ser	
115	

<210> 3786

<211> 484

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 30..431

<221> sig_peptide

<222> 30..170

<223> score 4.9

seq LSDGLSLAAPGWG/VP

<400> 3786

agaattagtt ctttctgccc acactagac atg gcg ctt gcc agc gtg ttg gag	53
Met Ala Leu Ala Ser Val Leu Glu	
-45 -40	
aga ccg cta ccg gtg aac cag cgc ggg ttt ttc gga ctt ggg ggt cgt	101
Arg Pro Leu Pro Val Asn Gln Arg Gly Phe Gly Leu Gly Gly Arg	
-35 -30 -25	
gca gat ctg ctg gat cta ggt cca ggg agt ctc agt gat ggt ctg agc	149
Ala Asp Leu Leu Asp Leu Gly Pro Gly Ser Leu Ser Asp Gly Leu Ser	
-20 -15 -10	
ctg gcc gcg cca ggc tgg ggt gtc cca gaa gag cca gga atc gaa atg	197
Leu Ala Ala Pro Gly Trp Gly Val Pro Glu Glu Pro Gly Ile Glu Met	
-5 1 5	
ctt cat gga aca acc acc ctg gcc ttc aag ttc cgc cat gga gtc ata	245
Leu His Gly Thr Thr Thr Leu Ala Phe Lys Phe Arg His Gly Val Ile	
10 15 20 25	
gtt gca gct gac tcc agg gct aca gcg ggt gct tac att gcc tcc cag	293
Val Ala Ala Asp Ser Arg Ala Thr Ala Gly Ala Tyr Ile Ala Ser Gln	
30 35 40	
acg gtg aag aag gtg ata gag atc aac cca tac ctg cta ggc acc atg	341
Thr Val Lys Lys Val Ile Glu Ile Asn Pro Tyr Leu Leu Gly Thr Met	
45 50 55	
gct ggg ggc gca cgg att gca gct tct ggg aac ggc tgt tgg ctc ggc	389
Ala Gly Gly Ala Arg Ile Ala Ala Ser Gly Asn Gly Cys Trp Leu Gly	
60 65 70	
aat gtc gaa tct atg agc ttc gaa ata agg aac gca tct ctg	431

Asn Val Glu Ser Met Ser Phe Glu Ile Arg Asn Ala Ser Leu

75

80

85

tagcagctgc ctccaaactg cttgccaaca tgggtgtatca gtacaaaggc atg

484

<210> 3787

<211> 515

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 57..428

<221> sig_peptide

<222> 57..146

<223> score 9.9

seq LLFGFTLVSGTGA/EK

<400> 3787

aaaatccccg cacctgagca tcggctcaca cctgcacccc gcccgggcat agcacc atg

59

Met

-30

cct gct tgt cgc cta ggc ccg cta gcc gcc gcc ctc ctc ctc agc ctg

107

Pro Ala Cys Arg Leu Gly Pro Leu Ala Ala Ala Leu Leu Leu Ser Leu

-25

-20

-15

ctg ctg ttc ggc ttc acc cta gtc tca ggc aca gga gca gag aag act

155

Leu Leu Phe Gly Phe Thr Leu Val Ser Gly Thr Gly Ala Glu Lys Thr

-10

-5

1

ggc gtg tgc ccc gag ctc cag gct gac cag aac tgc acg caa gag tgc

203

Gly Val Cys Pro Glu Leu Gln Ala Asp Gln Asn Cys Thr Gln Glu Cys

5

10

15

gtc tcg gac agc gaa tgc gcc gac aac ctc aag tgc tgc agc gcg ggc

251

Val Ser Asp Ser Glu Cys Ala Asp Asn Leu Lys Cys Cys Ser Ala Gly

20

25

30

35

tgt gcc acc ttc tgc tct ctg ccc aat gat aag gag ggt tcc tgc ccc

299

Cys Ala Thr Phe Cys Ser Leu Pro Asn Asp Lys Glu Gly Ser Cys Pro

40

45

50

cag gtg aac att aac ttt ccc cag ctc ggc ctc tgt cgg gac cag tgc

347

Gln Val Asn Ile Asn Phe Pro Gln Leu Gly Leu Cys Arg Asp Gln Cys

55

60

65

cag gtg gac agc cag tgt cct ggc cag atg aaa tgc tgc cgc aat ggc

395

Gln Val Asp Ser Gln Cys Pro Gly Gln Met Lys Cys Cys Arg Asn Gly

70

75

80

tgt ggg aag gtg tcc tgt gtc act ccc aat ttc tgagctccag ccaccaccag

448

Cys Gly Lys Val Ser Cys Val Thr Pro Asn Phe

85

90

gctgagcagt gaggagagaa agtttctgcc tggccctgca tctgggtcca gccacactgc

508

cctcccc

515

<210> 3788

<211> 912

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 22..450

<221> sig_peptide

<222> 22..132

<223> score 4.2

seq LADVCLDTPLCNG/HT

<400> 3788

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attcaacagk atgcacaaaa c atg ggc ctg ccc cag aac cgt atc att ttt      51
                        Met Gly Leu Pro Gln Asn Arg Ile Ile Phe
                        -35                                -30
tca cct gtt gct cct aaa gag gaa cac gtc agg aga ggc cag ctg gct      99
Ser Pro Val Ala Pro Lys Glu Glu His Val Arg Arg Gly Gln Leu Ala
-25                                -20                                -15
gat gtc tgc ttg gac act cca ctc tgt aat ggg cac acc aca ggg atg      147
Asp Val Cys Leu Asp Thr Pro Leu Cys Asn Gly His Thr Thr Gly Met
-10                                -5                                1                                5
gat gtc ctc tgg gca ggg acc ccc atg gtg act atg cca gga gag act      195
Asp Val Leu Trp Ala Gly Thr Pro Met Val Thr Met Pro Gly Glu Thr
                        10                                15                                20
ctt gct tct cga gtt gca gca tcc cag ctc act tgc tta ggt tgt ctt      243
Leu Ala Ser Arg Val Ala Ala Ser Gln Leu Thr Cys Leu Gly Cys Leu
                        25                                30                                35
gag ctt att gct aaa aac aga caa gaa tat gaa gac ata gct gtg aag      291
Glu Leu Ile Ala Lys Asn Arg Gln Glu Tyr Glu Asp Ile Ala Val Lys
                        40                                45                                50
ctg gga act gat cta gaa tac ctg aag aaa gtt cgt ggc aaa gtc tgg      339
Leu Gly Thr Asp Leu Glu Tyr Leu Lys Lys Val Arg Gly Lys Val Trp
                        55                                60                                65
aag caa aga ata tct agc cct ctg ttc aac acc aaa caa tac aca atg      387
Lys Gln Arg Ile Ser Ser Pro Leu Phe Asn Thr Lys Gln Tyr Thr Met
                        70                                75                                80                                85
gaa cta gag cgg ctc tat cta cag atg tgg gag cat tat gca gct ggc      435
Glu Leu Glu Arg Leu Tyr Leu Gln Met Trp Glu His Tyr Ala Ala Gly
                        90                                95                                100
anc aac ctg acc aca tgattaagcc tgttgaagtc actgagtcag cataaataaa      490
Xaa Asn Leu Thr Thr
                        105
gactgcacag gagaattacc cctataacctg agcctcaacc ttctggggga aagggaacta      550
gataacatac ttcttacttg tctgtacagt accttgttgc agatgggtga tatataatgg      610
taatagaata gcacagccag acttgcttcc tgcattgtag ggagagaaac aaaagatggg      670
aaactgcttt tccacaagga atctccgtag aaattttgcg gcgaccagat ggtgcatagg      730
tctggaaggt ctgatctccc ttggtcttcc atgggatggg tagtgtggag gggagatata      790
gattgtccgg ccgctttgtg attccatgga ttgattcagt cttctggatt ttttyttctt      850
tatatttttg gtactggagc ttttaaaaat gtttggtttc aggtattttt attcatgtga      910
ag                                                                912
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<210> 3789

<211> 458

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 100..444

<221> sig_peptide

<222> 100..216

<223> score 4.3

seq IHISWLSLSRVNC/SQ

<400> 3789

agtgagctaa gctgcggggc gcgggctcgg ccggggcacc ggtgagtcgc cggcgctgca 60
gagggaggcg gcactggtct cgacgtgggg cgccagcg atg aag ccg ccc agt 114
Met Lys Pro Pro Ser
-35

tca ata caa aca agt gag ttt gac tca tca gat gaa gag cct att gaa 162
Ser Ile Gln Thr Ser Glu Phe Asp Ser Ser Asp Glu Glu Pro Ile Glu
-30 -25 -20

gat gaa cag act cca att cat ata tca tgg cta tct ttg tca cga gtg 210
Asp Glu Gln Thr Pro Ile His Ile Ser Trp Leu Ser Leu Ser Arg Val
-15 -10 -5

aat tgt tct cag ttt ctc ggt tta tgt gct ctt cca ggt tgt aaa ttt 258
Asn Cys Ser Gln Phe Leu Gly Leu Cys Ala Leu Pro Gly Cys Lys Phe
1 5 10

aaa gat gtt aga aga aat gtc caa aaa gat aca gaa gaa cta aag agc 306
Lys Asp Val Arg Arg Asn Val Gln Lys Asp Thr Glu Glu Leu Lys Ser
15 20 25 30

tgt ggt ata caa gac ata ttt gtt ttc tgc acc aga ggg gaa ctg tca 354
Cys Gly Ile Gln Asp Ile Phe Val Phe Cys Thr Arg Gly Glu Leu Ser
35 40 45

aaa tat aga gtc cca aac ctt ctg gat ctc tac cag caa tgt gga att 402
Lys Tyr Arg Val Pro Asn Leu Leu Asp Leu Tyr Gln Gln Cys Gly Ile
50 55 60

atc acc cat cat cat cca atc gca gat gga ggg act ctg aca 444
Ile Thr His His His Pro Ile Ala Asp Gly Gly Thr Leu Thr
65 70 75

tagccagctg ctgt 458

<210> 3790

<211> 438

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 20..376

<221> sig_peptide

<222> 20..67

<223> score 6.5

seq VLXLFVCLFETES/XS

<400> 3790
taccagtgga atcaatcat atg ata ttt gtc ctt ywt ttg ttt gtt tgt ttg 52
Met Ile Phe Val Leu Xaa Leu Phe Val Cys Leu
-15 -10
ttt gag acg gag tct sgc tct gtt gcc cgg gct gga gtg cag tgg cac 100
Phe Glu Thr Glu Ser Xaa Ser Val Ala Arg Ala Gly Val Gln Trp His
-5 1 5 10
ggg ctt gtc tca ctg cga cct ctg cct cct ggg ttc aag cga ttc tca 148
Gly Leu Val Ser Leu Arg Pro Leu Pro Pro Gly Phe Lys Arg Phe Ser
15 20 25
tgc ctc agc ctt ctg agt agc tgg gat tac agg cgt gtg cca cca cgc 196
Cys Leu Ser Leu Leu Ser Ser Trp Asp Tyr Arg Arg Val Pro Pro Arg
30 35 40
tta gct aat ttt tgt att ttt agt aga gat ggc gtt atg cca ttt gac 244
Leu Ala Asn Phe Cys Ile Phe Ser Arg Asp Gly Val Met Pro Phe Asp
45 50 55
cag gct ggt ctt gag ctc ctg acc tca agc gat cct ccc gcc ttg gcc 292
Gln Ala Gly Leu Glu Leu Leu Thr Ser Ser Asp Pro Pro Ala Leu Ala
60 65 70 75
ttc cag ggt gct ggg atc gca ggt gtg agc cat gaa gcc tgg cct ggt 340
Phe Gln Gly Ala Gly Ile Ala Gly Val Ser His Glu Ala Trp Pro Gly
80 85 90
att tgt ctt ttt gtg att ggc tta ttt ctg tta gca taacgtcccc 386
Ile Cys Leu Phe Val Ile Gly Leu Phe Leu Leu Ala
95 100
aaggttcact catgtggcat gtatcggaat ttcttttctt tttgaggctg ad 438

<210> 3791
<211> 417
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 47..364

<221> sig_peptide
<222> 47..193
<223> score 5.9
seq FVFIFVXLRESLA/LL

<400> 3791
ttgtgacttt gattgcctac tggctaattgt tgccaactat tttttc atg att tta 55
Met Ile Leu
ttg gac att cac aca tat ttg ctg aag aaa tat cta ttt ata agc ttt 103
Leu Asp Ile His Thr Tyr Leu Leu Lys Lys Tyr Leu Phe Ile Ser Phe
-45 -40 -35
acc tat tat tta att ggg tta aat ttc ttt ttc tta ttc agt tgt tgg 151
Thr Tyr Tyr Leu Ile Gly Leu Asn Phe Phe Phe Leu Phe Ser Cys Trp
-30 -25 -20 -15
ttt ttt gtt ttt att ttt gtt tks ttg agg gag agt ctc gct ctg ctg 199
Phe Phe Val Phe Ile Phe Val Xaa Leu Arg Glu Ser Leu Ala Leu Leu

	-10		-5		1	
ccc agg ctg gag tgc agt ggc gtg atc tct gct cac tgc aag ctc tgc						247
Pro Arg Leu Glu Cys Ser Gly Val Ile Ser Ala His Cys Lys Leu Cys						
	5		10		15	
ctc ctg ggt tca cac cat tct cct gcc tca gcc tcc caa gta gct ggg						295
Leu Leu Gly Ser His His Ser Pro Ala Ser Ala Ser Gln Val Ala Gly						
	20		25		30	
act aca ggc gcc hgc cac tac gcg tgg cta att ttt tgt att ttt agt						343
Thr Thr Gly Ala Xaa His Tyr Ala Trp Leu Ile Phe Cys Ile Phe Ser						
	35		40		45	50
aga gat ggg gtt tca ctg tgt tagccaggat ggtctcgaac tcctgacctc						394
Arg Asp Gly Val Ser Leu Cys						
	55					
gtgatctgcc cacctcggcc tga						417

<210> 3792

<211> 447

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 51..443

<221> sig_peptide

<222> 51..161

<223> score 10.1

seq LLGLCVCLSGCST/ET

<400> 3792

agaacaatgc tgcttggtc cctgaattca gcacccttcc tagggaatgt atg ggt						56
					Met Gly	
gga tct ttt gcc ttg cag gat tct ttt tca tct ttg cag gga ctt ctg						104
Gly Ser Phe Ala Leu Gln Asp Ser Phe Ser Ser Leu Gln Gly Leu Leu						
	-35		-30		-25	-20
ggg ccg gag tat gta aaa ctc ctg ggt ctc tgt gtg tgc ctg agt ggc						152
Gly Pro Glu Tyr Val Lys Leu Leu Gly Leu Cys Val Cys Leu Ser Gly						
	-15		-10		-5	
tgc tct act gag act ctg cat aca cag ctc tgt ata tcg gac cca wgg						200
Cys Ser Thr Glu Thr Leu His Thr Gln Leu Cys Ile Ser Asp Pro Xaa						
	1		5		10	
ccc tgg tgg cat ggg ctc acg agg aga tcc cct gat ctg tgg gtt gca						248
Pro Trp Trp His Gly Leu Thr Arg Arg Ser Pro Asp Leu Trp Val Ala						
	15		20		25	
aag atc tgt ggg aga agt gtg gtt tcc tgg atg ggg tca cac aat cac						296
Lys Ile Cys Gly Arg Ser Val Val Ser Trp Met Gly Ser His Asn His						
	30		35		40	45
tca ctg ctt ccc ttg gct gga ggt ggg gct ttt ttt ttg gct cca tgc						344
Ser Leu Leu Pro Leu Ala Gly Gly Gly Ala Phe Phe Leu Ala Pro Cys						
	50		55		60	
tgc tcc tgg gcg ggc gat tgc cct acc cca ttt ttc ttc att ctc tgt						392
Cys Ser Trp Ala Gly Asp Cys Pro Thr Pro Phe Phe Phe Ile Leu Cys						
	65		70		75	

ggg tca agd bgt tca ctt ggt cag tcc att gtg rga mct gga tat ttc 440
 Gly Ser Xaa Xaa Ser Leu Gly Gln Ser Ile Val Xaa Xaa Gly Tyr Phe
 80 85 90

agt tgaa 447
 Ser

<210> 3793
 <211> 381
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 12..347

<221> sig_peptide
 <222> 12..158
 <223> score 7.7
 seq LCLLGSSDSPASA/SQ

<400> 3793
 tggactgttt t atg cat gtt gtt gtt gtt gtt gtt gtt gtt gtt gtt gtt gtt 50
 Met His Val Val Val Val Val Val Val Val Val Val Val Val Val Val
 -45 -40

gtt ttg aga cag agt ctt gct ctg ttg ccc agg ctg gag tgc agt ggc 98
 Val Leu Arg Gln Ser Leu Ala Leu Leu Pro Arg Leu Glu Cys Ser Gly
 -35 -30 -25

aca atc ttg gct cac tgc agc ctc tgc ctc ctg ggt tca agt gat tct 146
 Thr Ile Leu Ala His Cys Ser Leu Cys Leu Leu Gly Ser Ser Asp Ser
 -20 -15 -10 -5

cct gcc tca gcc tcc caa gta gct aga act aca ggc atg tgc cac cat 194
 Pro Ala Ser Ala Ser Gln Val Ala Arg Thr Thr Gly Met Cys His His
 1 5 10

acc cag cta att ttt gta ttt tta ata gag aca gga ttt ctc cat att 242
 Thr Gln Leu Ile Phe Val Phe Leu Ile Glu Thr Gly Phe Leu His Ile
 15 20 25

ggc cag gct gct ctt gaa ctc ctg acc tca ggt gat cca cct gcc tca 290
 Gly Gln Ala Ala Leu Glu Leu Leu Thr Ser Gly Asp Pro Pro Ala Ser
 30 35 40

gcc tcc caa agt gct ggg att aca ggc gtg asc acc aca cct ggc cgc 338
 Ala Ser Gln Ser Ala Gly Ile Thr Gly Val Xaa Thr Thr Pro Gly Arg
 45 50 55 60

ctt tca aat tagtaaccag tgcttcctat ctktttacrt atac 381
 Leu Ser Asn

<210> 3794
 <211> 352
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 28..330

<221> sig_peptide
 <222> 28..96
 <223> score 4.6
 seq LFFYFILWRRSLA/LS

<400> 3794
 tgttctcacd nrgtctttcc tttgtgc atg grs atg tct gtg tcc aaa ttt cct 54
 Met Xaa Met Ser Val Ser Lys Phe Pro
 -20 -15
 ttt ctt ttt ttt tat ttt att tta tgg aga cgg agt ctc gct ctg tct 102
 Phe Leu Phe Phe Tyr Phe Ile Leu Trp Arg Arg Ser Leu Ala Leu Ser
 -10 -5 1
 ccc agg ctg gag tgc agt ggc ccg atc ttg gct cac tgc aac ctc cgc 150
 Pro Arg Leu Glu Cys Ser Gly Pro Ile Leu Ala His Cys Asn Leu Arg
 5 10 15
 ctc ctg ggt tca agc aat tct cct acc tta gcc tcc cga gta gct ggg 198
 Leu Leu Gly Ser Ser Asn Ser Pro Thr Leu Ala Ser Arg Val Ala Gly
 20 25 30
 act aca ggt gca cgc tgc cac gcc tgg cta att ttt tgt att ttt agt 246
 Thr Thr Gly Ala Arg Cys His Ala Trp Leu Ile Phe Cys Ile Phe Ser
 35 40 45 50
 aga gac ggg ttt tca cca tgt tgc cca ggc tgg tct gga act cct gag 294
 Arg Asp Gly Phe Ser Pro Cys Cys Pro Gly Trp Ser Gly Thr Pro Glu
 55 60 65
 ctc agg caa tcc acc cay ctc ggc ctc cca agg tac taggattaca 340
 Leu Arg Gln Ser Thr His Leu Gly Leu Pro Arg Tyr
 70 75
 agcatgascc ac 352

<210> 3795
 <211> 421
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 8..415

<221> sig_peptide
 <222> 8..121
 <223> score 7
 seq LVMVWLGLLPLFS/GP

<400> 3795
 cctccta atg gca aat gca ata att aag aag cct tgt gca atg ccg gca 49
 Met Ala Asn Ala Ile Ile Lys Lys Pro Cys Ala Met Pro Ala
 -35 -30 -25
 cag cct cac aca ggg aat ctc ctg tgg cca cct ctt gtc atg gtg tgg 97
 Gln Pro His Thr Gly Asn Leu Leu Trp Pro Pro Leu Val Met Val Trp
 -20 -15 -10
 ctc ggg ctg ttg cct ctt ttc tct ggg ccc cac ttg caa gcc gtt cag 145

tca gca gag ttc ttc gtc act gtt gct gtc ttc gcc ttc ctc tac tct	413
Ser Ala Glu Phe Phe Val Thr Val Ala Val Phe Ala Phe Leu Tyr Ser	
65 70 75	
ttg gct gcc act gtc gtt tac att ttc ttc cag aac aaa tac cgg gaa	461
Leu Ala Ala Thr Val Val Tyr Ile Phe Phe Gln Asn Lys Tyr Arg Glu	
80 85 90	
aac acc ggg gcc cac tca ttg act tca ttg tca ctg tagtcttt	505
Asn Thr Gly Ala His Ser Leu Thr Ser Leu Ser Leu	
95 100 105	

<210> 3797
 <211> 389
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 18..380

<221> sig_peptide
 <222> 18..65
 <223> score 4.1
 seq VFFLTEAGSVAQA/GV

<400> 3797	
cactgttttt tctacta atg ttc tgg gtt ttt ttt ttg acg gag gct ggc	50
Met Phe Trp Val Phe Phe Leu Thr Glu Ala Gly	
-15 -10	
tct gta gcc cag gct gga gtg mag tgg tgt gat ctc ggc tca ctg caa	98
Ser Val Ala Gln Ala Gly Val Xaa Trp Cys Asp Leu Gly Ser Leu Gln	
-5 1 5 10	
cct ccg cct ccc agg atc aag caa ttc ccc tgc ctc agc cta cct agt	146
Pro Pro Pro Pro Arg Ile Lys Gln Phe Pro Cys Leu Ser Leu Pro Ser	
15 20 25	
agc tgg gac tac agg tgc aca cca cca cga cca gct aat ttt tgt att	194
Ser Trp Asp Tyr Arg Cys Thr Pro Arg Pro Ala Asn Phe Cys Ile	
30 35 40	
ttt tta gta gag acg ggg ttt ctc cgt gtt ggc cgg gct gat ctt gaa	242
Phe Leu Val Glu Thr Gly Phe Leu Arg Val Gly Arg Ala Asp Leu Glu	
45 50 55	
ctc cag acc tca agt gat gca ccc acc tgg gcc tct caa agt act ggg	290
Leu Gln Thr Ser Ser Asp Ala Pro Thr Trp Ala Ser Gln Ser Thr Gly	
60 65 70 75	
att gcg ggt gtg aac cac cas gcc cgg ccc ttt gct aat gtc ctt tta	338
Ile Ala Gly Val Asn His Xaa Ala Arg Pro Phe Ala Asn Val Leu Leu	
80 85 90	
cta tcc cgc gat cca rca tta tat tka ttc atc ctg ttt cca tagtkgcca	389
Leu Ser Arg Asp Pro Xaa Leu Tyr Xaa Phe Ile Leu Phe Pro	
95 100 105	

<210> 3798
 <211> 437
 <212> DNA

004220"6666666666

<213> Homo sapiens

<220>

<221> CDS

<222> 58..423

<221> sig_peptide

<222> 58..120

<223> score 5.8

seq ACVRVCLVWTSFC/QP

<400> 3798

ctgcaccgac taggctgagg tgctgggtact tgccccaacc cctacttttg tatttat 57
atg tgt gtg tgt gtg tgc gtg cgt gcg tgc gtg cgt gta tgt ttg gtc 105
Met Cys Val Cys Val Cys Val Arg Ala Cys Val Arg Val Cys Leu Val
-20 -15 -10
tgg acc agc ttc tgc cag ccc ctg gcc ttt act ttc ttc ctt gcc tat 153
Trp Thr Ser Phe Cys Gln Pro Leu Ala Phe Thr Phe Phe Leu Ala Tyr
-5 1 5 10
gca ggg caa aca aaa tgt gaa att ctg ccc tca gct gag ctg agt aag 201
Ala Gly Gln Thr Lys Cys Glu Ile Leu Pro Ser Ala Glu Leu Ser Lys
15 20 25
ggc tcc tgg ggg ttg gct gga gat ggg tgt ggc atc tgt cca ggc ctg 249
Gly Ser Trp Gly Leu Ala Gly Asp Gly Cys Gly Ile Cys Pro Gly Leu
30 35 40
gaa ccg tct caa gac agt gct ggc aaa gct gca gta ttg aga tgc tnn 297
Glu Pro Ser Gln Asp Ser Ala Gly Lys Ala Ala Val Leu Arg Cys Xaa
45 50 55
gga gct gat gcc acc tct ttg tct tcc cct aaa gga gaa cat ggg gat 345
Gly Ala Asp Ala Thr Ser Leu Ser Ser Pro Lys Gly Glu His Gly Asp
60 65 70 75
aac atg ggt gtg tgc cca caa cac tct agg tgc aga gcc cct gtg gca 393
Asn Met Gly Val Cys Pro Gln His Ser Arg Cys Arg Ala Pro Val Ala
80 85 90
aag tat tac agg gtg tgg gtg ggg att acc tgaatcgggg tctc 437
Lys Tyr Tyr Arg Val Trp Val Gly Ile Thr
95 100

<210> 3799

<211> 444

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 82..429

<221> sig_peptide

<222> 82..138

<223> score 5.8

seq HLMSLVTSTSASA/SA

<400> 3799

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atatttctaag ctgcgcttca cctgctacta atcttgctgt tactttctgct atcccatctt      60
taaattttta tcacaatttg a atg att ggc aac tat gat cat ctt atg tct      111
                               Met Ile Gly Asn Tyr Asp His Leu Met Ser
                               -15                               -10

tta gta aca tct aca tca gca tca gca tct gcg tca cca ttt caa tct      159
Leu Val Thr Ser Thr Ser Ala Ser Ala Ser Ala Ser Pro Phe Gln Ser
                               -5                               1                               5

gca tgg tat agt gaa tct gag ata act cag gga gca cgc tca aga tcg      207
Ala Trp Tyr Ser Glu Ser Glu Ile Thr Gln Gly Ala Arg Ser Arg Ser
                               10                               15                               20

cag aac cag caa cgg gat cat gat tca aaa aga cct aaa ctt tcc tgt      255
Gln Asn Gln Gln Arg Asp His Asp Ser Lys Arg Pro Lys Leu Ser Cys
                               25                               30                               35

aca aac tgt act acc tca gct ggg aga aat gtt gga aat ggt tta aac      303
Thr Asn Cys Thr Thr Ser Ala Gly Arg Asn Val Gly Asn Gly Leu Asn
                               40                               45                               50                               55

aca tta tca gat tca tct tgv tgg cat agt caa gtt cct aga tct tca      351
Thr Leu Ser Asp Ser Ser Xaa Trp His Ser Gln Val Pro Arg Ser Ser
                               60                               65                               70

tca atg gta ctt gga tca ttt tkg gac agw ctt aat gag aga gag gag      399
Ser Met Val Leu Gly Ser Phe Xaa Asp Xaa Leu Asn Glu Arg Glu Glu
                               75                               80                               85

aga ttt gga gag aag aac aga ttc ctc tat tagtaatctt atgga      444
Arg Phe Gly Glu Lys Asn Arg Phe Leu Tyr
                               90                               95

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<210> 3800

<211> 436

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 30..374

<221> sig_peptide

<222> 30..74

<223> score 8.6

seq PLLIICLLPAIEG/KN

<400> 3800

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actggggcac agtaggagga acccagaag atg ctg cct ctc ctg atc atc tgt      53
                               Met Leu Pro Leu Leu Ile Ile Cys
                               -15                               -10

ctc ctg cct gcc att gaa ggg aag aac tgc ctc cgc tgc tgg cca gaa      101
Leu Leu Pro Ala Ile Glu Gly Lys Asn Cys Leu Arg Cys Trp Pro Glu
                               -5                               1                               5

ctg tct gcc ttg ata gac tat gac ctg cag atc ctc tgg gtg acc cca      149
Leu Ser Ala Leu Ile Asp Tyr Asp Leu Gln Ile Leu Trp Val Thr Pro
                               10                               15                               20                               25

ggg cca ccc aca gaa ctt tct caa agt att cac tcc ttg ttc cta gag      197
Gly Pro Pro Thr Glu Leu Ser Gln Ser Ile His Ser Leu Phe Leu Glu

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	30		35		40	
gat aat aat ttt ctc aaa ccc tgg tac ctt gat cgt gac cat ttg gaa						245
Asp Asn Asn Phe Leu Lys Pro Trp Tyr Leu Asp Arg Asp His Leu Glu						
	45		50		55	
gaa gaa aca gcc aaa ttc ttc act caa gta cac caa gcc att aaa acg						293
Glu Glu Thr Ala Lys Phe Phe Thr Gln Val His Gln Ala Ile Lys Thr						
	60		65		70	
tta cga gat gat aaa aca gta ctt ctg gaa gag atc tac acg cac aag						341
Leu Arg Asp Asp Lys Thr Val Leu Leu Glu Glu Ile Tyr Thr His Lys						
	75		80		85	
aat ctc ttt act gag agg ctg aat aag ata atc tgatgggctg aaggagaarg						394
Asn Leu Phe Thr Glu Arg Leu Asn Lys Ile Ile						
	90		95		100	
acatacagtc cacactgaag gtcaccagct gtgctgactg ca						436

<210> 3801

<211> 424

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 54..377

<221> sig_peptide

<222> 54..104

<223> score 5.7

seq VVCCSCSWFFLFC/FV

<400> 3801

ttcttacagg agtaaggtag tgtctcactg tagttttaat ttgcatttcc ctg atg		56
	Met	
att agt gat gtt gta tgt tgt agt tgc tcc tgg ttt ttt ttg ttt tgt		104
Ile Ser Asp Val Val Cys Cys Ser Cys Ser Trp Phe Phe Leu Phe Cys		
-15	-10	-5
ttt gtt ttt gag atg gag tct cac tct gtc acc cag gct gga gtg cag		152
Phe Val Phe Glu Met Glu Ser His Ser Val Thr Gln Ala Gly Val Gln		
1	5	10
15		
tgg cgc gat ctt ggc tca ctg caa gct ctg cct ccc ggg ttc tgc cca		200
Trp Arg Asp Leu Gly Ser Leu Gln Ala Leu Pro Pro Gly Phe Ser Pro		
20	25	30
ttc tgc cta agc ctc ccg agt agc tgg gac tac agg tgc ctg cca cca		248
Phe Cys Leu Ser Leu Pro Ser Ser Trp Asp Tyr Arg Cys Leu Pro Pro		
35	40	45
agc tgc gct aat ttt ttt ttt kgw att ttt agw agt rac rng gtt twa		296
Ser Ser Ala Asn Phe Phe Phe Xaa Ile Phe Xaa Ser Xaa Xaa Val Xaa		
50	55	60
ccg wat tas cca gga tgg yct caa tct cct gac ctc atg atc cgc cca		344
Pro Xaa Xaa Pro Gly Trp Xaa Gln Ser Pro Asp Leu Met Ile Arg Pro		
65	70	75
80		
cct cgg cct ccc aaa gtg ctg gga ata cag gcg tracmacsgc gcctggccaa		397
Pro Arg Pro Pro Lys Val Leu Gly Ile Gln Ala		
85	90	

ktttkgcttt tttgccaga ctggagt

424

<210> 3802
<211> 370
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 25..345

<221> sig_peptide
<222> 25..87
<223> score 4.9
seq GVVAHACCPGTLG/CR

<400> 3802
cacaaagtgt tatataatta aaac atg aaa ctt gat aca tct cgg cct ggt 51
Met Lys Leu Asp Thr Ser Arg Pro Gly
-20 -15
gtg gtg gct cac gcc tgt tgt ccc ggc act ttg gga tgc cga ggc ggg 99
Val Val Ala His Ala Cys Cys Pro Gly Thr Leu Gly Cys Arg Gly Gly
-10 -5 1
tgg atc acg agg tca gga gat cga gac cag cct ggc caa cgt ggt gaa 147
Trp Ile Thr Arg Ser Gly Asp Arg Asp Gln Pro Gly Gln Arg Gly Glu
5 10 15 20
gcc cca tct cta cta aaa atg cta aaa aaa ttg gcc ggg cgt ggc ggt 195
Ala Pro Ser Leu Leu Lys Met Leu Lys Lys Leu Ala Gly Arg Gly Gly
25 30 35
cca cgc ctg tgg tcc cag cta ctt ggg agg ctg agg cag aag aat cgc 243
Pro Arg Leu Trp Ser Gln Leu Leu Gly Arg Leu Arg Gln Lys Asn Arg
40 45 50
ttg aac ctg gga rrc gga ggt tgc ggt gag ctg aga tca cgc cac tgc 291
Leu Asn Leu Gly Xaa Gly Gly Cys Gly Glu Leu Arg Ser Arg His Cys
55 60 65
act cca gcc tgg hga cag agc gag act ctg tct caa aat car aaa aaa 339
Thr Pro Ala Trp Xaa Gln Ser Glu Thr Leu Ser Gln Asn Gln Lys Lys
70 75 80
gaa act tgatacatct cttactttat atcca 370
Glu Thr
85

<210> 3803
<211> 453
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 46..450

<221> sig_peptide
<222> 46..105

<223> score 4.5
seq GTLVFTVITAVLG/SF

<400> 3803

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acactcacac aagacctgga attgacagga ctcccaacta gtaca atg aca gaa gat      57
                               Met Thr Glu Asp
                               -20
aag gtc act ggg acc ctg gtt ttc act gtc atc act gct gtg ctg ggt      105
Lys Val Thr Gly Thr Leu Val Phe Thr Val Ile Thr Ala Val Leu Gly
-15                               -10                               -5
tcc ttc cag ttt gga tat gac att ggt gtg atc aat gca cct caa cag      153
Ser Phe Gln Phe Gly Tyr Asp Ile Gly Val Ile Asn Ala Pro Gln Gln
1                               5                               10                               15
gta ata ata tct cac tat aga cat gtt ttg ggt gtt cca ctg gat gac      201
Val Ile Ile Ser His Tyr Arg His Val Leu Gly Val Pro Leu Asp Asp
20                               25                               30
cga aaa gct atc aac aac tat gtt atc aac agt aca gat gaa ctg ccc      249
Arg Lys Ala Ile Asn Asn Tyr Val Ile Asn Ser Thr Asp Glu Leu Pro
35                               40                               45
aca atc tca tac tca atg aac cca aaa cca acc cct tgg gct gag gaa      297
Thr Ile Ser Tyr Ser Met Asn Pro Lys Pro Thr Pro Trp Ala Glu Glu
50                               55                               60
gag act gtg gca gct gct caa cta atc acc atg ctc tgg tcc ctg tct      345
Glu Thr Val Ala Ala Ala Gln Leu Ile Thr Met Leu Trp Ser Leu Ser
65                               70                               75                               80
gta tcc agc ttt gca gtt ggt gga atg act gca tca ttc ttt ggt ggg      393
Val Ser Ser Phe Ala Val Gly Gly Met Thr Ala Ser Phe Phe Gly Gly
85                               90                               95
tgg ctt ggg gac aca ctt gga agg gct aat ttc agg cct ggt tcc tat      441
Trp Leu Gly Asp Thr Leu Gly Arg Ala Asn Phe Arg Pro Gly Ser Tyr
100                               105                               110
gta tat cgg tga      453
Val Tyr Arg
115

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<210> 3804
<211> 458
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 115..423

<221> sig_peptide
<222> 115..186
<223> score 4.5
seq CVLKCVCLPLILS/PP

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<400> 3804
tagtttgatc taaagaacca gcttatataa cttgctgttg ccatgtacat ttgtatgtct      60
ttgctgtgtc aaataactgg atctgatttt agctcttttt aagtgggtgaa agca atg      117

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                                Met
cat ttt tat tct tca aat tca gac att gaa tgt gta tta aaa tgt gtg      165
His Phe Tyr Ser Ser Asn Ser Asp Ile Glu Cys Val Leu Lys Cys Val
      -20                      -15                      -10
tgc tta cct tta atc ctc tcc cca ccg aca att agg aac acg ttt ctc      213
Cys Leu Pro Leu Ile Leu Ser Pro Pro Thr Ile Arg Asn Thr Phe Leu
      -5                      1                      5
caa tta ctg ttg gca aga cta cca aga aaa att gtt gaa tta gaa tcc      261
Gln Leu Leu Leu Ala Arg Leu Pro Arg Lys Ile Val Glu Leu Glu Ser
10                      15                      20                      25
cag cac cgg gca cgg tgg ctc acg cct gtg atc cta gca ctt tgg gag      309
Gln His Arg Ala Arg Trp Leu Thr Pro Val Ile Leu Ala Leu Trp Glu
      30                      35                      40
gcc aaa gca ggc gga tca cct gag gtc agg agt tcg aga cca gca ggg      357
Ala Lys Ala Gly Gly Ser Pro Glu Val Arg Ser Ser Arg Pro Ala Gly
      45                      50                      55
cca aca tgg cga aac ccc gac tct act aaa aat aca aaa att agc cag      405
Pro Thr Trp Arg Asn Pro Asp Ser Thr Lys Asn Thr Lys Ile Ser Gln
      60                      65                      70
gca tgg tgg tgg gcg ctg taatcccaac tactcaggag gctgaggcag gagaa      458
Ala Trp Trp Trp Ala Leu
      75

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<210> 3805
 <211> 371
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 24..338
 <221> sig_peptide
 <222> 24..125
 <223> score 8.2
 seq TLFLTLSSSTLS/FL

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<400> 3805
caagagggttt gtggtgattc gtt atg gca gca cag gaa act cat gca gca cat      53
                                Met Ala Ala Gln Glu Thr His Ala Ala His
                                -30                      -25
tta tat ttt tta cca aat ttg aga aat ttt cag aca tta ttt ctt ctg      101
Leu Tyr Phe Leu Pro Asn Leu Arg Asn Phe Gln Thr Leu Phe Leu Leu
      -20                      -15                      -10
aca ctt tcc agt tcc acc ctc tct ttc ctc ttt ttc ttt aac ttc agt      149
Thr Leu Ser Ser Ser Thr Leu Ser Phe Leu Phe Phe Phe Asn Phe Ser
      -5                      1                      5
gat ttg aat ctt agc tct ttt tat ttt tta ttt tta ttt tta ttg cga      197
Asp Leu Asn Leu Ser Ser Phe Tyr Phe Leu Phe Leu Phe Leu Leu Arg
10                      15                      20
tgg agt cat gct ctt gtc gcc cag gct gga gtg cag tgg tgt gat ctt      245
Trp Ser His Ala Leu Val Ala Gln Ala Gly Val Gln Trp Cys Asp Leu
25                      30                      35                      40

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ggc tca ctg caa cct ctg tct cca ggg ttc agg cta tca tcc tgc cca      293
Gly Ser Leu Gln Pro Leu Ser Pro Gly Phe Arg Leu Ser Ser Cys Pro
               45               50               55
act ccc gag tgg ctg gga ttg cag gca tgc acc tcc tca scc agc      338
Thr Pro Glu Trp Leu Gly Leu Gln Ala Cys Thr Ser Ser Xaa Ser
               60               65               70
tagttttttt gtatttttgt agagacaggg ata      371

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<210> 3806
 <211> 453
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 66..395

<221> sig_peptide
 <222> 66..149
 <223> score 4.5
 seq LMSPALAAHVTRS/SQ

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<400> 3806
caagaactca ctttcaggat tgagtattga tgaaattgtc caaagagtga cagaacacat      60
tctag atg aac aga aaa aga aaa agc caa acc cag gaa agg aca aga gga      110
      Met Asn Arg Lys Arg Lys Ser Gln Thr Gln Glu Arg Thr Arg Gly
               -25               -20               -15
ctt atg agc cca gct ctg gcs gcc cac gtg acc agg tcc tcc cag ggc      158
Leu Met Ser Pro Ala Leu Ala Ala His Val Thr Arg Ser Ser Gln Gly
               -10               -5               1
cca ccc ttg gcg gtt gtt gca cca tca ccc aaa acc aag ggg cag aaa      206
Pro Pro Leu Ala Val Val Ala Pro Ser Pro Lys Thr Lys Gly Gln Lys
               5               10               15
gca gaa gat gtc cct gtg agg gtt gca ctg ggt gca agt tcc tgt gaa      254
Ala Glu Asp Val Pro Val Arg Val Ala Leu Gly Ala Ser Ser Cys Glu
               20               25               30               35
ata tgt cac gag gtg ttc aaa tca aaa aac gtg cgt gtg ctc aaa tgt      302
Ile Cys His Glu Val Phe Lys Ser Lys Asn Val Arg Val Leu Lys Cys
               40               45               50
ggg cac aag tat cac aaa ggg tgt ttt aag cag tgg ctt aaa ggg cag      350
Gly His Lys Tyr His Lys Gly Cys Phe Lys Gln Trp Leu Lys Gly Gln
               55               60               65
agc gct tgc cca gcc tgc cag act tgt gat ctc ctg tca gaa gag      395
Ser Ala Cys Pro Ala Cys Gln Thr Cys Asp Leu Leu Ser Glu Glu
               70               75               80
tagcctgcac cttctggaag aggctggccc agtgagaatc gggagccgcc ttctgtct      453

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<210> 3807
 <211> 380
 <212> DNA
 <213> Homo sapiens

<220>

<221> CDS
 <222> 61..363

<221> sig_peptide
 <222> 61..198
 <223> score 3.6
 seq MWLLLFRLWDGLA/ME

<400> 3807
 ggctgccctt gaactcttga cctcaagtga tctcctgcc ttggcctcca gcgtgctggg 60
 atg aca gga atg aat cct ttt aat atg ctg ctt cag gca gca gtg cag 108
 Met Thr Gly Met Asn Pro Phe Asn Met Leu Leu Gln Ala Ala Val Gln
 -45 -40 -35
 cag gtt gga agc tac aca cgg cac ctg gaa aga tcc cac agc tct gtg 156
 Gln Val Gly Ser Tyr Thr Arg His Leu Glu Arg Ser His Ser Ser Val
 -30 -25 -20 -15
 tgg atg tgg ctg ctg ctc ttc agg ctg tgg gat ggt ttg gcg atg gaa 204
 Trp Met Trp Leu Leu Leu Phe Arg Leu Trp Asp Gly Leu Ala Met Glu
 -10 -5 1
 cca agc ggg ttc agt gct cac gac gtc tgt tca tgt tct ctc tca agc 252
 Pro Ser Gly Phe Ser Ala His Asp Val Cys Ser Cys Ser Leu Ser Ser
 5 10 15
 tta gag gtg act tta gtt gag gga ggt gag tta ggg aat atg gag gtg 300
 Leu Glu Val Thr Leu Val Glu Gly Gly Glu Leu Gly Asn Met Glu Val
 20 25 30
 acc aaa acc atg agg aac agg gtc agc ctg aag gga gcg ggc ttc cct 348
 Thr Lys Thr Met Arg Asn Arg Val Ser Leu Lys Gly Ala Gly Phe Pro
 35 40 45 50
 ctg tgt ccg gct gtg tagtaatggc cgcttct 380
 Leu Cys Pro Ala Val
 55

<210> 3808
 <211> 377
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 54..371

<221> sig_peptide
 <222> 54..140
 <223> score 3.9
 seq LVHSTVSVSLLEA/DS

<400> 3808
 caaaatccca aaaggtatga gaagtcttct tagtgaatat caaagaaaaa gaa atg 56
 Met
 aag aaa aag ctt tac agg aga aga ttc ctg cct cct tat gtg gaa ctc 104
 Lys Lys Lys Leu Tyr Arg Arg Arg Phe Leu Pro Pro Tyr Val Glu Leu
 -25 -20 -15


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gtt cat tcc aca gtt agc gtt tcc ctg ctt gag gcc gac agt ggc tcc      152
Val His Ser Thr Val Ser Val Ser Leu Leu Glu Ala Asp Ser Gly Ser
      -10                      -5                      1
ctg gcc cct gtg cct ggg tcc gta ccc aag gtg ggt cct tgc tgg tcc      200
Leu Ala Pro Val Pro Gly Ser Val Pro Lys Val Gly Pro Cys Trp Ser
5                      10                      15                      20
tgc tgg tgt ctc cat cgg tgg ccc ttt ggg ctg ctc tct ggt tct gga      248
Cys Trp Cys Leu His Arg Trp Pro Phe Gly Leu Leu Ser Gly Ser Gly
                        25                      30                      35
ttt tct ctt ctg act ttc ttc cag aaa gag gga aag aag ttg cca ttt      296
Phe Ser Leu Leu Thr Phe Phe Gln Lys Glu Gly Lys Lys Leu Pro Phe
                        40                      45                      50
tct aag aaa aga gca atc cat cct aag aac acc tct gac ctc act ggg      344
Ser Lys Lys Arg Ala Ile His Pro Lys Asn Thr Ser Asp Leu Thr Gly
                    55                      60                      65
ctc tta cta ctc act tgg ctg aag cac taactc      377
Leu Leu Leu Leu Thr Trp Leu Lys His
70                      75

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<210> 3809

<211> 408

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 67..381

<221> sig_peptide

<222> 67..186

<223> score 5

seq LTLFISAXFXSET/WQ

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aaacaa atg cct gct tgc ata ttg gaa gat gtt gaa att agt ttt aga      108
      Met Pro Ala Cys Ile Leu Glu Asp Val Glu Ile Ser Phe Arg
      -40                      -35                      -30
caa aag tgg tcc atc aat tca gac act ctg ctt gga tgc ctt acc ctt      156
Gln Lys Trp Ser Ile Asn Ser Asp Thr Leu Leu Gly Cys Leu Thr Leu
      -25                      -20                      -15
ttc att agt gca tks ttt rmt tct gaa act tgg cag aaa ctc gtt agc      204
Phe Ile Ser Ala Xaa Phe Xaa Ser Glu Thr Trp Gln Lys Leu Val Ser
      -10                      -5                      1                      5
cag tcc act gcc ttt ctg aca atg tgt gga gtc acg tat gct tgg tat      252
Gln Ser Thr Ala Phe Leu Thr Met Cys Gly Val Thr Tyr Ala Trp Tyr
      10                      15                      20
atg cct tta cta ctt tta aag ttc tac agt tta tta ctt gcc caa rwg      300
Met Pro Leu Leu Leu Leu Lys Phe Tyr Ser Leu Leu Leu Ala Gln Xaa
      25                      30                      35
tta cta aat cct ttt ctt atg tgt act gga nsg mga aaa aat tat agc      348
Leu Leu Asn Pro Phe Leu Met Cys Thr Gly Xaa Arg Lys Asn Tyr Ser
      40                      45                      50

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cag cac ttt gag agg aag ttt tca gaa caa tat taactggcac tactaactga 401
 Gln His Phe Glu Arg Lys Phe Ser Glu Gln Tyr
 55 60 65
 aggcacg 408

<210> 3810
 <211> 442
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 19..345

<221> sig_peptide
 <222> 19..141
 <223> score 6.1
 seq VLLALSLRMECSG/MI

<400> 3810
 agaagctagc agagaggt atg gaa cag att ctt ctt cac aac ctc aga ggg 51
 Met Glu Gln Ile Leu Leu His Asn Leu Arg Gly
 -40 -35
 aaa acc ctg ctg ata cct gga ttt caa act cct ggc ctc cag aac gac 99
 Lys Thr Leu Leu Ile Pro Gly Phe Gln Thr Pro Gly Leu Gln Asn Asp
 -30 -25 -20 -15
 aaa gtc ttg ctt gct ctg tcg ctc agg atg gag tgt agt ggt atg atc 147
 Lys Val Leu Leu Ala Leu Ser Leu Arg Met Glu Cys Ser Gly Met Ile
 -10 -5 1
 tta gct cac tac aac ctc tgc ctc cca ggt tca agt gat tct cct gcc 195
 Leu Ala His Tyr Asn Leu Cys Leu Pro Gly Ser Ser Asp Ser Pro Ala
 5 10 15
 tta cgc tcc caa gta act ggg act aca ggc aca cac cac cac acc cag 243
 Leu Arg Ser Gln Val Thr Gly Thr Thr Gly Thr His His His Thr Gln
 20 25 30
 cta att ttt gta ttt ttt gta gag acg ggg ttt tac cac gtt agc cgg 291
 Leu Ile Phe Val Phe Val Glu Thr Gly Phe Tyr His Val Ser Arg
 35 40 45 50
 gct ggt ctt gaa ctc ctg acc tca ggt gat cca hsc gcc tcg atc gcc 339
 Ala Gly Leu Glu Leu Thr Ser Gly Asp Pro Xaa Ala Ser Ile Ala
 55 60 65
 cat tat taacaatcaa atggctgttc ttcatggtac tggtacaaaa acagatatat 395
 His Tyr
 acaccaatgg aacagaacag aggcctcaga aacaacacca cacatct 442

<210> 3811
 <211> 423
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 12..320

004420"6666T560

<221> sig_peptide
 <222> 12..140
 <223> score 9.1
 seq CLFVCLFFXWSLA/LS

<400> 3811
 aaaatcccaa a atg yya cct agt gac aac tgc tgt tat tta tat ttc ttc 50
 Met Xaa Pro Ser Asp Asn Cys Cys Tyr Leu Tyr Phe Phe
 -40 -35
 tcc ctc cct ttc tcc tgc ccg caa ctg tat ata gtg ttt ttt gtt gtt 98
 Ser Leu Pro Phe Ser Cys Pro Gln Leu Tyr Ile Val Phe Phe Val Val
 -30 -25 -20 -15
 ttt tgt ttg ttt gtt tgt ttg ttt ttt tta tgg agt ctt gct ctg tct 146
 Phe Cys Leu Phe Val Cys Leu Phe Phe Xaa Trp Ser Leu Ala Leu Ser
 -10 -5 1
 ccc agg ctg gag tgc agt ggc gcg atc tca gct cac tgc aac ctc cac 194
 Pro Arg Leu Glu Cys Ser Gly Ala Ile Ser Ala His Cys Asn Leu His
 5 10 15
 ctc ccg ggt tca agc gat tct cct acc tca gcc tcc cga gta gct ggg 242
 Leu Pro Gly Ser Ser Asp Ser Pro Thr Ser Ala Ser Arg Val Ala Gly
 20 25 30
 att ata gac atg gca tca cca tgc ctg gct aat ttt tct att ttt agt 290
 Ile Ile Asp Met Ala Ser Pro Cys Leu Ala Asn Phe Ser Ile Phe Ser
 35 40 45 50
 agg gac ggg gtt ttg cca tgt tgg cga ggc tgatcgtgaa ctcctgacct 340
 Arg Asp Gly Val Leu Pro Cys Trp Arg Gly
 55 60
 cagatgatct gccagcctcg gctcccaaaa gtgctgggra tttacaggcg tgcgccatcg 400
 yaccggcct aatagttttg ctt 423

<210> 3812
 <211> 487
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 52..435

<400> 3812
 tctttgctgc tgcgtagttc gctcacctcc ctttctaact ccgctgccgc c atg gct 57
 Met Ala
 1
 cct gtg aaa aag ctt gtg gtg aag ggg ggc aaa aaa aag aag caa gtt 105
 Pro Val Lys Lys Leu Val Val Lys Gly Gly Lys Lys Lys Lys Gln Val
 5 10 15
 ctg aag ttc act ctt gat tgc acc cac cct gta gaa gat gga atc atg 153
 Leu Lys Phe Thr Leu Asp Cys Thr His Pro Val Glu Asp Gly Ile Met
 20 25 30
 gat gct gcc aat ttt gag cag ttt ttg caa gaa agg atc aaa gtg aac 201
 Asp Ala Ala Asn Phe Glu Gln Phe Leu Gln Glu Arg Ile Lys Val Asn

35	40	45	50	
gga aaa gct ggg aac ctt ggt gga ggg gtg gtg acc atc gaa agg agc				249
Gly Lys Ala Gly Asn Leu Gly Gly Gly Val Val Thr Ile Glu Arg Ser				
	55	60	65	
aag agc aag atc acc gtg aca tcc gag gtg cct ttc tcc aaa agg tat				297
Lys Ser Lys Ile Thr Val Thr Ser Glu Val Pro Phe Ser Lys Arg Tyr				
	70	75	80	
ttg aaa tat ctc acc aaa aaa tat ttg aag aag aat aat cta cgt gac				345
Leu Lys Tyr Leu Thr Lys Lys Tyr Leu Lys Lys Asn Asn Leu Arg Asp				
	85	90	95	
tgg ttg cgc gta gtt gct aac agc aaa gag agt tac gaa tta cgt tac				393
Trp Leu Arg Val Val Ala Asn Ser Lys Glu Ser Tyr Glu Leu Arg Tyr				
	100	105	110	
ttc cag att aac cag gac gaa gaa gag gag gaa gac gag gat				435
Phe Gln Ile Asn Gln Asp Glu Glu Glu Glu Glu Asp Glu Asp				
	115	120	125	
taaatttcat ttatctggaa aattttgtat gagttcttga ataaaaacttg gg				487

<210> 3813
 <211> 454
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 99..419

<400> 3813	
gccgccgtcg tctttctctg tctcggtctga ggcagccatc tttctcttgc cgcgtgctgg	60
tgttggagga ccctccctgc ttcagattta ccaacagc atg aat caa gaa aag tta	116
	Met Asn Gln Glu Lys Leu
	1 5
gcc aaa ctt cag gct cag gtc cgg ata ggg ggc aag ggt aca gct cgc	164
Ala Lys Leu Gln Ala Gln Val Arg Ile Gly Gly Lys Gly Thr Ala Arg	
	10 15 20
aga aag aag aag gtg gta cat aga aca gcc aca gct gat gac aaa aag	212
Arg Lys Lys Lys Val Val His Arg Thr Ala Thr Ala Asp Asp Lys Lys	
	25 30 35
ctt cag agt tct cta aaa aaa ctg gct gtg aat aat ata gct ggt att	260
Leu Gln Ser Ser Leu Lys Lys Leu Ala Val Asn Asn Ile Ala Gly Ile	
	40 45 50
gaa gag gtg aac atg att aaa gat gat ggg aca gtt att cat ttc aac	308
Glu Glu Val Asn Met Ile Lys Asp Asp Gly Thr Val Ile His Phe Asn	
	55 60 65 70
aat ccc aaa gtc caa gct tcc ctt tct gct aat acc ttt gca att act	356
Asn Pro Lys Val Gln Ala Ser Leu Ser Ala Asn Thr Phe Ala Ile Thr	
	75 80 85
ggt cat gca gaa gcc aaa cca atc aca gaa atg ctt cct gga aat att	404
Gly His Ala Glu Ala Lys Pro Ile Thr Glu Met Leu Pro Gly Asn Ile	
	90 95 100
aag tca gct tgg tgc tgacagttta acaagcctta ggaagtttagc tgaac	454
Lys Ser Ala Trp Cys	
	105

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 <213> Homo sapiens

<220>
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 tgcaacttcc ttcggtcgtc ccgaatccgg gttcatccga caccagccgc ctccacc 117
 atg ccg ccg aag ttc gac ccc aac gag atc aaa gtc gta tac ctg agg 165
 Met Pro Pro Lys Phe Asp Pro Asn Glu Ile Lys Val Val Tyr Leu Arg
 1 5 10 15
 tgc acc gga ggt gaa gtc ggt gcc act tct gcc ctg gcc ccc aag atc 213
 Cys Thr Gly Gly Glu Val Gly Ala Thr Ser Ala Leu Ala Pro Lys Ile
 20 25 30
 ggc ccc ctg ggt ctg tct cca aaa aaa gtt ggt gat gac att gcc aag 261
 Gly Pro Leu Gly Leu Ser Pro Lys Lys Val Gly Asp Asp Ile Ala Lys
 35 40 45
 gca acg ggt gac tgg aag ggc ctg agg att aca gtg aaa ctg acc att 309
 Ala Thr Gly Asp Trp Lys Gly Leu Arg Ile Thr Val Lys Leu Thr Ile
 50 55 60
 cag aac aga cag gcc cag att gag gtg gtg cct tct gcc tct gcc ctg 357
 Gln Asn Arg Gln Ala Gln Ile Glu Val Val Pro Ser Ala Ser Ala Leu
 65 70 75 80
 atc atc aaa gcc ctc aag gaa cca cca aga gac aga aag aaa cag aaa 405
 Ile Ile Lys Ala Leu Lys Glu Pro Pro Arg Asp Arg Lys Lys Gln Lys
 85 90 95
 aac att aaa cac agt ggg aat atc act ttt gat gag att gtc aac att 453
 Asn Ile Lys His Ser Gly Asn Ile Thr Phe Asp Glu Ile Val Asn Ile
 100 105 110
 gct cga cag atg cgg cac cga tcc tta gcc aga gaa ctc tct gga acc 501
 Ala Arg Gln Met Arg His Arg Ser Leu Ala Arg Glu Leu Ser Gly Thr
 115 120 125
 att aaa gag atc ctg ggg act gcc cag tca gtg ggc tgt aat gtt gat 549
 Ile Lys Glu Ile Leu Gly Thr Ala Gln Ser Val Gly Cys Asn Val Asp
 130 135 140
 ggc cgc cat cct cat gac atc atc gat gac atc aac agt ggt gct gtg 597
 Gly Arg His Pro His Asp Ile Ile Asp Asp Ile Asn Ser Gly Ala Val
 145 150 155 160
 gaa tgc cca gcc agt taagcaca
 Glu Cys Pro Ala Ser 621
 165

<210> 3815
 <211> 464
 <212> DNA
 <213> Homo sapiens

<220>

<221> CDS
<222> 61..369

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atg gcc caa ttt gtc cgt aac ctt gtg gag aag acc ccg gcg ctg gtg 108
Met Ala Gln Phe Val Arg Asn Leu Val Glu Lys Thr Pro Ala Leu Val
1 5 10 15
aac gct gct gtg act tac tcg aag cct cga ttg gcc aca ttt tgg tac 156
Asn Ala Ala Val Thr Tyr Ser Lys Pro Arg Leu Ala Thr Phe Trp Tyr
20 25 30
tac gcc aag gtt gag ctg gtt cct ccc acc cct gct gag atc cct aga 204
Tyr Ala Lys Val Glu Leu Val Pro Pro Thr Pro Ala Glu Ile Pro Arg
35 40 45
gct att cag agc ctg aaa aaa ata gtc aat agt gct cag act ggt agc 252
Ala Ile Gln Ser Leu Lys Lys Ile Val Asn Ser Ala Gln Thr Gly Ser
50 55 60
ttc aaa cag ctg aca gtt aag gaa gct gtg ctg aat ggt ttg gtg gcc 300
Phe Lys Gln Leu Thr Val Lys Glu Ala Val Leu Asn Gly Leu Val Ala
65 70 75 80
act gag gtg ttg atg tgg ttt tat gtc gga gag att ata ggc aag cgg 348
Thr Glu Val Leu Met Trp Phe Tyr Val Gly Glu Ile Ile Gly Lys Arg
85 90 95
ggc atc att ggc tat gat gtt tgaagaccaa tctttaacat ctgattatat 399
Gly Ile Ile Gly Tyr Asp Val
100
ttgatttatt atttgagtgt tgttggacca tgtgtgatca gactgctatc tgaataraat 459
aagat 464

<210> 3816
<211> 485
<212> DNA
<213> Homo sapiens

<220>
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<222> 76..426

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ctgcaggcac tcaga atg gtc cag cgt ttg aca tac cga cgt agg ctt tcc 111
Met Val Gln Arg Leu Thr Tyr Arg Arg Arg Leu Ser
1 5 10
tac aat aca gcc tct aac aaa act agg ctg tcc cga acc cct ggt aat 159
Tyr Asn Thr Ala Ser Asn Lys Thr Arg Leu Ser Arg Thr Pro Gly Asn
15 20 25
aga att gtt tac ctt tat acc aag aag gtt ggg aaa gca cca aaa tct 207
Arg Ile Val Tyr Leu Tyr Thr Lys Lys Val Gly Lys Ala Pro Lys Ser
30 35 40
gca tgt ggt gtg tgc cca ggc aga ctt cga ggg gtt cgt gct gta aga 255
Ala Cys Gly Val Cys Pro Gly Arg Leu Arg Gly Val Arg Ala Val Arg
45 50 55 60

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cct aaa gtt ctt atg aga ttg tcc aaa aca aag aaa cat gtc agc agg      303
Pro Lys Val Leu Met Arg Leu Ser Lys Thr Lys Lys His Val Ser Arg
               65               70               75
gcc tat ggt ggt tcc atg tgt gct aaa tgt gtt cgt gac agg atc aag      351
Ala Tyr Gly Gly Ser Met Cys Ala Lys Cys Val Arg Asp Arg Ile Lys
               80               85               90
cgt gct ttc ctt atc gag gag cag aaa atc gtt gtg aaa gtg ttg aag      399
Arg Ala Phe Leu Ile Glu Glu Gln Lys Ile Val Val Lys Val Leu Lys
               95               100               105
gca caa gca cag agt cag aaa gct aaa taaaaaaatg aaactttttt      446
Ala Gln Ala Gln Ser Gln Lys Ala Lys
               110               115
gagtaataaaa aatgaaaaga cgctgtgtgg ggatccact      485

<210> 3817
<211> 543
<212> DNA
<213> Homo sapiens

<220>
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<222> 134..484

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ctgccatccg aggagctgag gaagcctaga gctctcagaa gcagtccttt gagctggtgt      120
aggggcactc aga atg gtc cag cgt ttg aca tac cga cgt agg ctt tcc      169
               Met Val Gln Arg Leu Thr Tyr Arg Arg Arg Leu Ser
               1               5               10
tac aat aca gcc tct aac aaa act agg ctg tcc cga acc cct ggt aat      217
Tyr Asn Thr Ala Ser Asn Lys Thr Arg Leu Ser Arg Thr Pro Gly Asn
               15               20               25
aga att gtt tac ctt tat acc aag aag gtt ggg aaa gca cca aaa tct      265
Arg Ile Val Tyr Leu Tyr Thr Lys Lys Val Gly Lys Ala Pro Lys Ser
               30               35               40
gca tgt ggt gtg tgc cca ggc aga ctt cga ggg gtt cgt gct gta aga      313
Ala Cys Gly Val Cys Pro Gly Arg Leu Arg Gly Val Arg Ala Val Arg
               45               50               55               60
cct aaa gtt ctt atg aga ttg tcc aaa aca aag aaa cat gtc agc agg      361
Pro Lys Val Leu Met Arg Leu Ser Lys Thr Lys Lys His Val Ser Arg
               65               70               75
gcc tat ggt ggt tcc atg tgt gct aaa tgt gtt cgt gac agg atc aag      409
Ala Tyr Gly Gly Ser Met Cys Ala Lys Cys Val Arg Asp Arg Ile Lys
               80               85               90
cgt gct ttc ctt atc gag gag cag aaa atc gtt gtg aaa gtg ttg aag      457
Arg Ala Phe Leu Ile Glu Glu Gln Lys Ile Val Val Lys Val Leu Lys
               95               100               105
gca caa gca cag agt cag aaa gct aaa taaaaaaatg aaactttttt      504
Ala Gln Ala Gln Ser Gln Lys Ala Lys
               110               115
gagtaataaaa aatgaaaaga cgctgtgtgg ggatccact      543

<210> 3818

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<211> 610
 <212> DNA
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<220>
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 <222> 92..514

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 ggcagagagg ctgttcgcag agctgcggaa g atg aat gcc aga gga ctt gga 112
 Met Asn Ala Arg Gly Leu Gly
 1 5
 tct gag cta aag gac agt att cca gtt act gaa ctt tca gca agt gga 160
 Ser Glu Leu Lys Asp Ser Ile Pro Val Thr Glu Leu Ser Ala Ser Gly
 10 15 20
 cct ttt gaa agt cat gat ctt ctt cgg aaa ggt ttt tct tgt gtg aaa 208
 Pro Phe Glu Ser His Asp Leu Leu Arg Lys Gly Phe Ser Cys Val Lys
 25 30 35
 aat gaa ctt ttg cct agt cat ccc ctt gaa tta tca gaa aaa aat ttc 256
 Asn Glu Leu Leu Pro Ser His Pro Leu Glu Leu Ser Glu Lys Asn Phe
 40 45 50 55
 cag ctc aac caa gat aaa atg aat ttt tcc aca ctg aga aac att cag 304
 Gln Leu Asn Gln Asp Lys Met Asn Phe Ser Thr Leu Arg Asn Ile Gln
 60 65 70
 ggt cta ttt gct ccg cta aaa tta cag atg gaa ttc aag gca gtg cag 352
 Gly Leu Phe Ala Pro Leu Lys Leu Gln Met Glu Phe Lys Ala Val Gln
 75 80 85
 cag gtt cag cgt ctt cca ttt ctt tca agc tca aat ctt tca ctg gat 400
 Gln Val Gln Arg Leu Pro Phe Leu Ser Ser Ser Asn Leu Ser Leu Asp
 90 95 100
 gtt ttg agg ggt aat gat gag act att gga ttt gag gat att ctt aat 448
 Val Leu Arg Gly Asn Asp Glu Thr Ile Gly Phe Glu Asp Ile Leu Asn
 105 110 115
 gat cca tca caa agc gaa gtc atg gga gag cca cac ttg atg gtg gaa 496
 Asp Pro Ser Gln Ser Glu Val Met Gly Glu Pro His Leu Met Val Glu
 120 125 130 135
 tat aaa ctt ggt tta ctg taaatagtgt gctgttcatg gaaaccgagg 544
 Tyr Lys Leu Gly Leu Leu
 140
 gctgcatctt gtttatagtc atctttgtac tgtaatttga tgtacacaac attaaaagta 604
 ctgaca 610

<210> 3819
 <211> 458
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 49..354

004220" 666F560

<400> 3819
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 Met Asn Lys
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 ttg aaa tca tcg cag aag gat aaa gtt cgt cag ttt atg atc ttc aca 105
 Leu Lys Ser Ser Gln Lys Asp Lys Val Arg Gln Phe Met Ile Phe Thr
 5 10 15
 caa tct agt gaa aaa aca gca gta agt tgt ctt tct caa aat gac tgg 153
 Gln Ser Ser Glu Lys Thr Ala Val Ser Cys Leu Ser Gln Asn Asp Trp
 20 25 30 35
 aag tta gat gtt gca aca gat aat ttt ttc caa aat cct gaa ctt tat 201
 Lys Leu Asp Val Ala Thr Asp Asn Phe Phe Gln Asn Pro Glu Leu Tyr
 40 45 50
 ata cga gag agt gta aaa gga tca ttg gac agg aag aag tta gaa cag 249
 Ile Arg Glu Ser Val Lys Gly Ser Leu Asp Arg Lys Lys Leu Glu Gln
 55 60 65
 ctg tac aat aga tac aaa gac cct caa gat gag aat aaa att gga ata 297
 Leu Tyr Asn Arg Tyr Lys Asp Pro Gln Asp Glu Asn Lys Ile Gly Ile
 70 75 80
 gat ggc ata cag cag ttc tgt gat gac ctg gca ctc gat cca gcc agc 345
 Asp Gly Ile Gln Gln Phe Cys Asp Asp Leu Ala Leu Asp Pro Ala Ser
 85 90 95
 ata gtg tgt tgattattgc atggaagtgc agagnaaaca cagtgcgagt 394
 Ile Val Cys
 100
 tnccaaacag gagttcatgg atggcatgac agaattagat gtgacagcat agaaaaacta 454
 aagg 458

<210> 3820
 <211> 665
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 106..648

<400> 3820
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 cctctgaggt gtccctggcc agtgtccttc cacctgtcca caagc atg ggg aac atc 117
 Met Gly Asn Ile
 1
 ttc gcc aac ctc ttc aag ggc ctt ttt ggc aaa aaa gaa atg cgc atc 165
 Phe Ala Asn Leu Phe Lys Gly Leu Phe Gly Lys Lys Glu Met Arg Ile
 5 10 15 20
 ctc atg gtg ggc ctg gat gct gca ggg aag acc acg atc ctc tac aag 213
 Leu Met Val Gly Leu Asp Ala Ala Gly Lys Thr Thr Ile Leu Tyr Lys
 25 30 35
 ctt aag ctg ggt gag atc gtg acc acc att ccc acc ata ggc ttc aac 261
 Leu Lys Leu Gly Glu Ile Val Thr Thr Ile Pro Thr Ile Gly Phe Asn
 40 45 50
 gtg gaa acc gtg gag tac aag aac atc agc ttc act gtg tgg gac gtg 309
 Val Glu Thr Val Glu Tyr Lys Asn Ile Ser Phe Thr Val Trp Asp Val

55	60	65	
ggt ggc cag gac aag atc cgg ccc ctg tgg cgc cac tac ttc cag aac			357
Gly Gly Gln Asp Lys Ile Arg Pro Leu Trp Arg His Tyr Phe Gln Asn			
70	75	80	
aca caa ggc ctg atc ttc gtg gtg gac agc aat gac aga gag cgt gtg			405
Thr Gln Gly Leu Ile Phe Val Val Asp Ser Asn Asp Arg Glu Arg Val			
85	90	95	100
aac gag gcc cgt gag gag ctc atg agg atg ctg gcc gag gac gag ctc			453
Asn Glu Ala Arg Glu Glu Leu Met Arg Met Leu Ala Glu Asp Glu Leu			
105	110	115	
cgg gat gct gtc ctc ctg gtg ttc gcc aac aag cag gac ctc ccc aac			501
Arg Asp Ala Val Leu Leu Val Phe Ala Asn Lys Gln Asp Leu Pro Asn			
120	125	130	
gcc atg aat gcg gcc gag atc aca gac aag ctg ggg ctg cac tca cta			549
Ala Met Asn Ala Ala Glu Ile Thr Asp Lys Leu Gly Leu His Ser Leu			
135	140	145	
cgc cac agg aac tgg wac att cag gcc acc tgc gcc acc agc ggc gac			597
Arg His Arg Asn Trp Xaa Ile Gln Ala Thr Cys Ala Thr Ser Gly Asp			
150	155	160	
ggg ctc tat gaa gga ctg gac tgg ctg tcc aat cag ctc cgg aac cag			645
Gly Leu Tyr Glu Gly Leu Asp Trp Leu Ser Asn Gln Leu Arg Asn Gln			
165	170	175	180
aag tgaacgcgac cccctc			665
Lys			

<210> 3821
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 <212> DNA
 <213> Homo sapiens

<220>
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 <222> 62..481

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g atg tcg aag cga gga cgt ggt ggg tcc tct ggt gcg aaa ttc cgg att	109
Met Ser Lys Arg Gly Arg Gly Gly Ser Ser Gly Ala Lys Phe Arg Ile	
1	15
tcc ttg ggt ctt ccg gta gga gct gta atc aat tgt gct gac aac aca	157
Ser Leu Gly Leu Pro Val Gly Ala Val Ile Asn Cys Ala Asp Asn Thr	
20	30
gga gcc aaa aac ctg tat atc atc tcc gtg aag ggg atc aag gga cgg	205
Gly Ala Lys Asn Leu Tyr Ile Ile Ser Val Lys Gly Ile Lys Gly Arg	
35	45
ctg aac aga ctt ccc gct gct ggt gtg ggt gac atg gtg atg gcc aca	253
Leu Asn Arg Leu Pro Ala Ala Gly Val Gly Asp Met Val Met Ala Thr	
50	60
gtc aag aaa ggc aaa cca gag ctc aga aaa aag gta cat cca gca gtg	301
Val Lys Lys Gly Lys Pro Glu Leu Arg Lys Lys Val His Pro Ala Val	
65	75
gtc att cga caa cga aag tca tac cgt aga aaa gat ggc gtg ttt ctt	349
Val Ile Arg Gln Arg Lys Ser Tyr Arg Arg Lys Asp Gly Val Phe Leu	

	85	90	95	
tat ttt gaa gat aat gca gga gtc ata gtg aac aat aaa ggc gag atg				397
Tyr Phe Glu Asp Asn Ala Gly Val Ile Val Asn Asn Lys Gly Glu Met				
	100	105	110	
aaa ggt tct gcc att aca gga cca gta gca aag gag tgt gca gac ttg				445
Lys Gly Ser Ala Ile Thr Gly Pro Val Ala Lys Glu Cys Ala Asp Leu				
	115	120	125	
tgg ccc cgg att gca tcc aat gct ggc agc att gca tgattctcca gtatat				497
Trp Pro Arg Ile Ala Ser Asn Ala Gly Ser Ile Ala				
	130	135	140	

<210> 3822
<211> 453
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 37..360

<400> 3822	
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Met Ala Val Ala Arg Ala	
	1 5
ggg gtc ttg gga gtc cag tgg ctg caa agg gca tcc cgg aac gtg atg	102
Gly Val Leu Gly Val Gln Trp Leu Gln Arg Ala Ser Arg Asn Val Met	
	10 15 20
ccg ctg ggc gca cgg aca gcc tcc cac atg acc aag gac atg ttc ccg	150
Pro Leu Gly Ala Arg Thr Ala Ser His Met Thr Lys Asp Met Phe Pro	
	25 30 35
ggg ccc tat cct agg acc cca gaa gaa cgg gcc gcc gcc gcc aag aag	198
Gly Pro Tyr Pro Arg Thr Pro Glu Glu Arg Ala Ala Ala Ala Lys Lys	
	40 45 50
tat aat atg cgt gtg gaa gac tac gaa cct tac ccg gat gat ggc atg	246
Tyr Asn Met Arg Val Glu Asp Tyr Glu Pro Tyr Pro Asp Asp Gly Met	
	55 60 65 70
ggg tat ggc gac tac ccg aag ctc cct gac cgc tca cag cat gag aga	294
Gly Tyr Gly Asp Tyr Pro Lys Leu Pro Asp Arg Ser Gln His Glu Arg	
	75 80 85
gat cca tgg tat agc tgg gac cag ccg ggc ctg agg tta act ggg gtg	342
Asp Pro Trp Tyr Ser Trp Asp Gln Pro Gly Leu Arg Leu Thr Gly Val	
	90 95 100
aac cga tgc act ggc acc tagacatgta caacaggaac cgtgtggata	390
Asn Arg Cys Thr Gly Thr	
	105
catccccac acctgtttct tggcatgtca tgtgtatgca gctcttcggt ttcttggtt	450
tca	453

<210> 3823
<211> 572
<212> DNA
<213> Homo sapiens

SECRET

<222> 46..540

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Met Phe Phe Ser

gcg gcg ctc cgg gcc cgg gcg gct ggc ctc acc gcc cac tgg gga aga 105
Ala Ala Leu Arg Ala Arg Ala Ala Gly Leu Thr Ala His Trp Gly Arg
5 10 15 20

cat gta agg aat ttg cat aag aca gct atg caa aat gga gct gga gga 153
His Val Arg Asn Leu His Lys Thr Ala Met Gln Asn Gly Ala Gly Gly
25 30 35

gct tta ttt gtg cac aga gat act cct gag aat aac cct gat act cca 201
Ala Leu Phe Val His Arg Asp Thr Pro Glu Asn Asn Pro Asp Thr Pro
40 45 50

ttt gat ttc aca cca gaa aac tat aag agg ata gag gca att gta aaa 249
 Phe Asp Phe Thr Pro Glu Asn Tyr Lys Arg Ile Glu Ala Ile Val Lys
 55 60 65

aac tat cca gaa ggc cat aaa gca gca gct gtt ctt cca gtc ctg gat 297
 Asn Tyr Pro Glu Gly His Lys Ala Ala Ala Val Leu Pro Val Leu Asp
 70 75 80

tta gcc caa agg cag aat ggg tgg ttg ccc atc tct gct atg aac aag	345
Leu Ala Gln Arg Gln Asn Gly Trp Leu Pro Ile Ser Ala Met Asn Lys	
85 90 95 100	

85 90 95 393
gtt gca gaa gtt tta caa gta cct cca atg aga gta tat gaa gta gca
Val Ala Glu Val Leu Gln Val Pro Pro Met Arg Val Tyr Glu Val Ala
105 110 115

act ttt tat aca atg tat aat cga aag cca gtn gga aag tat cac att 441
Thr Phe Tyr Thr Met Tyr Asn Arg Lys Pro Val Gly Lys Tyr His Ile
120 125 130

cag gtc tgc act act aca ccc tgc atg ctt cga aac tct gac agc ata 489
Gln Val Cys Thr Thr Thr Pro Cys Met Leu Arg Asn Ser Asp Ser Ile
135 140 145

ctg gag gcc att cag aaa aag ctt gga aat aaa ggt tgg gga gac tac 537
Leu Glu Ala Ile Gln Lys Lys Leu Gly Asn Lys Gly Trp Gly Asp Tyr
150 155 160

acc tgacaaactt ttcactctta tagaagtgga at 572
Thr
165

<211> 522

<213> Homo sapiens

<221> CDS

<222> 85..444

<400> 3824

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                               Met Asn Ser Ser Asp Glu Glu Lys Gln
                               1           5

ctg cag ctc att acc agt ctg aag gag caa gca ata ggc gaa tat gaa      159
Leu Gln Leu Ile Thr Ser Leu Lys Glu Gln Ala Ile Gly Glu Tyr Glu
10           15           20           25
gac ctt aga gca gag aac cag aaa aca aag gag aag tgk gac aaa att      207
Asp Leu Arg Ala Glu Asn Gln Lys Thr Lys Glu Lys Xaa Asp Lys Ile
30           35           40
agg caa gaa cga gat gaa gcc gtt aaa aaa ctg gaa gaa ttt cag aaa      255
Arg Gln Glu Arg Asp Glu Ala Val Lys Lys Leu Glu Glu Phe Gln Lys
45           50           55
att tct cac atg gkc ata gag gaa gtt aat ttc atg cag aac cat ctt      303
Ile Ser His Met Xaa Ile Glu Glu Val Asn Phe Met Gln Asn His Leu
60           65           70
gaa ata gag aag act tgt cga gaa agt gct gaa gct ttg gca aca aag      351
Glu Ile Glu Lys Thr Cys Arg Glu Ser Ala Glu Ala Leu Ala Thr Lys
75           80           85
cta aat aaa gaa aat aaa acg ttg aaa aga atc agc atg ttg tac atg      399
Leu Asn Lys Glu Asn Lys Thr Leu Lys Arg Ile Ser Met Leu Tyr Met
90           95           100           105
gcc aag ctg gga cca gat gta ata act gaa gag ata aac atn gna      444
Ala Lys Leu Gly Pro Asp Val Ile Thr Glu Glu Ile Asn Xaa Xaa
110           115           120
tgatgaagat tcgactacag acacagacgg tgccgccgag acttgtgtct cagtacagtg      504
tcagaagcaa attaaaga      522

<210> 3825
<211> 462
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 42..344

<400> 3825
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                               Met Val Glu Lys Lys
                               1           5

act tgc gtt cgc tcc cag gac ccc ggg cag cgg cgg gtg ctg gac cgg      104
Thr Ser Val Arg Ser Gln Asp Pro Gly Gln Arg Arg Val Leu Asp Arg
10           15           20
gct gcc cgg cag cgt cgc atc aac cgg cag ctg gag gcc ctg gag aat      152
Ala Ala Arg Gln Arg Arg Ile Asn Arg Gln Leu Glu Ala Leu Glu Asn
25           30           35
gac aac ttc cag gat gac ccc cac gcg gga ctc cct cag ctc ggc aag      200
Asp Asn Phe Gln Asp Asp Pro His Ala Gly Leu Pro Gln Leu Gly Lys
40           45           50
aga ctg cct cag ttt gat gac gat gcg gac act gga aag aaa aag aag      248
Arg Leu Pro Gln Phe Asp Asp Asp Ala Asp Thr Gly Lys Lys Lys Lys
55           60           65

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aaa acc cga ggt gat cat ttt aaa ctt cgc ttc cga aaa aac ttt cag 296
 Lys Thr Arg Gly Asp His Phe Lys Leu Arg Phe Arg Lys Asn Phe Gln
 70 75 80 85
 gcc ctg ttg gag gag cag aac ttg agt gtg gcc gag ggc cta act acc 344
 Ala Leu Leu Glu Glu Gln Asn Leu Ser Val Ala Glu Gly Leu Thr Thr
 90 95 100
 tgacggcctg tgcgggaccc ccatcgcggc ccacagcgccc cttctgtgct gtctgtggct 404
 tcccatcccc ctacacctgt gtcagctgcg gtgcccggta ctgcactgtg cgctgtct 462

<210> 3826
 <211> 344
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 23..325

<400> 3826
 atgctctgca gagaaatcaa ag atg gcg gtt gta tct gct gtt cgc tgg ctg 52
 Met Ala Val Val Ser Ala Val Arg Trp Leu
 1 5 10
 ggc ctc cgc agc agg ctt ggc cag ccg ctg acg ggt cgg cgg gcg ggt 100
 Gly Leu Arg Ser Arg Leu Gly Gln Pro Leu Thr Gly Arg Arg Ala Gly
 15 20 25
 ttg tgt gaa cag gca cgc agc tgc aga ttt tat tct ggt agt gca acc 148
 Leu Cys Glu Gln Ala Arg Ser Cys Arg Phe Tyr Ser Gly Ser Ala Thr
 30 35 40
 ctc tca aag gtt gaa gga act gat gta aca ggg att gaa gaa gta gta 196
 Leu Ser Lys Val Glu Gly Thr Asp Val Thr Gly Ile Glu Glu Val Val
 45 50 55
 att cca aaa aag aaa act tgg gat aaa gta gcc gtt ctt cag gca ctt 244
 Ile Pro Lys Lys Lys Thr Trp Asp Lys Val Ala Val Leu Gln Ala Leu
 60 65 70
 gca tcc aca gta aac agg gat acc aca gct gtg cct tat gtg ttt caa 292
 Ala Ser Thr Val Asn Arg Asp Thr Thr Ala Val Pro Tyr Val Phe Gln
 75 80 85 90
 gat gat cct tac ctt atg cca gcg aaa cac ata taataaatgc attcacaca 344
 Asp Asp Pro Tyr Leu Met Pro Ala Lys His Ile
 95 100

<210> 3827
 <211> 492
 <212> DNA
 <213> Homo sapiens

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 <222> 162..464

<400> 3827
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actgggcgac tctgtgcctc gctgaggaaa aataactaaa c atg ggc aaa gga gat 176
                                   Met Gly Lys Gly Asp
                                   1 5
cct aag aag ccg aga ggc aaa atg tca tca tat gca ttt ttt gtg caa 224
Pro Lys Lys Pro Arg Gly Lys Met Ser Ser Tyr Ala Phe Phe Val Gln
                                   10 15 20
act tgt cgg gag gag cat aag aag aag cac cca gat gct tca gtc aac 272
Thr Cys Arg Glu Glu His Lys Lys Lys His Pro Asp Ala Ser Val Asn
                                   25 30 35
ttc tca gag ttt tct aag aag tgc tca gag agg tgg aag acc atg tct 320
Phe Ser Glu Phe Ser Lys Lys Cys Ser Glu Arg Trp Lys Thr Met Ser
                                   40 45 50
gct aaa gag aaa gga aaa ttt gaa gat atg gca aaa gcg gac aag gcc 368
Ala Lys Glu Lys Gly Lys Phe Glu Asp Met Ala Lys Ala Asp Lys Ala
                                   55 60 65
cgt tat gaa aga gaa atg aaa acc tat atc cct ccc aaa ggg gag aca 416
Arg Tyr Glu Arg Glu Met Lys Thr Tyr Ile Pro Pro Lys Gly Glu Thr
                                   70 75 80 85
aaa aag aag ttc aag gat ccc aat gca ccc aag agg cct cac tgc tgt 464
Lys Lys Lys Phe Lys Asp Pro Asn Ala Pro Lys Arg Pro His Cys Cys
                                   90 95 100
tgargtggtg gtggtcacaa atctcctc 492

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<222> 72..419

<400> 3828
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ggctgttccc t atg gca gaa ggc aac cac aga aaa aag cca ctt aag gtg 110
                                   Met Ala Glu Gly Lys His Arg Lys Lys Pro Leu Lys Val
                                   1 5 10
ttg gaa tcc ctg ggc aaa gat ttc ctc act ggt gtt ttg gat aac ttg 158
Leu Glu Ser Leu Gly Lys Asp Phe Leu Thr Gly Val Leu Asp Asn Leu
                                   15 20 25
gtg gaa caa aat gta ctg aac tgg aag gaa gag gaa aaa aag aaa tat 206
Val Glu Gln Asn Val Leu Asn Trp Lys Glu Glu Glu Lys Lys Lys Tyr
                                   30 35 40 45
tac gat gct aaa act gaa gac aaa gtt cgg gtc atg gca gac tct atg 254
Tyr Asp Ala Lys Thr Glu Asp Lys Val Arg Val Met Ala Asp Ser Met
                                   50 55 60
caa gag aag caa cgt atg gca gga caa atg ctt ctt caa acc ttt ttt 302
Gln Glu Lys Gln Arg Met Ala Gly Gln Met Leu Leu Gln Thr Phe Phe
                                   65 70 75
aac ata gac caa ata tcc ccc aat aaa aaa gct cat ccg aat atg gag 350
Asn Ile Asp Gln Ile Ser Pro Asn Lys Lys Ala His Pro Asn Met Glu
                                   80 85 90

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<221> CDS
<222> 286..603

<400> 3830

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cctgcagagg cccggagaac acaaccctcc cgagaagccc aggactttgc agaccctca 180
gttccctggg attgagacag cacttctga ctgttacctt ggggccagag ccaaaccgt 240
cactgacccc ccagcccagg cgcccagcca ctccccaccg ctacc atg gcc gaa gac 297
Met Ala Glu Asp

1
gca gac atg cgc aat gag ctg gag gag atg cag cga agg gct gac cag 345
Ala Asp Met Arg Asn Glu Leu Glu Glu Met Gln Arg Arg Ala Asp Gln
5 10 15 20
ttg gct gat gag tcg ctg gaa agc acc cgt cgt atg ctg caa ctg gtt 393
Leu Ala Asp Glu Ser Leu Glu Ser Thr Arg Arg Met Leu Gln Leu Val
25 30 35
gaa gag agt aaa gat gct ggt atc agg act ttg gtt atg ttg gat gaa 441
Glu Glu Ser Lys Asp Ala Gly Ile Arg Thr Leu Val Met Leu Asp Glu
40 45 50
caa gga gaa caa ctg gaa cgc att gag gaa ggg atg gac caa atc aat 489
Gln Gly Glu Gln Leu Glu Arg Ile Glu Glu Gly Met Asp Gln Ile Asn
55 60 65
aag gac akc rra gaa gca gaa aag aat ttg acg gac cta gga aaa ttc 537
Lys Asp Xaa Xaa Glu Ala Glu Lys Asn Leu Thr Asp Leu Gly Lys Phe
70 75 80
tgc ggg ctt tgt gtg tgt cct gkr aca agc tta aat caa gtg atg ctt 585
Cys Gly Leu Cys Val Cys Pro Xaa Thr Ser Leu Asn Gln Val Met Leu
85 90 95 100
aca aaa agc ctg ggg caa taatcaggac ggagtggtgg ccagccagcc 633
Thr Lys Ser Leu Gly Gln
105
tgctcgtgta gtggacgaac gggag 658

<210> 3831
<211> 449
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 52..408

<400> 3831

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Met Ala
1
gct ata gct gca tcc gag gtg ctg gtg gac agc gcg gag gag ggg tcc 105
Ala Ile Ala Ala Ser Glu Val Leu Val Asp Ser Ala Glu Gly Ser
5 10 15
ctc gct gcg gcg gcg gas ctg gcc gct cag aag cgc gaa cag aga ctg 153
Leu Ala Ala Ala Ala Xaa Leu Ala Ala Gln Lys Arg Glu Gln Arg Leu

20	25	30	
cgc aaa ttc cgg gag ctg cac ctg atg cgg aat gaa gct cgt aaa tta			201
Arg Lys Phe Arg Glu Leu His Leu Met Arg Asn Glu Ala Arg Lys Leu			
35	40	45	50
aat cac cag gaa gtt gtg gaa gaa gat aaa aga cta aaa tta cct gca			249
Asn His Gln Glu Val Val Glu Glu Asp Lys Arg Leu Lys Leu Pro Ala			
55	60	65	
aat tgg gaa gcc aaa aaa gct cgt ttg gag tgg gaa cta aag gaa gag			297
Asn Trp Glu Ala Lys Lys Ala Arg Leu Glu Trp Glu Leu Lys Glu Glu			
70	75	80	
gaa aag aaa aag gaa tgt gcg gca aga sga gaa gac tat grg aaa gtg			345
Glu Lys Lys Lys Glu Cys Ala Ala Arg Xaa Glu Asp Tyr Xaa Lys Val			
85	90	95	
aag ttg ctg gag atc agt gca gaa gat gca gaa aga tgg gag agg aaa			393
Lys Leu Leu Glu Ile Ser Ala Glu Asp Ala Glu Arg Trp Glu Arg Lys			
100	105	110	
agr aga gga aaa mcc tgatctggga tttcagatta tgctgctgcc agttacgcc a			449
Arg Arg Gly Lys Xaa			
115			
<210> 3832			
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<222> 95..406			
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aactgggggat gattacagtt cttcctaaaa aagg atg gct gct ctt ttt cta aag			115
Met Ala Ala Leu Phe Leu Lys			
1			5
agg tta aca cta caa act gta aag tct gaa aat agt tgc att aga tgt			163
Arg Leu Thr Leu Gln Thr Val Lys Ser Glu Asn Ser Cys Ile Arg Cys			
10			15
20			
ttt ggt aaa cac atc ctg caa aag aca gca cca gca cag ttg tcc cct			211
Phe Gly Lys His Ile Leu Gln Lys Thr Ala Pro Ala Gln Leu Ser Pro			
25			30
35			
att gct tct gcc cca aga ctc tcc ttc cta att cat gca aaa gcc ttt			259
Ile Ala Ser Ala Pro Arg Leu Ser Phe Leu Ile His Ala Lys Ala Phe			
40			45
50			55
agt acc gct gaa gac acc cag aat gaa gga aaa aag aca aaa aag aat			307
Ser Thr Ala Glu Asp Thr Gln Asn Glu Gly Lys Lys Thr Lys Lys Asn			
60			65
70			
aaa aca gct ttt agt aac gtt gga aga raa att agt cag cga gtt att			355
Lys Thr Ala Phe Ser Asn Val Gly Arg Xaa Ile Ser Gln Arg Val Ile			
75			80
85			
cac tta ttt gat gag arg gca atg att tgg gaa aca tgc acc gag caa			403
His Leu Phe Asp Glu Xaa Ala Met Ile Trp Glu Thr Cys Thr Glu Gln			
90			95
100			
atg tgattagact tatggatgag cgagacctgc gactgggttca aaggaacacc			456

Met
agcacagasc tgcagagtat cagctcatga c

487

<210> 3833
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<222> 47..409

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Met Lys Val
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gag ctg tgc agt ttt agc ggg tac aag atc tac ccc gga cac ggg agg 103
Glu Leu Cys Ser Phe Ser Gly Tyr Lys Ile Tyr Pro Gly His Gly Arg
5 10 15
cgc tac gcc agg acc gac ggg aag gtt ttc cag ttt ctt aat gcg aaa 151
Arg Tyr Ala Arg Thr Asp Gly Lys Val Phe Gln Phe Leu Asn Ala Lys
20 25 30 35
tgc gag tcg gct ttc ctt tcc aag agg aat cct cgg cag ata aac tgg 199
Cys Glu Ser Ala Phe Leu Ser Lys Arg Asn Pro Arg Gln Ile Asn Trp
40 45 50
act gtc ctc tac aga agg aag cac aaa aag gga cag tcg gaa gaa att 247
Thr Val Leu Tyr Arg Arg Lys His Lys Lys Gly Gln Ser Glu Glu Ile
55 60 65
caa aag aaa aga acc cgc cga gca gtc aaa ttc cag agg gcc att act 295
Gln Lys Lys Arg Thr Arg Arg Ala Val Lys Phe Gln Arg Ala Ile Thr
70 75 80
ggt gca tct ctt gct gat ata atg gcc aag agg aat cag aaa cct gaa 343
Gly Ala Ser Leu Ala Asp Ile Met Ala Lys Arg Asn Gln Lys Pro Glu
85 90 95
gtt aga aag gct caa cga gaa caa gct atc agg sac ctr cwa agg mag 391
Val Arg Lys Ala Gln Arg Glu Gln Ala Ile Arg Xaa Leu Xaa Arg Xaa
100 105 110 115
cac cta agc aaa aga ttg tgaagcctgt gaaagtttca gctccccgag 439
His Leu Ser Lys Arg Leu
120
ttggtgaaa acgctaaact gg 461

<210> 3834
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<212> DNA
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<220>
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<222> 75..398

<400> 3834

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gtgtactatt agcc atg gtc aac ccc acc gtg ttc ttc gac att gcc gtc      110
          Met Val Asn Pro Thr Val Phe Phe Asp Ile Ala Val
          1          5          10
gac ggc gag ccc ttg ggc cgc gtc tcc ttt gag ctg ttt gca gac aag      158
Asp Gly Glu Pro Leu Gly Arg Val Ser Phe Glu Leu Phe Ala Asp Lys
          15          20          25
gtc cca aag aca gca gaa aat ttt cgt gct ctg agc act gga gag aaa      206
Val Pro Lys Thr Ala Glu Asn Phe Arg Ala Leu Ser Thr Gly Glu Lys
          30          35          40
gga ttt ggt tat aag ggt tcc tgc ttt cac aga att att cca ggg ttt      254
Gly Phe Gly Tyr Lys Gly Ser Cys Phe His Arg Ile Ile Pro Gly Phe
          45          50          55          60
atg tgt cag ggt ggt gac ttc aca cgc cat aat ggc act ggt ggc aag      302
Met Cys Gln Gly Gly Asp Phe Thr Arg His Asn Gly Thr Gly Gly Lys
          65          70          75
tcc atc tat ggg gag ggt cag cct gct ttt gtt atc aag cct tcc cag      350
Ser Ile Tyr Gly Glu Gly Gln Pro Ala Phe Val Ile Lys Pro Ser Gln
          80          85          90
cgg aac cta ggg gng aga gac aca gcc agg asc aan scc agg ttc cag      398
Arg Asn Leu Gly Xaa Arg Asp Thr Ala Arg Xaa Xaa Xaa Arg Phe Gln
          95          100          105
taggaaggcc a      409

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 <211> 739
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 <213> Homo sapiens

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gtgtactatt agcc atg gtc aac ccc acc gtg ttc ttc gac att gcc gtc      110
          Met Val Asn Pro Thr Val Phe Phe Asp Ile Ala Val
          1          5          10
gac ggc gag ccc ttg ggc cgc gtc tcc ttt gag ctg ttt gca gac aag      158
Asp Gly Glu Pro Leu Gly Arg Val Ser Phe Glu Leu Phe Ala Asp Lys
          15          20          25
gtc cca aag aca gca gaa aat ttt cgt gct ctg agc act gga gag aaa      206
Val Pro Lys Thr Ala Glu Asn Phe Arg Ala Leu Ser Thr Gly Glu Lys
          30          35          40
gga ttt ggt tat aag ggt tcc tgc ttt cac aga att att cca ggg ttt      254
Gly Phe Gly Tyr Lys Gly Ser Cys Phe His Arg Ile Ile Pro Gly Phe
          45          50          55          60
atg tgt cag ggt ggt gac ttc aca cgc cat aat ggc act ggt ggc aag      302
Met Cys Gln Gly Gly Asp Phe Thr Arg His Asn Gly Thr Gly Gly Lys
          65          70          75
tcc atc tat ggg gag aaa ttt gaa gat gag aac ttc atc cta aag cat      350
Ser Ile Tyr Gly Glu Lys Phe Glu Asp Glu Asn Phe Ile Leu Lys His
          80          85          90

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acg ggt cct gkc atc ttg tcc atg gca aat gct gga ccc aac aca aat	398
Thr Gly Pro Xaa Ile Leu Ser Met Ala Asn Ala Gly Pro Asn Thr Asn	
95 100 105	
ggt tcc cag ttt ttc atc tgc act gcc aag act gag tgg ttg gat ggc	446
Gly Ser Gln Phe Phe Ile Cys Thr Ala Lys Thr Glu Trp Leu Asp Gly	
110 115 120	
aag cat gtg gtg ttt ggc aaa gtg aaa gaa ggc atg aat att gtg gag	494
Lys His Val Val Phe Gly Lys Val Lys Glu Gly Met Asn Ile Val Glu	
125 130 135 140	
gcc atg gag cgc ttt ggg tcc agg aat ggc aag acc agc aag aag atc	542
Ala Met Glu Arg Phe Gly Ser Arg Asn Gly Lys Thr Ser Lys Lys Ile	
145 150 155	
acc att gct gac tgt gga caa ctc gaa taagtttgac ttgtgtttta	589
Thr Ile Ala Asp Cys Gly Gln Leu Glu	
160 165	
tcttaaccac cagatcwttc cttctgtagc tcaggagagc acccctccac cccatttgct	649
cgcagtatcc tagaatcttt gtgctctcgc tgcagttccc tttgggttcc atgttttct	709
tggtccctcc catgcctagc tggattgcag	739

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Met Ala Asp Gln Leu Thr Glu Glu Gln Ile Ala Glu Phe Lys Glu Ala	
1 5 10 15	
ttc tcc ctc ttt gac aag gat gga gat ggc act atc acc acc aag gag	153
Phe Ser Leu Phe Asp Lys Asp Gly Asp Gly Thr Ile Thr Thr Lys Glu	
20 25 30	
ttg ggg aca gtg atg aga tcc ctg gga cag aac ccc act gaa gca gag	201
Leu Gly Thr Val Met Arg Ser Leu Gly Gln Asn Pro Thr Glu Ala Glu	
35 40 45	
ctg cag gat atg atc aat gag gtg gat gca gat ggg aac ggg acc att	249
Leu Gln Asp Met Ile Asn Glu Val Asp Ala Asp Gly Asn Gly Thr Ile	
50 55 60	
gac ttc ccg gag ttc ctg acc atg atg gcc aga aag atg aag gac aca	297
Asp Phe Pro Glu Phe Leu Thr Met Met Ala Arg Lys Met Lys Asp Thr	
65 70 75 80	
gac agt gag gag gag atc cga gag gcg ttc cgt gtc ttt gac aag gat	345
Asp Ser Glu Glu Glu Ile Arg Glu Ala Phe Arg Val Phe Asp Lys Asp	
85 90 95	
ggg aat ggc tac atc agc gcc gca gag ctg cgt cac gta atg acg aac	393
Gly Asn Gly Tyr Ile Ser Ala Ala Glu Leu Arg His Val Met Thr Asn	
100 105 110	
ctg ggg gag aag ctg acc gat gag gag gtg gat gag atg atc agg gag	441
Leu Gly Glu Lys Leu Thr Asp Glu Glu Val Asp Glu Met Ile Arg Glu	

115	120	125	
gct gac atc gat gga gat ggc cag gtc aat tat gaa gag ttt gta cag			489
Ala Asp Ile Asp Gly Asp Gly Gln Val Asn Tyr Glu Glu Phe Val Gln			
130	135	140	
atg atg act gca aag tgaaggcccc ccgggcagct ggcgatgccc gttctcttga			544
Met Met Thr Ala Lys			
145			
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 <212> DNA
 <213> Homo sapiens

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1	
aag aag ggt ggc gag aag aaa aag ggc cgt tct gcc atc aac gaa gtg	103
Lys Lys Gly Gly Glu Lys Lys Lys Gly Arg Ser Ala Ile Asn Glu Val	
5 10 15 20	
nta acc cga gaa tac acc atc aac att cac aag cgc atc cat gga gtg	151
Xaa Thr Arg Glu Tyr Thr Ile Asn Ile His Lys Arg Ile His Gly Val	
25 30 35	
ggc ttc aag aag cgt gca cct cgg gca ctc aaa gag att cgg aaa ttt	199
Gly Phe Lys Lys Arg Ala Pro Arg Ala Leu Lys Glu Ile Arg Lys Phe	
40 45 50	
gcc atg aag gag atg gga act cca gat gtg cgc att gac acc agg ctc	247
Ala Met Lys Glu Met Gly Thr Pro Asp Val Arg Ile Asp Thr Arg Leu	
55 60 65	
aac aaa gct gtc tgg gcc aaa gga ata agg aat gtg cca tac cga atc	295
Asn Lys Ala Val Trp Ala Lys Gly Ile Arg Asn Val Pro Tyr Arg Ile	
70 75 80	
cgt gtg cgg ctg tcc aga aaa cgt aat gag gat gaa gat tca cca aat	343
Arg Val Arg Leu Ser Arg Lys Arg Asn Glu Asp Glu Asp Ser Pro Asn	
85 90 95 100	
aag cta tat act ttg gtt acc tat gta cct gtt acc act ttc aaa aat	391
Lys Leu Tyr Thr Leu Val Thr Tyr Val Pro Val Thr Thr Phe Lys Asn	
105 110 115	
cta cag aca gtc aat gtg gat gag aac taatcgctga tcgtcagatc	438
Leu Gln Thr Val Asn Val Asp Glu Asn	
120 125	
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SECRET

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gac atg atg gac ttg ccc agg tcg cgc atc aac gcc ggc atg cta gct																	105	
Asp Met Met Asp Leu Pro Arg Ser Arg Ile Asn Ala Gly Met Leu Ala																		
															5	10	15	
caa ttc atc gac aag cct gtc tgc ttc gta ggg agg ctg gaa aag att																	153	
Gln Phe Ile Asp Lys Pro Val Cys Phe Val Gly Arg Leu Glu Lys Ile																		
															20	25	30	
cat ccc acc gga aaa atg ttt att ctt tca gat gga gaa gga aaa aat																	201	
His Pro Thr Gly Lys Met Phe Ile Leu Ser Asp Gly Glu Gly Lys Asn																		
															35	40	45	50

gga acc atc gag ttg atg gaa ccc ctt gat gaa gaa atc tct gga att	249
Gly Thr Ile Glu Leu Met Glu Pro Leu Asp Glu Glu Ile Ser Gly Ile	
55 60 65	
gtg gaa gtg gtt gga aga gta acc gcc aag gcc acc atc ttg tgt aca	297
Val Glu Val Val Gly Arg Val Thr Ala Lys Ala Thr Ile Leu Cys Thr	
70 75 80	
tct tat gtc cag ttt aaa gaa gat agc cat cct ttt gat ctt gga ctt	345
Ser Tyr Val Gln Phe Lys Glu Asp Ser His Pro Phe Asp Leu Gly Leu	
85 90 95	
tac aat gaa gct gtg aaa att atc cat gac ttc cct cag ttt tat cct	393
Tyr Asn Glu Ala Val Lys Ile Ile His Asp Phe Pro Gln Phe Tyr Pro	
100 105 110	
tta ggg att gtg caa cat gat tgatcttgat ggattttcat acgattgtaa	444
Leu Gly Ile Val Gln His Asp	
115 120	
atgagctata ttaaagtcta ttaaaggaag cccttcttgt ttgagggaga gatttctgtg	504
ctttctcata ttttaattgc tgtttttaag atattccaac ctagagtttt tgatggaact	564
gatataattga cagttctcac cgaagtcctt ttataaagaa ttgctactcc aatatatggt	624
cagattagat gcaagaataa agca	648
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cccgcgcct cccgcccccg cagttccttg gagagcttgg agccgcgcgc cggagggaat	180
aggaaaagctt ggttacaacc cgggacaccc ggagcttcag g atg gtt cgt act aag	236
Met Val Arg Thr Lys	
1 5	
aca tgg acc ctg aag aag cac ttt gtt ggc tat cct act aat agt gac	284
Thr Trp Thr Leu Lys Lys His Phe Val Gly Tyr Pro Thr Asn Ser Asp	
10 15 20	
ttt gag ttg aag aca gct gag ctc cca ccc tta aaa aat gga gag gtc	332
Phe Glu Leu Lys Thr Ala Glu Leu Pro Pro Leu Lys Asn Gly Glu Val	
25 30 35	
ctg ctt gaa gct ttg ttc ctc acc gtg gat ccc tac atg aga gtg gca	380
Leu Leu Glu Ala Leu Phe Leu Thr Val Asp Pro Tyr Met Arg Val Ala	
40 45 50	
gcc aaa aga ttg aag gaa ggt gat aca atg atg ggg cag caa gtg gcc	428
Ala Lys Arg Leu Lys Glu Gly Asp Thr Met Met Gly Gln Gln Val Ala	
55 60 65	
aaa gtt gtg gaa agt aaa aat gta gcc cta cca aaa gga act att gta	476
Lys Val Val Glu Ser Lys Asn Val Ala Leu Pro Lys Gly Thr Ile Val	
70 75 80 85	
ctg gct tct cca ggc tgg aca acg cac tcc att tct gat ggg aaa gat	524
Leu Ala Ser Pro Gly Trp Thr Thr His Ser Ile Ser Asp Gly Lys Asp	

90 95 100 540
 ctg gaa agc tgc tgac
 Leu Glu Ser Cys
 105

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 <222> 149..625

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 ctagtttttc agaagaagtg aagtcaag atg aag aac cat ttg ctt ttc tgg 172
 Met Lys Asn His Leu Leu Phe Trp
 1 5
 gga gtc ctg gcg gtt ttt att aag gct gtt cat gtg aaa gcc caa gaa 220
 Gly Val Leu Ala Val Phe Ile Lys Ala Val His Val Lys Ala Gln Glu
 10 15 20
 gat gaa agg att gtt ctt gtt gac aac aaa tgt aag tgt gcc cgg att 268
 Asp Glu Arg Ile Val Leu Val Asp Asn Lys Cys Lys Cys Ala Arg Ile
 25 30 35 40
 act tcc agg atc atc cgt tct tcc gaa gat cct aat gag gac att gtg 316
 Thr Ser Arg Ile Ile Arg Ser Ser Glu Asp Pro Asn Glu Asp Ile Val
 45 50 55
 gag aga aac atc cga att att gtt cct ctg aac aac agg gag aat atc 364
 Glu Arg Asn Ile Arg Ile Ile Val Pro Leu Asn Asn Arg Glu Asn Ile
 60 65 70
 tct gat ccc acc tca cca ttg aga acc aga ttt gtg tac cat ttg tct 412
 Ser Asp Pro Thr Ser Pro Leu Arg Thr Arg Phe Val Tyr His Leu Ser
 75 80 85
 gac ctc tgt aaa aaa tgt gat cct aca gaa gtg gag ctg gat aat cag 460
 Asp Leu Cys Lys Lys Cys Asp Pro Thr Glu Val Glu Leu Asp Asn Gln
 90 95 100
 ata gtt act gct acc cag agc aat atc tgt gat gaa gac agt gct aca 508
 Ile Val Thr Ala Thr Gln Ser Asn Ile Cys Asp Glu Asp Ser Ala Thr
 105 110 115 120
 gag acc tgc tac act tat gac aga aac aag tgc tac aca gct gtg gtc 556
 Glu Thr Cys Tyr Thr Tyr Asp Arg Asn Lys Cys Tyr Thr Ala Val Val
 125 130 135
 cca ctc gta tat ggt ggt gag acc aaa atg gtg gaa aca gcc tta acc 604
 Pro Leu Val Tyr Gly Gly Glu Thr Lys Met Val Glu Thr Ala Leu Thr
 140 145 150
 cca gat gcc tgc tat cct gac taatttaagt cattgtctgac tgcataagctc 655
 Pro Asp Ala Cys Tyr Pro Asp
 155
 tttttcttga gaggtctctc attttgattc agaaagttan gcatatttat taccaatgaa 715
 ttgtgaaacca gggctttttt ttt 738

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 <211> 727
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 <213> Homo sapiens

<220>
 <221> CDS
 <222> 138..614

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 tttgcacact ccttatagat aacacacctt aaccctgact ttttttgctc cagtttttca 120
 gaagaagtga agtcaag atg aag aac cat ttg ctt ttc tgg gga gtc ctg 170
 Met Lys Asn His Leu Leu Phe Trp Gly Val Leu
 1 5 10
 gcg gtt ttt att aag gct gtt cat gtg aaa gcc caa gaa gat gaa agg 218
 Ala Val Phe Ile Lys Ala Val His Val Lys Ala Gln Glu Asp Glu Arg
 15 20 25
 att gtt ctt gtt gac aac aaa tgt aag tgt gcc cgg att act tcc agg 266
 Ile Val Leu Val Asp Asn Lys Cys Lys Cys Ala Arg Ile Thr Ser Arg
 30 35 40
 atc atc cgt tct tcc gaa gat cct aat gag gac att gtg gag aga aac 314
 Ile Ile Arg Ser Ser Glu Asp Pro Asn Glu Asp Ile Val Glu Arg Asn
 45 50 55
 atc cga att att gtt cct ctg aac aac agg gag aat atc tct gat ccc 362
 Ile Arg Ile Ile Val Pro Leu Asn Asn Arg Glu Asn Ile Ser Asp Pro
 60 65 70 75
 acc tca cca ttg aga acc aga ttt gtg tac cat ttg tct gac ctc tgt 410
 Thr Ser Pro Leu Arg Thr Arg Phe Val Tyr His Leu Ser Asp Leu Cys
 80 85 90
 aaa aaa tgt gat cct aca gaa gtg gag ctg gat aat cag ata gtt act 458
 Lys Lys Cys Asp Pro Thr Glu Val Glu Leu Asp Asn Gln Ile Val Thr
 95 100 105
 gct acc cag agc aat atc tgt gat gaa gac agt gct aca gag acc tgc 506
 Ala Thr Gln Ser Asn Ile Cys Asp Glu Asp Ser Ala Thr Glu Thr Cys
 110 115 120
 tac act tat gac aga aac aag tgc tac aca gct gtg gtc cca ctc gta 554
 Tyr Thr Tyr Asp Arg Asn Lys Cys Tyr Thr Ala Val Val Pro Leu Val
 125 130 135
 tat ggt ggt gag acc aaa atg gtg gaa aca gcc tta acc cca gat gcc 602
 Tyr Gly Gly Glu Thr Lys Met Val Glu Thr Ala Leu Thr Pro Asp Ala
 140 145 150 155
 tgc tat cct gac taatttaagt cattgctgac tgcatagctc tttttcttga 654
 Cys Tyr Pro Asp
 gaggtctccc attttgatcc agaaagttn gcatatttat taccaatgaa tttgaaacca 714
 gggctttttt ttt 727

<210> 3843
 <211> 504
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<220>

<221> CDS
<222> 60..491

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 atg tcg acc aag aat ttc cga gtc agt gac ggg gac tgg att tgc cct 107
 Met Ser Thr Lys Asn Phe Arg Val Ser Asp Gly Asp Trp Ile Cys Pro
 1 5 10 15
 gac aaa aaa tgt gga aat gta aac ttt gct aga aga acc agc tgt aat 155
 Asp Lys Lys Cys Gly Asn Val Asn Phe Ala Arg Arg Thr Ser Cys Asn
 20 25 30
 cga tgt ggt cgg gag aaa aca act gag gcc aag atg atg aaa gct ggg 203
 Arg Cys Gly Arg Glu Lys Thr Thr Glu Ala Lys Met Met Lys Ala Gly
 35 40 45
 ggc act gaa ata gga aag aca ctt gca gaa aag agc cga ggc cta ttt 251
 Gly Thr Glu Ile Gly Lys Thr Leu Ala Glu Lys Ser Arg Gly Leu Phe
 50 55 60
 agt gct aat gac tgg caa tgt aaa act tgc agc aat gtg aat tgg gcc 299
 Ser Ala Asn Asp Trp Gln Cys Lys Thr Cys Ser Asn Val Asn Trp Ala
 65 70 75 80
 aga aga tca gag tgt aat atg tgt aat act cca aag tat gct aaa tta 347
 Arg Arg Ser Glu Cys Asn Met Cys Asn Thr Pro Lys Tyr Ala Lys Leu
 85 90 95
 gaa gaa aga aca gga tat ggt ggt ggt ttt aat gaa aga gaa aat gtt 395
 Glu Glu Arg Thr Gly Tyr Gly Gly Gly Phe Asn Glu Arg Glu Asn Val
 100 105 110
 gaa tat ata gaa aga rag aat ctg atg gtg aat atg atg agt ttg gac 443
 Glu Tyr Ile Glu Arg Xaa Asn Leu Met Val Asn Met Met Ser Leu Asp
 115 120 125
 gta aaa aga naa aat aca gag gga aag cag ttg gtc ctg cat cta tat 491
 Val Lys Arg Xaa Asn Thr Glu Gly Lys Gln Leu Val Leu His Leu Tyr
 130 135 140
 taaaggaagt tga 504

<210> 3844
<211> 501
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 45..392

<400> 3844
 tttgttccca aagggttgtg cgtcaccgag tcgttgggcgc tgtc atg gcg ggt gtg 56
 Met Ala Gly Val
 1
 ctg aag aag acc act ggc ctt gtg gga ttg gct gtg tgc aat act cct 104
 Leu Lys Lys Thr Thr Gly Leu Val Gly Leu Ala Val Cys Asn Thr Pro
 5 10 15 20
 cac gag agg cta aga ata ttg tac aca aag att ctt gat gtt ctt gag 152
 His Glu Arg Leu Arg Ile Leu Tyr Thr Lys Ile Leu Asp Val Leu Glu

	25		30		35	
gaa atc cct aaa aat gca gca tat aga aag tat aca gaa cag att aca						200
Glu Ile Pro Lys Asn Ala Ala Tyr Arg Lys Tyr Thr Glu Gln Ile Thr						
	40		45		50	
aat gag aag ctg gct atg gtt aaa gcg gaa cca gat gtt aaa aaa tta						248
Asn Glu Lys Leu Ala Met Val Lys Ala Glu Pro Asp Val Lys Lys Leu						
	55		60		65	
gaa gac caa ctt caa ggc ggt caa tta gaa gag gtg att ctt cag gct						296
Glu Asp Gln Leu Gln Gly Gly Gln Leu Glu Glu Val Ile Leu Gln Ala						
	70		75		80	
gaa cat gaa cta aat ctg gca aga aaa atg agg gaa tgg aaa cta tgg						344
Glu His Glu Leu Asn Leu Ala Arg Lys Met Arg Glu Trp Lys Leu Trp						
	85		90		95	
gag cca tta gtg gaa gag cct cct gcc gat cag tgg aaa tgg cca ata						392
Glu Pro Leu Val Glu Glu Pro Pro Ala Asp Gln Trp Lys Trp Pro Ile						
	105		110		115	
taattattaa gtgactttgg tgtgttcacg ggaaactgat gtaattaaat attctgttat						452
attaagagcg tggtcttatt actgacattt tgtaatcaag aaaagtgat						501

<210> 3845
 <211> 449
 <212> DNA
 <213> Homo sapiens

 <220>
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 <222> 125..436

 <400> 3845
 ctacgcgggg caggccagcc ctggggcgcc ttaaaaaccg gagctggcgc ttggcatcgc
 cactctgggc aggatccaac gtcgctccag ctgctcttga cgactccaca gataccccga
 agcc atg gca agc aag ggc ttg cag gac ctg aag caa cag gtg gag ggg
 Met Ala Ser Lys Gly Leu Gln Asp Leu Lys Gln Gln Val Glu Gly
 1 5 10 15
 acc gcc cag gaa gcc gtg tca gcg gcc gga gcg gca gct cag caa gtg
 Thr Ala Gln Glu Ala Val Ser Ala Ala Gly Ala Ala Gln Gln Val
 20 25 30
 gtg gac cag gcc aca gag gcg ggg cag aaa gcc atg gac cag ctg gcc
 Val Asp Gln Ala Thr Glu Ala Gly Gln Lys Ala Met Asp Gln Leu Ala
 35 40 45
 aag acc acc cag gaa acc atc gac aag act gct aac cag gcc tct gac
 Lys Thr Thr Gln Glu Thr Ile Asp Lys Thr Ala Asn Gln Ala Ser Asp
 50 55 60
 acc ttc tct ggg atc ggg aaa aaa ttc ggc ctg gag ctt ccc ttg ctc
 Thr Phe Ser Gly Ile Gly Lys Lys Phe Gly Leu Glu Leu Pro Leu Leu
 65 70 75
 cct gag gga agg cct aga ggc ctc atc ctt gtg ggg ccc caa ggt cct
 Pro Glu Gly Arg Pro Arg Gly Leu Ile Leu Val Gly Pro Gln Gly Pro
 80 85 90 95
 agc atg agg ctg gac ttc gta tgg tgg tgaagaacag agt
 Ser Met Arg Leu Asp Phe Val Trp Trp
 100

<210> 3846
 <211> 602
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 34..495

<400> 3846
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 Met Ala Ala Ser Arg Arg Leu
 1 5
 atg aag gag ctt gaa gaa atc cgc aaa tgt ggg atg aaa aac ttc cgt 102
 Met Lys Glu Leu Glu Glu Ile Arg Lys Cys Gly Met Lys Asn Phe Arg
 10 15 20
 aac atc cag gtt gat gaa gct aat tta ttg act tgg caa ggg ctt att 150
 Asn Ile Gln Val Asp Glu Ala Asn Leu Leu Thr Trp Gln Gly Leu Ile
 25 30 35
 gtt cct gac aac cct cca tat gat aag gga gcc ttc aga atc gaa atc 198
 Val Pro Asp Asn Pro Pro Tyr Asp Lys Gly Ala Phe Arg Ile Glu Ile
 40 45 50 55
 aac ttt cca gca gag tac cca ttc aaa cca ccg aag atc aca ttt aaa 246
 Asn Phe Pro Ala Glu Tyr Pro Phe Lys Pro Pro Lys Ile Thr Phe Lys
 60 65 70
 aca aag atc tat cac cca aac atc gac gaa aag ggg cag gtc tgt ctg 294
 Thr Lys Ile Tyr His Pro Asn Ile Asp Glu Lys Gly Gln Val Cys Leu
 75 80 85
 cca gta att agt gcc gaa aac tgg aag cca gca acc aaa acc gac caa 342
 Pro Val Ile Ser Ala Glu Asn Trp Lys Pro Ala Thr Lys Thr Asp Gln
 90 95 100
 gta atc cag tcc ctc ata gca ctg gtg aat gac ccc cag cct gag cac 390
 Val Ile Gln Ser Leu Ile Ala Leu Val Asn Asp Pro Gln Pro Glu His
 105 110 115
 ccg ctt cgg gct gac cta gct gaa gaa tac tct aag gac cgt aaa aaa 438
 Pro Leu Arg Ala Asp Leu Ala Glu Glu Tyr Ser Lys Asp Arg Lys Lys
 120 125 130 135
 ttc tgt aag aat gct gaa gag ttt aca aag aaa tat ggg gaa aag cga 486
 Phe Cys Lys Asn Ala Glu Glu Phe Thr Lys Lys Tyr Gly Glu Lys Arg
 140 145 150
 cct gtg gac taaaatctgc cacgattggt tccagcaagt gtgagcagag 535
 Pro Val Asp
 acngcgtgca gtgcattcag acaccccgca aagcaggact ctgtggaaat tgacacgtgc 595
 caccgsc 602

<210> 3847
 <211> 506
 <212> DNA
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<220>
 <221> CDS
 <222> 34..399

004220"6667560

<400> 3847
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Met Ala Ala Ser Arg Arg Leu
1 5
acg aag gac aac cct cca tat gat aag gga gcc ttc aga atc gaa atc 102
Thr Lys Asp Asn Pro Pro Tyr Asp Lys Gly Ala Phe Arg Ile Glu Ile
10 15 20
aac ttt cca gca gag tac cca ttc aaa cca ccg aag atc aca ttt aaa 150
Asn Phe Pro Ala Glu Tyr Pro Phe Lys Pro Pro Lys Ile Thr Phe Lys
25 30 35
aca aag atc tat cac cca aac atc gac gaa aag ggg cag gtc tgt ctg 198
Thr Lys Ile Tyr His Pro Asn Ile Asp Glu Lys Gly Gln Val Cys Leu
40 45 50 55
cca gta att agt gcc gaa aac tgg aag cca gca acc aaa acc gac caa 246
Pro Val Ile Ser Ala Glu Asn Trp Lys Pro Ala Thr Lys Thr Asp Gln
60 65 70
gta atc cag tcc ctc ata gca ctg gtg aat gac ccc cag cct gag cac 294
Val Ile Gln Ser Leu Ile Ala Leu Val Asn Asp Pro Gln Pro Glu His
75 80 85
ccg ctt cgg gct gac cta gct gaa gaa tac tct aag gac cgt aaa aaa 342
Pro Leu Arg Ala Asp Leu Ala Glu Glu Tyr Ser Lys Asp Arg Lys Lys
90 95 100
ttc tgt aag aat gct gaa gag ttt aca aag aaa tat ggg gaa aag cga 390
Phe Cys Lys Asn Ala Glu Glu Phe Thr Lys Lys Tyr Gly Glu Lys Arg
105 110 115
cct gtg gac taaaatctgc cacgattggt tccagcaagt gtgagcagag 439
Pro Val Asp
120
acngcgtgca gtgcattcag acaccccgca aagcaggact ctgtggaaat tgacacgtgc 499
cascgsc 506

<210> 3848
<211> 720
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 61..687

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atg agt atg ctc agg ctt cag aag agg ctc gcc tct agt gtc ctc cgc 108
Met Ser Met Leu Arg Leu Gln Lys Arg Leu Ala Ser Ser Val Leu Arg
1 5 10 15
tgt ggc aag aag aag gtc tgg tta gac ccc aat gag acc aat gaa atc 156
Cys Gly Lys Lys Lys Val Trp Leu Asp Pro Asn Glu Thr Asn Glu Ile
20 25 30
gcc aat gcc aac tcc cgt cag cag atc cgg aag ctc atc aaa gat ggg 204
Ala Asn Ala Asn Ser Arg Gln Gln Ile Arg Lys Leu Ile Lys Asp Gly
35 40 45

ctg atc atc cgc aag cct gtg acg gtc cat tcc cgg gct cga tgc cgg	252
Leu Ile Ile Arg Lys Pro Val Thr Val His Ser Arg Ala Arg Cys Arg	
50 55 60	
aaa aac acc ttg gcc cgc cgg aag ggc agg cac atg ggc ata ggt aag	300
Lys Asn Thr Leu Ala Arg Arg Lys Gly Arg His Met Gly Ile Gly Lys	
65 70 75 80	
cgg aag ggt aca gcc aat gcc cga atg cca gag aag gtc aca tgg atg	348
Arg Lys Gly Thr Ala Asn Ala Arg Met Pro Glu Lys Val Thr Trp Met	
85 90 95	
agg aga atg agg att ttg cgc cgg ctg ctc aga aga tac cgt gaa tct	396
Arg Arg Met Arg Ile Leu Arg Arg Leu Leu Arg Arg Tyr Arg Glu Ser	
100 105 110	
aag aag atc gat cgc cac atg tat cac agc ctg tac ctg aag gtg aag	444
Lys Lys Ile Asp Arg His Met Tyr His Ser Leu Tyr Leu Lys Val Lys	
115 120 125	
ggg aat gtg ttc aaa aac aag cgg att ctc atg gaa cac atc cac aag	492
Gly Asn Val Phe Lys Asn Lys Arg Ile Leu Met Glu His Ile His Lys	
130 135 140	
ctg aag gca gac aag gcc cgc aag aag ctc ctg gct gac cag gct gag	540
Leu Lys Ala Asp Lys Ala Arg Lys Lys Leu Leu Ala Asp Gln Ala Glu	
145 150 155 160	
gcc cgc agg tct aag acc aag gaa gca cgc aag cgc cgt gaa gag cgc	588
Ala Arg Arg Ser Lys Thr Lys Glu Ala Arg Lys Arg Arg Glu Glu Arg	
165 170 175	
ctc crg ggc caa gaa gga rgg aga tca nna aga ctt tat cca agg agg	636
Leu Xaa Gly Gln Glu Gly Xaa Arg Ser Xaa Arg Leu Tyr Pro Arg Arg	
180 185 190	
aag aga cca aga aat aaa acc tcc cac ttt gtc tgt aca tac tgg cct	684
Lys Arg Pro Arg Asn Lys Thr Ser His Phe Val Cys Thr Tyr Trp Pro	
195 200 205	
ctg tgattatatt yatcagccat taaaataaaa caa	720
Leu	

<210> 3849
 <211> 367
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 6..332

<400> 3849	
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Met Gly Gly Ala Gly Pro Glu Arg Ala Leu Ser Phe Arg Cys Cys	
1 5 10 15	
ggc cgc asc atg agt atg ctc agg ctt cag aag agg ctc gcc tct agt	98
Gly Arg Xaa Met Ser Met Leu Arg Leu Gln Lys Arg Leu Ala Ser Ser	
20 25 30	
gtc ctc cgc tgt ggc aag aag aag gtc tgg tta gac ccc aat gag acc	146
Val Leu Arg Cys Gly Lys Lys Lys Val Trp Leu Asp Pro Asn Glu Thr	
35 40 45	
aat gaa atc gcc aat gcc aac tcc cgt cag cag atc cgg aag ctc atc	194

Asn	Glu	Ile	Ala	Asn	Ala	Asn	Ser	Arg	Gln	Gln	Ile	Arg	Lys	Leu	Ile		
	50						55					60					
aaa	gat	ggg	ctg	atc	atc	cgc	aag	cct	gtg	acg	gtc	cat	tcc	cgg	gct		242
Lys	Asp	Gly	Leu	Ile	Ile	Arg	Lys	Pro	Val	Thr	Val	His	Ser	Arg	Ala		
	65						70				75						
cga	tgc	cgg	aaa	aac	acc	ttg	gcc	cgc	cgg	aag	ggc	agg	cac	atg	ggc		290
Arg	Cys	Arg	Lys	Asn	Thr	Leu	Ala	Arg	Arg	Lys	Gly	Arg	His	Met	Gly		
	80				85					90					95		
ata	ggt	aag	cgg	aag	ggt	aca	gcc	aat	gcc	crc	ccc	tcc	ggc				332
Ile	Gly	Lys	Arg	Lys	Gly	Thr	Ala	Asn	Ala	Xaa	Pro	Ser	Gly				
				100					105								
tagctcgctg	gctcccggt	cctcccgacg	tctcc														367

<210> 3850
 <211> 361
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 5..346

<400>	3850																
aaca	atg	gcc	caa	gtt	ttg	ttc	agc	agg	aat	atg	aga	ttg	aat	gta	gct		49
	Met	Ala	Gln	Val	Leu	Phe	Ser	Arg	Asn	Met	Arg	Leu	Asn	Val	Ala		
	1				5					10				15			
tta	act	ttc	tgg	aga	aag	aga	agt	ata	agt	gaa	ctt	gta	gct	tat	ttg		97
Leu	Thr	Phe	Trp	Arg	Lys	Arg	Ser	Ile	Ser	Glu	Leu	Val	Ala	Tyr	Leu		
				20				25					30				
ttg	agg	ata	gaa	gat	ctt	ggc	gtt	gtg	gta	gat	tgc	ctt	cct	gtg	ctc		145
Leu	Arg	Ile	Glu	Asp	Leu	Gly	Val	Val	Val	Asp	Cys	Leu	Pro	Val	Leu		
			35				40				45						
acc	aat	tgt	tta	cag	gaa	gaa	aaa	caa	tat	atc	tca	ctt	ggc	tgc	tgt		193
Thr	Asn	Cys	Leu	Gln	Glu	Glu	Lys	Gln	Tyr	Ile	Ser	Leu	Gly	Cys	Cys		
	50					55					60						
gtt	gac	ttg	ttg	cct	cta	gta	aag	tca	cta	ctt	aaa	agc	aaa	ttt	gaa		241
Val	Asp	Leu	Leu	Pro	Leu	Val	Lys	Ser	Leu	Leu	Lys	Ser	Lys	Phe	Glu		
	65				70					75							
gaa	tat	gtt	ata	gtt	ggt	tta	aac	tgg	ctt	caa	gca	gtc	att	aaa	agg		289
Glu	Tyr	Val	Ile	Val	Gly	Leu	Asn	Trp	Leu	Gln	Ala	Val	Ile	Lys	Arg		
	80				85				90					95			
tgg	tgg	tca	gaa	cta	tca	tcc	aaa	aca	gaa	att	ata	aat	gat	gga	aat		337
Trp	Trp	Ser	Glu	Leu	Ser	Ser	Lys	Thr	Glu	Ile	Ile	Asn	Asp	Gly	Asn		
				100					105					110			
att	caa	att	taaaacaaca	attaa													361
Ile	Gln	Ile															

<210> 3851
 <211> 493
 <212> DNA
 <213> Homo sapiens

<220>

<221> CDS
<222> 120..470

<400> 3851
gggtctctgt aagagtcaca cgctttgggc atccttgaaa agaattcttct gaggcctcag 60
cattttatct gagtcttctg aatcccactt agaactgtgt tgagctctca cccatcacg 119
atg agc aac aaa ttc ctg ggc acc tgg aaa ctt gtc tct agt gag aac 167
Met Ser Asn Lys Phe Leu Gly Thr Trp Lys Leu Val Ser Ser Glu Asn
1 5 10 15
ttt gac gat tac atg aaa gct ctg ggt gtg ggg tta gcc acc aga aaa 215
Phe Asp Asp Tyr Met Lys Ala Leu Gly Val Gly Leu Ala Thr Arg Lys
20 25 30
ctg gga aat ttg gcc aaa ccc act gtg atc atc agc aag aaa gga gat 263
Leu Gly Asn Leu Ala Lys Pro Thr Val Ile Ile Ser Lys Lys Gly Asp
35 40 45
att ata act ata cga act gaa agt acc ttt aaa aat aca gaa atc tcc 311
Ile Ile Thr Ile Arg Thr Glu Ser Thr Phe Lys Asn Thr Glu Ile Ser
50 55 60
ttc aag cta ggc cag gaa ttt gaa gaa acc aca gct gac aat aga aag 359
Phe Lys Leu Gly Gln Glu Phe Glu Glu Thr Thr Ala Asp Asn Arg Lys
65 70 75 80
acc aag agc atc gta acc ctg cag aga gga tca ctg aat caa gtg cag 407
Thr Lys Ser Ile Val Thr Leu Gln Arg Gly Ser Leu Asn Gln Val Gln
85 90 95
aga tgg gat ggc aaa gag aca acc ata aag aga gct agt gar tgg gaa 455
Arg Trp Asp Gly Lys Glu Thr Thr Ile Lys Arg Ala Ser Glu Trp Glu
100 105 110
aat ggt agc gga atg traaatgaag ggcgtggtgt gca 493
Asn Gly Ser Gly Met
115

<210> 3852
<211> 478
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 84..416

<400> 3852
tagaaggtaa cttccggtga cgggggttgca tcaacttctc tcaagcttgg cgtttggttg 60
gtgggggttac acgcgggttc aac atg cgt atc gaa aag tgt tat ttc tgt tcg 113
Met Arg Ile Glu Lys Cys Tyr Phe Cys Ser
1 5 10
ggg ccc atc tat cct gga cac ggc atg atg ttc gtc cgc aac gat tgc 161
Gly Pro Ile Tyr Pro Gly His Gly Met Met Phe Val Arg Asn Asp Cys
15 20 25
aag gtg ttc aga ttt tgc aaa tct aaa tgt cat aaa aac ttt aaa aag 209
Lys Val Phe Arg Phe Cys Lys Ser Lys Cys His Lys Asn Phe Lys Lys
30 35 40
aag cgc aat cct cgc aaa gtt agg tgg acc aaa gca ttc cgg aaa gca 257

Lys Arg Asn Pro Arg Lys Val Arg Trp Thr Lys Ala Phe Arg Lys Ala
 45 50 55
 gct ggt aaa gag ctt aca gtg gat aat tca ttt gaa ttt gaa aaa cgt 305
 Ala Gly Lys Glu Leu Thr Val Asp Asn Ser Phe Glu Phe Glu Lys Arg
 60 65 70
 aga aat gaa cct atc aaa tac cag cga gag cta tgg aat aaa act att 353
 Arg Asn Glu Pro Ile Lys Tyr Gln Arg Glu Leu Trp Asn Lys Thr Ile
 75 80 85 90
 gat gcg atg aag aga gtt gaa gaa atc aaa cag aag cgc cna gct aaa 401
 Asp Ala Met Lys Arg Val Glu Glu Ile Lys Gln Lys Arg Xaa Ala Lys
 95 100 105
 ttt ata atg aac aga tgaagaaaat taaagagcta caggangngt tcaggatatc 456
 Phe Ile Met Asn Arg
 110
 aaagaagtca agcaaaccatc ca 478

 <210> 3853
 <211> 518
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> CDS
 <222> 66..458

 <400> 3853
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 ccatc atg aac gac acc gta act atc cgc act aga aag ttc atg acc aac 110
 Met Asn Asp Thr Val Thr Ile Arg Thr Arg Lys Phe Met Thr Asn
 1 5 10 15
 cga cta ctt cag agg aaa caa atg gtc att gat gtc ctt cac ccc ggg 158
 Arg Leu Leu Gln Arg Lys Gln Met Val Ile Asp Val Leu His Pro Gly
 20 25 30
 aag gcg aca gtg cct aag aca gaa att cgg gaa aaa cta gcc aaa atg 206
 Lys Ala Thr Val Pro Lys Thr Glu Ile Arg Glu Lys Leu Ala Lys Met
 35 40 45
 tac aag acc aca ccg gat gtc atc ttt gta ttt gga ttc aga act cat 254
 Tyr Lys Thr Thr Pro Asp Val Ile Phe Val Phe Gly Phe Arg Thr His
 50 55 60
 ttt ggt ggt ggc aag aca act ggc ttt ggc atg att tat gat tcc ctg 302
 Phe Gly Gly Gly Lys Thr Thr Gly Phe Gly Met Ile Tyr Asp Ser Leu
 65 70 75
 gat tat gca aag aaa aat gaa ccc aaa cat aga ctt gca aga cat ggc 350
 Asp Tyr Ala Lys Lys Asn Glu Pro Lys His Arg Leu Ala Arg His Gly
 80 85 90 95
 ctg tat gag aag aaa aag acc tca aga aag caa cga aag gaa cgc aag 398
 Leu Tyr Glu Lys Lys Lys Thr Ser Arg Lys Gln Arg Lys Glu Arg Lys
 100 105 110
 aac aga atg aag aaa gtc agg ggg act gca aag gcc aat gtt ggt gct 446
 Asn Arg Met Lys Lys Val Arg Gly Thr Ala Lys Ala Asn Val Gly Ala
 115 120 125
 ggc aaa aag aag tgagctggag attggatcac agccgaagga gtaaaggtgc 498
 Gly Lys Lys Lys

130
tgcaatgatg ttagctgtgg

518

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<211> 716
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 26..706

<400> 3854
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Met Ala Ala Gly Met Tyr Leu Glu His
1 5
tat ctg gac agt att gaa aac ctt ccc ttt gaa tta cag aga aac ttt 100
Tyr Leu Asp Ser Ile Glu Asn Leu Pro Phe Glu Leu Gln Arg Asn Phe
10 15 20 25
cag ctc atg agg gac cta gac caa aga aca gag gac ctg aag gct gaa 148
Gln Leu Met Arg Asp Leu Asp Gln Arg Thr Glu Asp Leu Lys Ala Glu
30 35 40
att gac aag ttg gcc act gag tat atg agt agt gcc cgc agc ctg agc 196
Ile Asp Lys Leu Ala Thr Glu Tyr Met Ser Ser Ala Arg Ser Leu Ser
45 50 55
tcc gag gaa aaa ttg gcc ctt ctc aaa cag atc cag gaa gcc tat ggc 244
Ser Glu Glu Lys Leu Ala Leu Leu Lys Gln Ile Gln Glu Ala Tyr Gly
60 65 70
aag tgc aag gaa ttt ggt gac gac aag gtg cag ctt gcc atg cag acc 292
Lys Cys Lys Glu Phe Gly Asp Asp Lys Val Gln Leu Ala Met Gln Thr
75 80 85
tat gag atg gtg gac aaa cac att cgg cgg ctg gac aca gac ctg gcc 340
Tyr Glu Met Val Asp Lys His Ile Arg Arg Leu Asp Thr Asp Leu Ala
90 95 100 105
cgt ttt gag gct gat ctc aag gag aaa cag att gag tca agt gac tat 388
Arg Phe Glu Ala Asp Leu Lys Glu Lys Gln Ile Glu Ser Ser Asp Tyr
110 115 120
gac agc tct tcc agc aaa ggc aaa aag agc cgg act caa aag gag aag 436
Asp Ser Ser Ser Ser Lys Gly Lys Lys Ser Arg Thr Gln Lys Glu Lys
125 130 135
aaa gct gct cgt gct cgt tcc aaa ggg raa aac tcg gat gaa gaa gcc 484
Lys Ala Ala Arg Ala Arg Ser Lys Gly Xaa Asn Ser Asp Glu Glu Ala
140 145 150
ccc aag act rcc cag aag aag tta aag ctc gtg cgc aca agt cct gag 532
Pro Lys Thr Xaa Gln Lys Lys Leu Lys Leu Val Arg Thr Ser Pro Glu
155 160 165
tat ggg awg ccc tca gtg acc ttt ggc agt gtc cac ccc tct gat gtg 580
Tyr Gly Xaa Pro Ser Val Thr Phe Gly Ser Val His Pro Ser Asp Val
170 175 180 185
ttg gat atg cct gtg gat ccc aac gaa ccc acc tat tgc ctt tgt cac 628
Leu Asp Met Pro Val Asp Pro Asn Glu Pro Thr Tyr Cys Leu Cys His
190 195 200
cag gtc tcc tat gga gag atg att ggc tgt gac acc ctg att gtt cca 676

Gln Val Ser Tyr Gly Glu Met Ile Gly Cys Asp Thr Leu Ile Val Pro
 205 210 215
 ttg agt nnt tcc att ttg cct gtg tgg ggc tgacaaccaa 716
 Leu Ser Xaa Ser Ile Leu Pro Val Trp Gly
 220 225

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 <212> DNA
 <213> Homo sapiens

<220>
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 <222> 212..514

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 ctttctgtgt ttgttctctg cctgccaag gccgtagagc tgggtgcgtgc gggtagcggg 180
 gctctccgag gagccgcacg ccggcggcac c atg gtc cac ctc act act ctc 232
 Met Val His Leu Thr Thr Leu
 1 5
 ctc tgc aag gcc tac cgt ggg ggc cac tta acc atc cgc ctt gcc ctg 280
 Leu Cys Lys Ala Tyr Arg Gly Gly His Leu Thr Ile Arg Leu Ala Leu
 10 15 20
 ggt ggc tgc acc aat cgg ccg ttc tac cgc att gtg gct gct cac aac 328
 Gly Gly Cys Thr Asn Arg Pro Phe Tyr Arg Ile Val Ala Ala His Asn
 25 30 35
 aag tgt ccc agg gat ggc cgt ttc gta gag cag ctg ggc tcc tat gat 376
 Lys Cys Pro Arg Asp Gly Arg Phe Val Glu Gln Leu Gly Ser Tyr Asp
 40 45 50 55
 cca ttg ccc aac agt cat gga gaa aaa ctc gtt gcc ctc aac cta gac 424
 Pro Leu Pro Asn Ser His Gly Glu Lys Leu Val Ala Leu Asn Leu Asp
 60 65 70
 agg atc cgt cat tgg att ggc tgc ggg gcc cac ctc tct aag cct atg 472
 Arg Ile Arg His Trp Ile Gly Cys Gly Ala His Leu Ser Lys Pro Met
 75 80 85
 gaa aag ctt ctg ggt ctt gct ggc ttt ttc ctc tgc atc cta 514
 Glu Lys Leu Leu Gly Leu Ala Gly Phe Phe Leu Cys Ile Leu
 90 95 100
 tgatgtcaca aatgctgaga gactgcgaag gaaacgggca cgtgaagtcc tgtagcttc 574
 tcagaaaaca gatgcagaag ctacagat 602

<210> 3856
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<220>
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 <222> 18..392

<400> 3856

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actagtttct aaggatc atg tct gcg agc cag gat tcc cga tcc aga gac      50
          Met Ser Ala Ser Gln Asp Ser Arg Ser Arg Asp
              1              5              10

aat ggc ccc gat ggg atg gag ccc gaa ggc gtc atc gag agt aac tgg      98
Asn Gly Pro Asp Gly Met Glu Pro Glu Gly Val Ile Glu Ser Asn Trp
              15              20              25

aat gag att gtt gac agc ttt gat gac atg aac ctc tcg gag tcc ctt      146
Asn Glu Ile Val Asp Ser Phe Asp Asp Met Asn Leu Ser Glu Ser Leu
              30              35              40

ctc cgt ggc atc tac gcc tat ggt ttt gag aag ccc tct gcc atc cag      194
Leu Arg Gly Ile Tyr Ala Tyr Gly Phe Glu Lys Pro Ser Ala Ile Gln
              45              50              55

cag cga gcc att cta cct tgt atc aag ggt tat gat gtg att gct caa      242
Gln Arg Ala Ile Leu Pro Cys Ile Lys Gly Tyr Asp Val Ile Ala Gln
              60              65              70              75

gcc caa tct ggg act ggg aaa acg gcc aca ttt gcc ata tca att ctg      290
Ala Gln Ser Gly Thr Gly Lys Thr Ala Thr Phe Ala Ile Ser Ile Leu
              80              85              90

cag cag att gaa tta gat cta aaa gcc acc cag gcc ttg gtc cta gca      338
Gln Gln Ile Glu Leu Asp Leu Lys Ala Thr Gln Ala Leu Val Leu Ala
              95              100              105

ccc act cga gaa ttg gct cag cag ata cag aag gtg gtc atg gca ctc      386
Pro Thr Arg Glu Leu Ala Gln Gln Ile Gln Lys Val Val Met Ala Leu
              110              115              120

ttg tgg taagaagtg      401
Leu Trp
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<210> 3857

<211> 425

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 18..341

<400> 3857

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          Met Ser Ala Ser Gln Asp Ser Arg Ser Arg Asp
              1              5              10

aat ggc ccc gat ggg atg gag ccc gaa ggc gtc atc gag agt aac tgg      98
Asn Gly Pro Asp Gly Met Glu Pro Glu Gly Val Ile Glu Ser Asn Trp
              15              20              25

aat gag att gtt gac agc ttt gat gac atg aac ctc tcg gag tcc ctt      146
Asn Glu Ile Val Asp Ser Phe Asp Asp Met Asn Leu Ser Glu Ser Leu
              30              35              40

ctc cgt ggc atc tac gcc tat ggt ttt gag aag ccc tct gcc atc cag      194
Leu Arg Gly Ile Tyr Ala Tyr Gly Phe Glu Lys Pro Ser Ala Ile Gln
              45              50              55

cag cga gcc att cta cct tgt atc aag ggt tat gat gtg att gct caa      242
Gln Arg Ala Ile Leu Pro Cys Ile Lys Gly Tyr Asp Val Ile Ala Gln

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60	65	70	75	
gcc caa tct ggg act ggg aaa acg gcc aca ttt gcc ata tcg att ctg				290
Ala Gln Ser Gly Thr Gly Lys Thr Ala Thr Phe Ala Ile Ser Ile Leu				
	80	85	90	
cag cag att gaa tta gat cta aaa gcc acc cag nct ttc tca ggt cat				338
Gln Gln Ile Glu Leu Asp Leu Lys Ala Thr Gln Xaa Phe Ser Gly His				
	95	100	105	
ttt taataataga agagtctagg attaataattg ttataaacat caagcttaat				391
Phe				
agttgttttt tttataaaga aatgtttcca ttag				425

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 <211> 443
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 114..434

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	Met
	1
gac cca agt ggg gtc aaa gtg ctg gaa aca gca gag gac atc cag gag	164
Asp Pro Ser Gly Val Lys Val Leu Glu Thr Ala Glu Asp Ile Gln Glu	
	5 10 15
agg cgg cag cag gtc cta gac cga tac cac cgc ttc aag gaa ctc tca	212
Arg Arg Gln Gln Val Leu Asp Arg Tyr His Arg Phe Lys Glu Leu Ser	
	20 25 30
acc ctt agg cgt cag aag ctg gaa gat tcc tat cga ttc cag ttc ttt	260
Thr Leu Arg Arg Gln Lys Leu Glu Asp Ser Tyr Arg Phe Gln Phe Phe	
	35 40 45
caa aga gat gct gaa gag ctg gag aaa tgg ata cag gaa aaa ctt cag	308
Gln Arg Asp Ala Glu Leu Glu Lys Trp Ile Gln Glu Lys Leu Gln	
	50 55 60 65
att gca tct gat gag aat tat aaa gac cca acc aac ttg cag gga aag	356
Ile Ala Ser Asp Glu Asn Tyr Lys Asp Pro Thr Asn Leu Gln Gly Lys	
	70 75 80
ctt cag aag cat caa gca ttt gaa gct gaa gtg cag gcc aac tca gga	404
Leu Gln Lys His Gln Ala Phe Glu Ala Glu Val Gln Ala Asn Ser Gly	
	85 90 95
gcc att gtt aag ctg gat gaa ctg gaa acc tgatgatct	443
Ala Ile Val Lys Leu Asp Glu Leu Glu Thr	
	100 105

<210> 3859
 <211> 446
 <212> DNA
 <213> Homo sapiens

<220>

SECRET

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<210> 3860
<211> 377
<212> DNA
<213> Homo sapiens
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Leu Met Ser Xaa Ser Thr Ala Asn Ala Lys Lys Asp Pro Ser Cys Lys
80 85 90 95
acc tgt aat atc agt gtt gga cgt taa 377
Thr Cys Asn Ile Ser Val Gly Arg
100

<210> 3861
<211> 741
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 62..412

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g atg aag ttc gtg tac aaa gaa gag cat ccg ttc gag aag cgc cgc tct 109
Met Lys Phe Val Tyr Lys Glu Glu His Pro Phe Glu Lys Arg Arg Ser
1 5 10 15
gag ggc gag aag atc cga aag aaa tac ccg gac cgg gtg ccg gtg ata 157
Glu Gly Glu Lys Ile Arg Lys Lys Tyr Pro Asp Arg Val Pro Val Ile
20 25 30
gta gaa aag gct ccc aaa gct cgg ata gga gac ctg gac aaa aag aaa 205
Val Glu Lys Ala Pro Lys Ala Arg Ile Gly Asp Leu Asp Lys Lys Lys
35 40 45
tac ctg gtg cct tct gat ctc aca gtt ggt cag ttc tac ttc ttg atc 253
Tyr Leu Val Pro Ser Asp Leu Thr Val Gly Gln Phe Tyr Phe Leu Ile
50 55 60
cgg aag cga att cat ctc cga gct gag gat gcc ttg ttt ttt gtc 301
Arg Lys Arg Ile His Leu Arg Ala Glu Asp Ala Leu Phe Phe Phe Val
65 70 75 80
aac aat gtc att cca ccc acc agt gcc aca atg ggt cag ctg tac cag 349
Asn Asn Val Ile Pro Thr Ser Ala Thr Met Gly Gln Leu Tyr Gln
85 90 95
gaa cac cat gaa gaa gac ttc ttt ctc tac att gcc tac agt gac gaa 397
Glu His His Glu Glu Asp Phe Phe Leu Tyr Ile Ala Tyr Ser Asp Glu
100 105 110
agt gtc tac ggt ctg tgaagctgct gccctgagc tggagggggg tctcattcta 452
Ser Val Tyr Gly Leu
115
caaagagaga ggtggcccc ctttcttgam cntcctcctc cttcaagctc aaacaccacc 512
tcccttattc aggaccggca cttcttaatg tttgtggctt tctctccagc ctctcttagg 572
aggggtaatg gtggagtgg catcttgtaa ctctccttctc tcccttctctc ccctttctct 632
gccgccttt cccatcctgc ttagacttctc ttgattgtca gtctgtgtca catccagtga 692
ttgttttggg ttctgttccc tttctgactg cccaagggggc tcagaaccc 741

<210> 3862
<211> 655
<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 196..513

<400> 3862

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acctggtgcc ttctgatctc acagttggtc agttctactt cttgatccgg aagcgaattc 180
atctccgagc tgagg atg cct tgt ttt tct ttg tca aca atg tca ttc cac 231
Met Pro Cys Phe Ser Leu Ser Thr Met Ser Phe His
1 5 10
cca cca gtg cca caa tgg gtc agc tgt acc agg aac acc atg aag aag 279
Pro Pro Val Pro Gln Trp Val Ser Cys Thr Arg Asn Thr Met Lys Lys
15 20 25
act tct ttc tct aca ttg cct aca gtg acg aaa gtg tct acg gtc tgt 327
Thr Ser Phe Ser Thr Leu Pro Thr Val Thr Lys Val Ser Thr Val Cys
30 35 40
gaa gct gct gcc cct gag ctg gag ggg ggt ctc att cta caa aga gag 375
Glu Ala Ala Ala Pro Glu Leu Glu Gly Gly Leu Ile Leu Gln Arg Glu
45 50 55 60
agg tgg ccc ccc ttt ctt grm cnt cct cct cct tca agc tca aac acc 423
Arg Trp Pro Pro Phe Leu Xaa Xaa Pro Pro Pro Ser Ser Ser Asn Thr
65 70 75
acc tcc ctt att cag gac cgg cac ttc tta atg ttt gtg gct ttc tct 471
Thr Ser Leu Ile Gln Asp Arg His Phe Leu Met Phe Val Ala Phe Ser
80 85 90
cca gcc tct ctt agg agg ggt aat ggt gga gtt ggc atc ttg 513
Pro Ala Ser Leu Arg Arg Gly Asn Gly Gly Val Gly Ile Leu
95 100 105
taactctcct ttctcctttc ttcccctttc tctgcccgcc ttcccatcc tgctgtagac 573
ttcttgattg tcagtctgtg tcacatccag tgattgtttt gggttctgtt ccctttctga 633
ctgcccagg ggctcagaac cc 655

<210> 3863

<211> 697

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 62..412

<400> 3863

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g atg aag ttc gtg tac aaa gaa gag cat ccg ttc gag aag cgc cgc tct 109
Met Lys Phe Val Tyr Lys Glu Glu His Pro Phe Glu Lys Arg Arg Ser
1 5 10 15
gag ggc gag aag atc cga aag aaa tac ccg gac cgg gtg ccg gtg ata 157
Glu Gly Glu Lys Ile Arg Lys Lys Tyr Pro Asp Arg Val Pro Val Ile
20 25 30

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gta gaa aag gct ccc aaa gct cgg ata gga gac ctg gac aaa aag aaa      205
Val Glu Lys Ala Pro Lys Ala Arg Ile Gly Asp Leu Asp Lys Lys Lys
      35              40              45
tac ctg gtg cct tct gat ctc aca gtt ggt cag ttc tac ttc ttg atc      253
Tyr Leu Val Pro Ser Asp Leu Thr Val Gly Gln Phe Tyr Phe Leu Ile
      50              55              60
cgg aag cga att cat ctc cga gct gag gat gcc ttg ttt ttc ttt gtc      301
Arg Lys Arg Ile His Leu Arg Ala Glu Asp Ala Leu Phe Phe Phe Val
      65              70              75              80
aac aat gtc att cca ccc acc agt gcc aca atg ggt cag ctg tac cag      349
Asn Asn Val Ile Pro Pro Thr Ser Ala Thr Met Gly Gln Leu Tyr Gln
      85              90              95
gaa cac cat gaa gaa gac ttc ttt ctc tac att gcc tac agt gac gaa      397
Glu His His Glu Glu Asp Phe Phe Leu Tyr Ile Ala Tyr Ser Asp Glu
      100             105             110
agt gtc tac ggt ctg tgaagctgct gccctttct tgacctctc ctccttcaag      452
Ser Val Tyr Gly Leu
      115
ctcaaacacc acctccctta ttcaggaccg gcacttctta atgtttgtgg ctttctctsc      512
aagccttctc ttaagraggg gtaatggtgg agttggcatc ttgtaactct cctttctcct      572
ttcttccctt ttctctgccc gcctttccca tctgtctgta gacttcttga ttgtcagtct      632
gtgtcacatc cagtgattgt tttggtttct gttcccttcc tgactgccca aggggctcag      692
aaccc                                           697

<210> 3864
<211> 801
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 409..783

<400> 3864
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cgtttawcag tgcaaggaaa acagcgctat agtactgcgt cacaactagc gcagactccg      180
gcagtattta ggcggtgcgg cttgggaact agaatccgct tctgtcttc cgcctcaggc      240
tagaggcgca gcgcttcgcc gtgggacttc ctctgcctgg ctccgctctt tgccccggaa      300
gtactcacag cggacggtgg tttttgggca cgtttctgag cagcgcttcc tttttgtccg      360
acatcttgac gaggtgcgg tgtctgctgc tattctccga gcttcgca atg ccg cct      417
                                           Met Pro Pro
                                           1
aag gac gac aag aag aag aag gac gct gga aag tcg gcc aag aaa gac      465
Lys Asp Asp Lys Lys Lys Lys Asp Ala Gly Lys Ser Ala Lys Lys Asp
      5              10              15
aaa gac cca gtg aac aaa tcc ggg ggc aag gcc aaa aag aag aag tgg      513
Lys Asp Pro Val Asn Lys Ser Gly Gly Lys Ala Lys Lys Lys Lys Trp
      20              25              30              35
tcc aaa ggc aaa gtt cgg gac aag ctc aat aac tta gtc ttg ttt gac      561
Ser Lys Gly Lys Val Arg Asp Lys Leu Asn Asn Leu Val Leu Phe Asp
      40              45              50
aaa gct acc tat gat aaa ctc tgt aag gaa gtt ccc aac tat aaa ctt      609

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Lys	Ala	Thr	Tyr	Asp	Lys	Leu	Cys	Lys	Glu	Val	Pro	Asn	Tyr	Lys	Leu		
			55					60				65					
ata	acc	cca	gct	gtg	gtc	tct	gag	aga	ctg	aag	att	cga	ggc	tcc	ctg	657	
Ile	Thr	Pro	Ala	Val	Val	Ser	Glu	Arg	Leu	Lys	Ile	Arg	Gly	Ser	Leu		
		70					75					80					
gcc	agg	gca	gcc	ctt	cag	gag	ctc	ctt	agt	aaa	gga	ctt	atc	aaa	ctg	705	
Ala	Arg	Ala	Ala	Leu	Gln	Glu	Leu	Leu	Ser	Lys	Gly	Leu	Ile	Lys	Leu		
		85				90					95						
gtt	tca	aag	cac	aga	gct	caa	gta	att	tac	acc	aga	aat	acc	aag	ggc	753	
Val	Ser	Lys	His	Arg	Ala	Gln	Val	Ile	Tyr	Thr	Arg	Asn	Thr	Lys	Gly		
100					105					110					115		
gga	gat	gct	cca	gct	gct	ggc	gaa	gat	gca	tgaataggctc	caaccacc					801	
Gly	Asp	Ala	Pro	Ala	Ala	Gly	Glu	Asp	Ala								
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<211> 416

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 6..398

<400> 3865

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	1				5				10					15			
cag	att	act	cga	gag	gga	aag	ggc	gct	tct	gcc	aga	aat	act	aac	ttg	98	
Gln	Ile	Thr	Arg	Glu	Gly	Lys	Gly	Ala	Ser	Ala	Arg	Asn	Thr	Asn	Leu		
			20				25						30				
ttt	ctg	ttt	tgt	ttt	ggc	gag	cag	aag	tgg	tcc	aaa	ggc	aaa	gtt	cgg	146	
Phe	Leu	Phe	Cys	Phe	Gly	Glu	Gln	Lys	Trp	Ser	Lys	Gly	Lys	Val	Arg		
			35				40					45					
gac	aag	ctc	aat	aac	tta	gtc	ttg	ttt	gac	aaa	gct	acc	tat	gat	aaa	194	
Asp	Lys	Leu	Asn	Asn	Leu	Val	Leu	Phe	Asp	Lys	Ala	Thr	Tyr	Asp	Lys		
		50					55				60						
ctc	tgt	aag	gaa	gtt	ccc	aac	tat	aaa	ctt	ata	acc	cca	gct	gtg	gtc	242	
Leu	Cys	Lys	Glu	Val	Pro	Asn	Tyr	Lys	Leu	Ile	Thr	Pro	Ala	Val	Val		
		65				70				75							
tct	gag	aga	ctg	aag	att	cga	ggc	tcc	ctg	gcc	agg	gca	gcc	ctt	cag	290	
Ser	Glu	Arg	Leu	Lys	Ile	Arg	Gly	Ser	Leu	Ala	Arg	Ala	Ala	Leu	Gln		
		80			85			90					95				
gag	ctc	ctt	agt	aaa	gga	ctt	atc	aaa	ctg	gtt	tca	aag	cac	aga	gct	338	
Glu	Leu	Leu	Ser	Lys	Gly	Leu	Ile	Lys	Leu	Val	Ser	Lys	His	Arg	Ala		
			100				105						110				
caa	gta	att	tac	acc	aga	aat	acc	aag	ggc	gga	gat	gct	cca	gct	gct	386	
Gln	Val	Ile	Tyr	Thr	Arg	Asn	Thr	Lys	Gly	Gly	Asp	Ala	Pro	Ala	Ala		
			115				120					125					
ggc	gaa	gat	gca	tgaataggctc	caaccacc											416	
Gly	Glu	Asp	Ala														
			130														

<210> 3866
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 <212> DNA
 <213> Homo sapiens

<220>
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 <222> 30..476

<400> 3866
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 cgg ctg gtg tca tcg gtg tcc ttc ctc cgc tgc cgc mcc cgc aag gct 101
 Arg Leu Val Ser Ser Val Ser Phe Leu Arg Cys Arg Xaa Arg Lys Ala
 10 15 20
 tcg ccg tca tcg agg cca ttt cca gcg act tgt cgc acg ctt ttc tat 149
 Ser Pro Ser Ser Arg Pro Phe Pro Ala Thr Cys Arg Thr Leu Phe Tyr
 25 30 35 40
 ata ctt cgt tcc ccg cca acc gca acc att gac gcc atg tcg ggt tat 197
 Ile Leu Arg Ser Pro Pro Thr Ala Thr Ile Asp Ala Met Ser Gly Tyr
 45 50 55
 tcg agt gac cga gac cgc ggc cgg gac cga ggg ttt ggt gca cct cga 245
 Ser Ser Asp Arg Asp Arg Gly Arg Asp Arg Gly Phe Gly Ala Pro Arg
 60 65 70
 ttt gga gga agt agg gca ggg ccc tta tct gga aag aag ttt gga aac 293
 Phe Gly Gly Ser Arg Ala Gly Pro Leu Ser Gly Lys Lys Phe Gly Asn
 75 80 85
 cct ggg gag aaa tta gtt aaa aag aag tgg aat ctt gat gag ctg cct 341
 Pro Gly Glu Lys Leu Val Lys Lys Lys Trp Asn Leu Asp Glu Leu Pro
 90 95 100
 aaa ttt gag aag aat ttt tat caa gag cac cct gat ttg gct agg cgc 389
 Lys Phe Glu Lys Asn Phe Tyr Gln Glu His Pro Asp Leu Ala Arg Arg
 105 110 115 120
 aca gca caa gag gtg gaa aca tac aga aga agc aag gaa att aca gtt 437
 Thr Ala Gln Glu Val Glu Thr Tyr Arg Arg Ser Lys Glu Ile Thr Val
 125 130 135
 aga ggt cac aac tgc ccg nwn naa gtt ctn gak ttt tta tgaagccaat 486
 Arg Gly His Asn Cys Pro Xaa Xaa Val Leu Xaa Phe Leu
 140 145
 ttccctgcaa atgtcatgga tggtattgca agacagaatt tcaactg 532

<210> 3867
 <211> 665
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 68..583

<400> 3867

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tttgggct atg gcc tcc aac ttt aag aag gca aac atg gca tca agt tct 109
      Met Ala Ser Asn Phe Lys Lys Ala Asn Met Ala Ser Ser Ser
      1          5          10
cag cga aaa aga atg agc cct aag cct gag ctt act gaa gag caa aag 157
Gln Arg Lys Arg Met Ser Pro Lys Pro Glu Leu Thr Glu Glu Gln Lys
15          20          25          30
cag gag atc cgg gaa gct ttt gat ctt ttc gat gcg gat gga act ggc 205
Gln Glu Ile Arg Glu Ala Phe Asp Leu Phe Asp Ala Asp Gly Thr Gly
      35          40          45
acc ata gat gtt aaa gaa ctg aag gtg gca atg agg gcc ctg ggc ttt 253
Thr Ile Asp Val Lys Glu Leu Lys Val Ala Met Arg Ala Leu Gly Phe
      50          55          60
gaa ccc aag aaa gaa gaa att aag aaa atg ata agt gaa att gat aag 301
Glu Pro Lys Lys Glu Glu Ile Lys Lys Met Ile Ser Glu Ile Asp Lys
      65          70          75
gaa ggg aca gga aaa atg aac ttt ggt gac ttt tta act gtg atg acc 349
Glu Gly Thr Gly Lys Met Asn Phe Gly Asp Phe Leu Thr Val Met Thr
      80          85          90
cag aaa atg tct gag aaa rat act aaa gaa gaa atc ctg aaa gct ttc 397
Gln Lys Met Ser Glu Lys Xaa Thr Lys Glu Glu Ile Leu Lys Ala Phe
95          100          105          110
aag ctc ttt gat gat gat gaa act ggg aag att tcg ttc aaa aat ctg 445
Lys Leu Phe Asp Asp Asp Glu Thr Gly Lys Ile Ser Phe Lys Asn Leu
      115          120          125
aaa cgc gtg gcc aag gag ttg ggt gag aac ctg act gat gag gag ctg 493
Lys Arg Val Ala Lys Glu Leu Gly Glu Asn Leu Thr Asp Glu Glu Leu
      130          135          140
cag gaa atg att gat gaa gct gat cga gat gga gat gga gag gtc agt 541
Gln Glu Met Ile Asp Glu Ala Asp Arg Asp Gly Asp Gly Glu Val Ser
      145          150          155
gag caa gag ttc ctg cgc atc atg aaa aag acc agc ctc tat 583
Glu Gln Glu Phe Leu Arg Ile Met Lys Lys Thr Ser Leu Tyr
      160          165          170
taagatcagt gtcttctttt tctactgcrn gcacatgtaa ctagatttag tgcttgccat 643
ggtagtgaaat ctggcttttg ag 665

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<210> 3868

<211> 450

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 106..423

<400> 3868

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ctgaagcggc ggccagagaa gactcaaggc caccagcctc gggcc atg cct ttc ttg 117
      Met Pro Phe Leu
      1

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gac atc cag aaa agg ttc ggc ctt aac ata gat cga tgg ttg aca atc 165
Asp Ile Gln Lys Arg Phe Gly Leu Asn Ile Asp Arg Trp Leu Thr Ile

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5	10	15	20	
cag agt ggt gaa	cag ccc tac aag atg gct ggt cga tgc cat gct ttt			213
Gln Ser Gly Glu	Gln Pro Tyr Lys Met Ala Gly Arg Cys His Ala Phe			
	25	30	35	
gaa aaa gaa tgg	ata gaa tgt gca cat gga atc ggt tat act cgg gca			261
Glu Lys Glu Trp	Ile Glu Cys Ala His Gly Ile Gly Tyr Thr Arg Ala			
	40	45	50	
gag aaa gag tgc	aag ata gaa tat gat gat ttc gta gag tgt ttg ctt			309
Glu Lys Glu Cys	Lys Ile Glu Tyr Asp Asp Phe Val Glu Cys Leu Leu			
	55	60	65	
cgg cag aaa acg	atg aga cgt gca ggt acc atc agg aag cag cgg gat			357
Arg Gln Lys Thr	Met Arg Arg Ala Gly Thr Ile Arg Lys Gln Arg Asp			
	70	75	80	
aag ctg ata aag	gaa gga aag tac acc cct cca cct cac cac att ggc			405
Lys Leu Ile Lys	Glu Gly Lys Tyr Thr Pro Pro Pro His His Ile Gly			
	85	90	95	100
aag ggg gag cct	cgg ccc tgaacagagc agctgctgat atctgga			450
Lys Gly Glu Pro	Arg Pro			
	105			
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cttttatattg attgttatac tcac atg atc ata aat att agc cat gtt tgg				111
Met Ile Ile Asn Ile Ser His Val Trp				
	1	5		
tgc tgt gga gaa	atg aag gcc atc gaa gac ggc aat ttg gag gaa atg			159
Cys Cys Gly Glu	Met Lys Ala Ile Glu Asp Gly Asn Leu Glu Glu Met			
	10	15	20	25
gaa gag gaa gta	cgg ctt aag aag cga aaa aga cga aga aat gtg gat			207
Glu Glu Glu Val	Arg Leu Lys Lys Arg Lys Arg Arg Arg Asn Val Asp			
	30	35	40	
aaa gat cct gca	aaa gaa gat gtg gaa aaa gct aag aag aga aga ggc			255
Lys Asp Pro Ala	Lys Glu Asp Val Glu Lys Ala Lys Lys Arg Arg Gly			
	45	50	55	
cgc cct ccc gct	gag aaa ctg tca cca aat ccc ccc aaa ctg aca aag			303
Arg Pro Pro Ala	Glu Lys Leu Ser Pro Asn Pro Pro Lys Leu Thr Lys			
	60	65	70	
cag atg aac gct	atc atc gat act gtg ata aac tac aaa gat agt tca			351
Gln Met Asn Ala	Ile Ile Asp Thr Val Ile Asn Tyr Lys Asp Ser Ser			
	75	80	85	
ggg cga cas tca	gtg aag tct tca ttc agt tac ctt caa gga aag aat			399
Gly Arg Xaa Ser	Val Lys Ser Ser Phe Ser Tyr Leu Gln Gly Lys Asn			
	90	95	100	105
tac cag aat act	atg aat taattaagga agccagtgga tttcaaaaaa			447

Tyr Gln Asn Thr Met Asn
110

<210> 3870
<211> 531
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 57..443

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Met
1
gct aaa agc tta cgg agt aag tgg aaa aga aag atg cgt gct gaa aag 107
Ala Lys Ser Leu Arg Ser Lys Trp Lys Arg Lys Met Arg Ala Glu Lys
5 10 15
aga aaa aag aat gcc cca aag gag gcc agc agg ctt aaa agt att ctc 155
Arg Lys Lys Asn Ala Pro Lys Glu Ala Ser Arg Leu Lys Ser Ile Leu
20 25 30
aaa cta gac ggt gat gtt tta atg aaa gat gtt caa gag ata gca act 203
Lys Leu Asp Gly Asp Val Leu Met Lys Asp Val Gln Glu Ile Ala Thr
35 40 45
gtg gtg gta ccc aaa ccc aaa cat tgc caa gag aaa atg caa tgt gag 251
Val Val Val Pro Lys Pro Lys His Cys Gln Glu Lys Met Gln Cys Glu
50 55 60 65
gta aaa gat gaa aaa gat gac atg aaa atg gag act gat att aag aga 299
Val Lys Asp Glu Lys Asp Asp Met Lys Met Glu Thr Asp Ile Lys Arg
70 75 80
aac aaa aag act ctt cta gac cag cat gga cag tac cca ata tgg atg 347
Asn Lys Lys Thr Leu Leu Asp Gln His Gly Gln Tyr Pro Ile Trp Met
85 90 95
aac caa agg caa aga aaa agg ctg aag gca aag cga gag aaa aga aag 395
Asn Gln Arg Gln Arg Lys Arg Leu Lys Ala Lys Arg Glu Lys Arg Lys
100 105 110
ggg aaa agc aaa gca aaa gca gtg aaa gtg gca aag ggt ttg gcc tgg 443
Gly Lys Ser Lys Ala Lys Ala Val Lys Val Ala Lys Gly Leu Ala Trp
115 120 125
tagactctta aaaccttgga aaatgccaca tgggatagat gacggattag aatgtataca 503
catgtatact ttgatttcaa ctgccacc 531

<210> 3871
<211> 471
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 106..429

004220-0540

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 ttaccccggc tctccgcccc tccttctcgc ggcgctcgag ggacc atg gcc gat cct 117
 Met Ala Asp Pro

1
 cgc gtg aga cag atc aag atc aag acc ggc gtg gtg aag cgg ttg gtc 165
 Arg Val Arg Gln Ile Lys Ile Lys Thr Gly Val Val Lys Arg Leu Val
 5 10 15 20
 aaa gaa aaa gtg atg tat gaa aaa gag gca aaa caa caa gaa gaa aag 213
 Lys Glu Lys Val Met Tyr Glu Lys Glu Ala Lys Gln Gln Glu Glu Lys
 25 30 35
 att gaa aaa atg aga gct gaa gac ggt gaa aat tat gac att aaa aag 261
 Ile Glu Lys Met Arg Ala Glu Asp Gly Glu Asn Tyr Asp Ile Lys Lys
 40 45 50
 cag gca gag atc cta caa gaa tcc agg atg atg atc cca gat tgc cag 309
 Gln Ala Glu Ile Leu Gln Glu Ser Arg Met Met Ile Pro Asp Cys Gln
 55 60 65
 cgc agg ttg gaa gcc gca tat ttg gat ctt caa cgg ata cta gaa aat 357
 Arg Arg Leu Glu Ala Ala Tyr Leu Asp Leu Gln Arg Ile Leu Glu Asn
 70 75 80
 gaa aaa gac ttg gaa gaa gct gag gaa tat aaa gaa gca cgt tta gta 405
 Glu Lys Asp Leu Glu Glu Ala Glu Glu Tyr Lys Glu Ala Arg Leu Val
 85 90 95 100
 ctg gat tca gtg aag tta gaa gcc tgaaactttt ctcgtatggg gtgggttttg 459
 Leu Asp Ser Val Lys Leu Glu Ala
 105
 cattaaatcc kg 471

<210> 3872
 <211> 559
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 33..365

<400> 3872
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 Met Val Arg Met Asn Val Leu
 1 5
 gca gat gct ctc aag agt atc aac aat gcc gaa aag aga ggc aaa cgc 101
 Ala Asp Ala Leu Lys Ser Ile Asn Asn Ala Glu Lys Arg Gly Lys Arg
 10 15 20
 cag gtg ctt att agg ccg tgc tcc aaa gtc atc gtc cgg ttt ctc act 149
 Gln Val Leu Ile Arg Pro Cys Ser Lys Val Ile Val Arg Phe Leu Thr
 25 30 35
 gtg atg atg aag cat ggt tac att ggc gaa ttt gaa atc att gat gac 197
 Val Met Met Lys His Gly Tyr Ile Gly Glu Phe Glu Ile Ile Asp Asp
 40 45 50 55
 cac aga gct ggg aaa att gtt gtg aac ctc aca ggc agg cta aac aag 245
 His Arg Ala Gly Lys Ile Val Val Asn Leu Thr Gly Arg Leu Asn Lys
 60 65 70

kkt gga gtg cag tgg cac gat ctt ggc tac tgc aac ctc tgt ctc cca 293
 Xaa Gly Val Gln Trp His Asp Leu Gly Tyr Cys Asn Leu Cys Leu Pro
 75 80 85
 ggt tca agc gat tct cct gcc tca gcc tcc cta gta gct gag att aca 341
 Gly Ser Ser Asp Ser Pro Ala Ser Ala Ser Leu Val Ala Glu Ile Thr
 90 95 100
 gtg tgg ggt gat cag ccc cag att tgacgtgcaa ctcaaagacc tggaaaaatg 395
 Val Trp Gly Asp Gln Pro Gln Ile
 105 110
 gcagaataat ctgcttccat cccgccagtt tggtttcatt gtactgacaa cctcagctgg 455
 catcatggac catgaagaag caagacgaaa acacacagga ggaaaatcct gggattcttt 515
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 <210> 3873
 <211> 527
 <212> DNA
 <213> Homo sapiens

 <220>
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 <222> 99..494

 <400> 3873
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 ccgtctgccca tcggcgccat cctgcaatct aagccaca atg gtg cgc atg aat gtc 116
 Met Val Arg Met Asn Val
 1 5
 ctg gca gat gct ctc aag agt atc aac aat gcc gaa aag aga ggc aaa 164
 Leu Ala Asp Ala Leu Lys Ser Ile Asn Asn Ala Glu Lys Arg Gly Lys
 10 15 20
 cgc cag gtg ctt att agg ccg tgc tcc aaa gtc atc gtc cgg ttt ctc 212
 Arg Gln Val Leu Ile Arg Pro Cys Ser Lys Val Ile Val Arg Phe Leu
 25 30 35
 act gtg atg atg aag cat ggt tac att ggc gaa ttt gaa atc att gat 260
 Thr Val Met Met Lys His Gly Tyr Ile Gly Glu Phe Glu Ile Ile Asp
 40 45 50
 gac cac aga gct ggg aaa att gtt gtg aac ctc aca ggc agg cta aac 308
 Asp His Arg Ala Gly Lys Ile Val Val Asn Leu Thr Gly Arg Leu Asn
 55 60 65 70
 aag tgt ggg gtg atc agc ccc aga ttt gac gtg caa ctc aaa gac ctg 356
 Lys Cys Gly Val Ile Ser Pro Arg Phe Asp Val Gln Leu Lys Asp Leu
 75 80 85
 gaa aaa tgg cag aat aat ctg ctt cca tcc cgc cag ttt ggt ttc att 404
 Glu Lys Trp Gln Asn Asn Leu Leu Pro Ser Arg Gln Phe Gly Phe Ile
 90 95 100
 gta ctg aca act cag ctg gca tca tgg acc atg aag aag caa gac gaa 452
 Val Leu Thr Thr Gln Leu Ala Ser Trp Thr Met Lys Lys Gln Asp Glu
 105 110 115
 aac aca cag gag gaa aat cct ggg att ctt ttt cta ggg atg 494
 Asn Thr Gln Glu Glu Asn Pro Gly Ile Leu Phe Leu Gly Met
 120 125 130
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<210> 3874
 <211> 482
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 15..479

<400> 3874

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cgc cgc gtg ast tgc ttt ttg cgg ctg ggg agg tct acg ctt cta gag		98
Arg Arg Val Xaa Cys Phe Leu Arg Leu Gly Arg Ser Thr Leu Leu Glu		
	15 20 25	
ctt gag cca gcg ggg cga ccc tgc agt ggc agg act cgg cac cgc gcc		146
Leu Glu Pro Ala Gly Arg Pro Cys Ser Gly Arg Thr Arg His Arg Ala		
	30 35 40	
ctc cac cgc cgg ttg gtg gcc tgc gtg aca gtt tcc tcc cgt cga cat		194
Leu His Arg Arg Leu Val Ala Cys Val Thr Val Ser Ser Arg Arg His		
	45 50 55 60	
cga aag gaa gcc gga cgt ggg cgg gca gag agc ttc atc gca gta gga		242
Arg Lys Glu Ala Gly Arg Gly Arg Ala Glu Ser Phe Ile Ala Val Gly		
	65 70 75	
atg gca gcc cca tct atg aag gaa aga cag gtc tgc tgg ggg gcc cgg		290
Met Ala Ala Pro Ser Met Lys Glu Arg Gln Val Cys Trp Gly Ala Arg		
	80 85 90	
gat gag tac tgg aag tgt tta gat gag aac tta gag gat gct tct caa		338
Asp Glu Tyr Trp Lys Cys Leu Asp Glu Asn Leu Glu Asp Ala Ser Gln		
	95 100 105	
tgc aag aag tta aga agc tct ttc gaa tca agt tgt ccc caa cag tgg		386
Cys Lys Lys Leu Arg Ser Ser Phe Glu Ser Ser Cys Pro Gln Gln Trp		
	110 115 120	
ata aaa tat ttt gat aaa aga aga gac tac tta aaa ttc aaa gaa aaa		434
Ile Lys Tyr Phe Asp Lys Arg Arg Asp Tyr Leu Lys Phe Lys Glu Lys		
	125 130 135 140	
ttt gaa gca gga caa ttt gag cct tca gaa aca act gca aaa tcc tag		482
Phe Glu Ala Gly Gln Phe Glu Pro Ser Glu Thr Thr Ala Lys Ser		
	145 150 155	

<210> 3875
 <211> 620
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 188..568

<400> 3875

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tggatatctt cggggacctg aagaagatga acaagcgcca stctattacc aggttttaaa 180
cttcgcc atg atc gtg tct tct gca ctc atg ata tgg aaa ggc ttg atc 229
      Met Ile Val Ser Ser Ala Leu Met Ile Trp Lys Gly Leu Ile
      1           5           10
gtg ctc aca ggc agt gag agc ccc atc gtg gtg gtg ctg agt ggc agt 277
Val Leu Thr Gly Ser Glu Ser Pro Ile Val Val Val Leu Ser Gly Ser
15           20           25           30
atg gag ccg gcc ttt cac aga gga gac ctc ctg ttc ctc aca aat ttc 325
Met Glu Pro Ala Phe His Arg Gly Asp Leu Leu Phe Leu Thr Asn Phe
      35           40           45
cgg gaa gac cca atc aga gct ggt gaa ata gtt gtt ttt aaa gtt gaa 373
Arg Glu Asp Pro Ile Arg Ala Gly Glu Ile Val Val Phe Lys Val Glu
      50           55           60
gga cga gac att cca ata gtt cac aga gta atc aaa gtt cat gaa aaa 421
Gly Arg Asp Ile Pro Ile Val His Arg Val Ile Lys Val His Glu Lys
      65           70           75
gat aat gga gac atc aaa ttt ctg act aaa gga gat aat aat gaa gtt 469
Asp Asn Gly Asp Ile Lys Phe Leu Thr Lys Gly Asp Asn Asn Glu Val
      80           85           90
gat gat aga ggc ttg tac aaa gaa ggc cag aac tgg ctg gaa aag aag 517
Asp Asp Arg Gly Leu Tyr Lys Glu Gly Gln Asn Trp Leu Glu Lys Lys
      95           100           105           110
gac gtg gtg gga aga gca aga ggg ttt tta cca tat gtg gta tgg tca 565
Asp Val Val Gly Arg Ala Arg Gly Phe Leu Pro Tyr Val Val Trp Ser
      115           120           125
cca taataatgaa tgactatcca aaattcaagt atgctctttt ggctgtaatg gg 620
Pro

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<210> 3876
 <211> 508
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> CDS
 <222> 68..502

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gnccaaa atg aag ttt aat ccc ttt gtg act tcc gac cga agc aag aat 109
      Met Lys Phe Asn Pro Phe Val Thr Ser Asp Arg Ser Lys Asn
      1           5           10
cgc aaa agg cat ttc aat gca cct tcc cac att cga agg aag att atg 157
Arg Lys Arg His Phe Asn Ala Pro Ser His Ile Arg Arg Lys Ile Met
15           20           25           30
tct tcc cct ctt tcc aaa gag ctg aga cag aag tac aac gtg cga tcc 205
Ser Ser Pro Leu Ser Lys Glu Leu Arg Gln Lys Tyr Asn Val Arg Ser
      35           40           45
atg ccc atc cga aag gat gat gaa gtt cag gtt gta cgt gga cac tat 253
Met Pro Ile Arg Lys Asp Asp Glu Val Gln Val Val Arg Gly His Tyr
      50           55           60
aaa ggt cag caa att ggc aaa gta gtc cag gtt tac agg aag aaa tat 301

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agc act gac ccc cct cac cat gac cat cat gat gag ttt tgc nnw atg 623
 Ser Thr Asp Pro Pro His His Asp His His Asp Glu Phe Cys Xaa Met
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 ccc tgaatcctga tgggtttccct aaagttatta cggaaamagm cccctgcttt 676
 Pro
 cgaatttaca tgttcatgat gt 698

<210> 3878
 <211> 662
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 207..590

<400> 3878
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 ccgtcgctcg ctcccttctc ggacgtggta cctgttcccg gtgtccctga ggacgtgcgg 120
 gccaggtttg cggggccaag tgttgccggc acgcacctca cgtcgagaat cgggaggagg 180
 agactrcaag gataggccca ggagta atg gag tcc aaa gag gaa cga gcg tta 233
 Met Glu Ser Lys Glu Glu Arg Ala Leu
 1 5
 aac aat ctc atc gtg gaa aat gtc aac cag gaa aat gat gaa aaa gat 281
 Asn Asn Leu Ile Val Glu Asn Val Asn Gln Glu Asn Asp Glu Lys Asp
 10 15 20 25
 gaa aag gag caa gtw gct aat aaa ggg gag ccc ttg gcc cta cct ttg 329
 Glu Lys Glu Gln Val Ala Asn Lys Gly Glu Pro Leu Ala Leu Pro Leu
 30 35 40
 rat gyt rgt gaa tac tgt gtg cct aga gga aat cgt agg cgg ttc cgc 377
 Xaa Xaa Xaa Glu Tyr Cys Val Pro Arg Gly Asn Arg Arg Arg Phe Arg
 45 50 55
 gtt agg cag ccc atc ctg cag tat aga tgg gat atg atg cat agg ctt 425
 Val Arg Gln Pro Ile Leu Gln Tyr Arg Trp Asp Met Met His Arg Leu
 60 65 70
 gga gaa cca cag gca agg atg ana gaa gag aat atg gaa agg att ggg 473
 Gly Glu Pro Gln Ala Arg Met Xaa Glu Glu Asn Met Glu Arg Ile Gly
 75 80 85
 gag gag gtg aga cag ctg atg gaa aag ctg agg gaa aag cag ttg agt 521
 Glu Glu Val Arg Gln Leu Met Glu Lys Leu Arg Glu Lys Gln Leu Ser
 90 95 100 105
 cat agt ctg cgg gca gtc agc act gac ccc cct cac cat gac cat cat 569
 His Ser Leu Arg Ala Val Ser Thr Asp Pro Pro His His Asp His His
 110 115 120
 gat gag ttt tgc nnw atg ccc tgaatcctga tgggtttccct aaagttatta 620
 Asp Glu Phe Cys Xaa Met Pro
 125
 cggaaamagm cccctgcttt cgaatttaca tgttcatgat gt 662

<210> 3879
 <211> 461
 <212> DNA
 <213> Homo sapiens


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20 25 30 35
gtc att ttt tgt ctc agt gca gac aaa aag tgc atc att gta gaa gaa 262
Val Ile Phe Cys Leu Ser Ala Asp Lys Lys Cys Ile Ile Val Glu Glu
40 45 50
ggc aaa gag atc ttg gtt gga gat gtt ggt gta acc ata act gat cct 310
Gly Lys Glu Ile Leu Val Gly Asp Val Gly Val Thr Ile Thr Asp Pro
55 60 65
ttc aag cat ttt gtg gga atg ctt cct gaa aaa gat tgt cgc tat gct 358
Phe Lys His Phe Val Gly Met Leu Pro Glu Lys Asp Cys Arg Tyr Ala
70 75 80
ttg tat gat gca agc ttt gaa aca aaa gaa tcc aga aaa gaa gag ttg 406
Leu Tyr Asp Ala Ser Phe Glu Thr Lys Glu Ser Arg Lys Glu Glu Leu
85 90 95
atg ttt ttt ttg tgg gca cca gaa cta gca cct ctg aaa agt aaa atg 454
Met Phe Phe Leu Trp Ala Pro Glu Leu Ala Pro Leu Lys Ser Lys Met
100 105 110 115
atc tat gca agc tcc aag gat gca att aaa aag aaa ttt caa ggc ata 502
Ile Tyr Ala Ser Ser Lys Asp Ala Ile Lys Lys Lys Phe Gln Gly Ile
120 125 130
aaa cat gaa tgt caa gca aat gga cca gaa gat ctc aat cgg gct tgt 550
Lys His Glu Cys Gln Ala Asn Gly Pro Glu Asp Leu Asn Arg Ala Cys
135 140 145
att gct gaa aag tta ggt gga tcc tta att gta gcc ttt gaa gga tgc 598
Ile Ala Glu Lys Leu Gly Gly Ser Leu Ile Val Ala Phe Glu Gly Cys
150 155 160
cct gtg tagattattc agtgccacaa attgaaagct tccatgttta atgttatcct 654
Pro Val
165
cttgctatat aaataaagca aatatattta ggccagggtc tcactgaggg ggagctgtct 714
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agtctaaagt tttattgatg tgaaattaaa ttcttattgg ccaaagtcct gtwtgatga 834
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Gly Gly Lys Pro Leu Ser Gly Leu Leu Asn Ala Leu Ala Gln Asp Thr
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ttc cac ggg tac ccc ggc atc aca gag gag ctg cta cgg agc cag cta	149
Phe His Gly Tyr Pro Gly Ile Thr Glu Glu Leu Leu Arg Ser Gln Leu	
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Tyr Pro Glu Val Pro Pro Glu Glu Phe Arg Pro Phe Leu Ala Lys Met	
40 45 50 55	
agg ggg att ctt aag tct att gcg tct gca gac atg gat ttc aac cag	245
Arg Gly Ile Leu Lys Ser Ile Ala Ser Ala Asp Met Asp Phe Asn Gln	
60 65 70	
ctg gag gca ttc ttg act gct caa acc aaa aag caa ggt ggg atc aca	293
Leu Glu Ala Phe Leu Thr Ala Gln Thr Lys Lys Gln Gly Gly Ile Thr	
75 80 85	
tct gac caa gct gct gtc att tcc aaa ttc tgg aag agc cac aag aca	341
Ser Asp Gln Ala Ala Val Ile Ser Lys Phe Trp Lys Ser His Lys Thr	
90 95 100	
aaa atc cgt gag agc ctc atg aac cag agc cgc tgg aat agc ggg ctt	389
Lys Ile Arg Glu Ser Leu Met Asn Gln Ser Arg Trp Asn Ser Gly Leu	
105 110 115	
cgg ggc cnt gag ctg gag agt tgatggcaag tctcagtcaa ggcactcagc	440
Arg Gly Xaa Glu Leu Glu Ser	
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Ser Gly Thr Leu Arg Glu Tyr Lys Val Val Gly Arg Cys Leu Pro Thr	
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ccc aaa tgc cac acg ccg ccc ctc tac cgc atg cga atc ttt gcg cct	151
Pro Lys Cys His Thr Pro Pro Leu Tyr Arg Met Arg Ile Phe Ala Pro	
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aat cat gtc gtc gcc aag tcc cgc ttc tgg tac ttt gta tct cag tta	199
Asn His Val Val Ala Lys Ser Arg Phe Trp Tyr Phe Val Ser Gln Leu	
40 45 50	
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Lys Lys Met Lys Lys Ser Ser Gly Glu Ile Val Tyr Cys Gly Gln Val	
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Phe Glu Lys Ser Pro Leu Arg Val Lys Asn Phe Gly Ile Trp Leu Arg	
70 75 80	
tat gac tcc cgg agc ggc acc cac aac atg tac cgg gaa tac cgg gac	343
Tyr Asp Ser Arg Ser Gly Thr His Asn Met Tyr Arg Glu Tyr Arg Asp	


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ggc acc gcg ccc gag ccc act cca ttc aga tca tgaagggtgga ggagatcgcg 444
Gly Thr Ala Pro Glu Pro Thr Pro Phe Arg Ser
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ctgccccacc ggtcctgcg ccgtcagcac aagcca 540

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                                Met Gln Leu Lys Pro Met
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gag atc aac ccc gag atg ctg aac aaa gtg ctg tcc cgg ctg ggg gtc 164
Glu Ile Asn Pro Glu Met Leu Asn Lys Val Leu Ser Arg Leu Gly Val
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gcc ggc cag tgg cgc ttc gtg gac gtg ctg ggg ctg gaa gag gag tct 212
Ala Gly Gln Trp Arg Phe Val Asp Val Leu Gly Leu Glu Glu Ser
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ctg ggc tgc gtg cca gcg cct gcc tgc gcg ctg ctg ctg ctg ttt ccc 260
Leu Gly Ser Val Pro Ala Pro Ala Cys Ala Leu Leu Leu Phe Pro
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ctc acg gcc cag cat gag aac ttc agg aaa aag cag att gaa gag ctg 308
Leu Thr Ala Gln His Glu Asn Phe Arg Lys Lys Gln Ile Glu Glu Leu
      55              60              65              70
aag ttc tca tgc tgg gcc gtg agg kga aac agc agc ngc agt tgc gcg 356
Lys Phe Ser Cys Trp Ala Val Arg Xaa Asn Ser Ser Xaa Ser Ser Ala
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gtc ccg cgg gtc tgt ctc ttg ott caa cag tgt ttg gac gga aca gat 404
Val Pro Arg Val Cys Leu Leu Leu Gln Gln Cys Leu Asp Gly Thr Asp
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Pro Gly Thr Leu Phe Gln Pro Pro Thr Ala Leu Arg Phe Pro Leu Arg
      105              110              115
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Leu Pro His Leu
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cccaccaggg aagtggaagt tgcattgagc tgagatggca ctccagtgca ctccagcctg 564
ggtgacagag caagactccg tctcaaaaaa aacaaaaaaa acaaaaacaaa acaaaaaagc 624
agaaaataga gtcaaagagc tcctctgctg tctkmaaata tcgacaattt cacaggatcc 684
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 Met Gln Leu Lys Pro Met
 1 5
 gag atc aac ccc gag atg ctg aac aaa gtg ctg tcc cgg ctg ggg gtc 164
 Glu Ile Asn Pro Glu Met Leu Asn Lys Val Leu Ser Arg Leu Gly Val
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 gcc ggc cag tgg cgc ttc gtg gac gtg ctg ggg ctg gaa gag gag tct 212
 Ala Gly Gln Trp Arg Phe Val Asp Val Leu Gly Leu Glu Glu Glu Ser
 25 30 35
 ctg ggc tgc gtg cca gcg cct gcc tgc gcg ctg ctg ctg ctg ttt ccc 260
 Leu Gly Ser Val Pro Ala Pro Ala Cys Ala Leu Leu Leu Leu Phe Pro
 40 45 50
 ctc acg gcc cag cat gag aac ttc agg aaa aag cag att gaa gag ctg 308
 Leu Thr Ala Gln His Glu Asn Phe Arg Lys Lys Gln Ile Glu Glu Leu
 55 60 65 70
 aag ttc tca tgc tgg gcc gtg agg kga aac agc agc ngc agt tgc gcg 356
 Lys Phe Ser Cys Trp Ala Val Arg Xaa Asn Ser Ser Xaa Ser Ser Ala
 75 80 85
 gtc ccg cgg gtc tgt ctc ttg ctt caa cag tgt ttg gac gga aca gat 404
 Val Pro Arg Val Cys Leu Leu Leu Gln Gln Cys Leu Asp Gly Thr Asp
 90 95 100
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 Pro Gly Thr Leu Phe Gln Pro Pro Thr Asp Pro Leu
 105 110
 tacacagtag actgagccag ggagatcgct tgagcccaaa aggctgaatc tgcagtgagc 510
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 Met Gln Leu Lys Pro Met

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Glu	Ile	Asn	Pro	Glu	Met	Leu	Asn	Lys	Val	Leu	Ser	Arg	Leu	Gly	Val					
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gcc	ggc	cag	tgg	cgc	ttc	gtg	gac	gtg	ctg	ggg	ctg	gaa	gag	gag	tct	212				
Ala	Gly	Gln	Trp	Arg	Phe	Val	Asp	Val	Leu	Gly	Leu	Glu	Glu	Glu	Ser					
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Leu	Gly	Ser	Val	Pro	Ala	Pro	Ala	Cys	Ala	Leu	Leu	Leu	Leu	Phe	Pro					
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Leu	Thr	Ala	Gln	His	Glu	Asn	Phe	Arg	Lys	Lys	Gln	Ile	Glu	Glu	Leu					
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Lys	Phe	Ser	Cys	Trp	Ala	Val	Arg	Xaa	Asn	Ser	Ser	Xaa	Ser	Ser	Ala					
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Val	Pro	Arg	Val	Cys	Leu	Leu	Leu	Gln	Gln	Cys	Leu	Asp	Gly	Thr	Asp					
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ccg	ggg	act	ctc	ttc	cag	cac	acc	ctg	gaa	gaa	gca	cag	cta	tct	ttc	452				
Pro	Gly	Thr	Leu	Phe	Gln	His	Thr	Leu	Glu	Glu	Ala	Gln	Leu	Ser	Phe					
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Leu	Ile	Phe																		
			120																	
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Phe	Trp	Ser	Arg	Phe	Arg	Lys	Glu	Lys	Glu	Pro	Val	Val	Val	Glu	Thr																		
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gta	gaa	gag	aaa	aag	gaa	cct	atc	cta	gtg	tgt	cca	cct	tta	cga	agc		197																
Val	Glu	Glu	Lys	Lys	Glu	Pro	Ile	Leu	Val	Cys	Pro	Pro	Leu	Arg	Ser																		
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cga	gca	tac	aca	cca	cct	gaa	gat	ctc	cag	agt	cgt	ttg	gaa	tct	tac		245																
Arg	Ala	Tyr	Thr	Pro	Pro	Glu	Asp	Leu	Gln	Ser	Arg	Leu	Glu	Ser	Tyr																		
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gtt aaa gaa gtt ttt ggt tca tct ctt cct agt aat tgg caa gac atc      293
Val Lys Glu Val Phe Gly Ser Ser Leu Pro Ser Asn Trp Gln Asp Ile
      75                      80                      85

tcc ctg gaa gat agt cgt cta aag ttc aat ctt ctg gct cat tta gct      341
Ser Leu Glu Asp Ser Arg Leu Lys Phe Asn Leu Leu Ala His Leu Ala
90                      95                      100                      105

gat gac ttg ggt cat gta gtc cct aac tcc aga ctc cac cag atg tgc      389
Asp Asp Leu Gly His Val Val Pro Asn Ser Arg Leu His Gln Met Cys
      110                      115                      120

agg gtt aga rat gtt ctt gat ttc tat aat gtc cct att caa gag atc      437
Arg Val Arg Xaa Val Leu Asp Phe Tyr Asn Val Pro Ile Gln Glu Ile
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atc ttg gtg gag aag gct cag gat gag atc cca gca ctg tcc gtg tcc      103
Ile Leu Val Glu Lys Ala Gln Asp Glu Ile Pro Ala Leu Ser Val Ser
      10                      15                      20

cgg ccc cag acc ggc ctg tcc ttc ctg ggc cct gag cct gag gac ctg      151
Arg Pro Gln Thr Gly Leu Ser Phe Leu Gly Pro Glu Pro Glu Asp Leu
      25                      30                      35

gag gac ctg tac agc cgc tac aag aag ctg cag caa gag ctg gag ttc      199
Glu Asp Leu Tyr Ser Arg Tyr Lys Lys Leu Gln Gln Glu Leu Glu Phe
      40                      45                      50

ctg gag gtg cag gag gaa tac atc aaa gat gag caa aag aac ctg aaa      247
Leu Glu Val Gln Glu Glu Tyr Ile Lys Asp Glu Gln Lys Asn Leu Lys
      55                      60                      65

aag gaa ttt ctc cat gcc cag gag gag gtg aag cga atc caa agc atc      295
Lys Glu Phe Leu His Ala Gln Glu Glu Val Lys Arg Ile Gln Ser Ile
      70                      75                      80                      85

ccg ctg gtc atc gga caa ttt ctg gag gct gtg gat cag aat aca gcc      343
Pro Leu Val Ile Gly Gln Phe Leu Glu Ala Val Asp Gln Asn Thr Ala
      90                      95                      100

atc gtg ggc tct acc aca ggc tcc aac tat tat gtg cgc atc ctg agc      391
Ile Val Gly Ser Thr Thr Gly Ser Asn Tyr Tyr Val Arg Ile Leu Ser
      105                      110                      115

acc atc gat cgg gag ctg ctc aag ccc aac gcc tca gtg gcc ctc cac      439
Thr Ile Asp Arg Glu Leu Leu Lys Pro Asn Ala Ser Val Ala Leu His
      120                      125                      130

aag cac agc aat gca ctg gtg gac gtg ctg ccc ccg aag ccg aca gca      487
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140

145

497

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Glu Pro Ala Lys Ser Ala Pro Ala Pro Lys Lys Gly Ser Lys Lys Ala
5 10 15
gtg acc aag gcg cag aag aag gat ggc aag aag cgc aag cgc agt cgt 153
Val Thr Lys Ala Gln Lys Lys Asp Gly Lys Lys Arg Lys Arg Ser Arg
20 25 30
aag gag agc tac tcc gtg tat gtg tac aag gtg cta aaa cag gtt cac 201
Lys Glu Ser Tyr Ser Val Tyr Val Tyr Lys Val Leu Lys Gln Val His
35 40 45 50
ccc gat acy ggc atc tcm tcy aar gcc atg ggs atc atg aat tcc tty 249
Pro Asp Thr Gly Ile Ser Ser Lys Ala Met Gly Ile Met Asn Ser Phe
55 60 65
gty aac gac atc ttc gar cgc atc gcm ggc gag gct tcc cgy ctg gcs 297
Val Asn Asp Ile Phe Glu Arg Ile Ala Gly Glu Ala Ser Arg Leu Ala
70 75 80
cay tac aac aag cgc tcg acc att acc tcc agg gag atc cag acs gcc 345
His Tyr Asn Lys Arg Ser Thr Ile Thr Ser Arg Glu Ile Gln Thr Ala
85 90 95
gtg cgy ctg ctg ctt ccc ggr gag ctg gcc aag cac gcw gtg tca gag 393
Val Arg Leu Leu Leu Pro Gly Glu Leu Ala Lys His Ala Val Ser Glu
100 105 110
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Gly Thr Lys Ala Val Thr Lys Tyr Thr Ser Ser Lys
115 120 125
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SECRET

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2424

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Ser	Pro	Phe	Tyr	Leu	Arg	Pro	Pro	Ser	Phe	Leu	Arg	Ala	Pro	Ser	Trp		
45					50				55					60			
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Phe	Asp	Thr	Gly	Leu	Ser	Glu	Met	Arg	Leu	Glu	Lys	Asp	Arg	Phe	Ser		
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Val	Leu	Gly	Asp	Val	Ile	Glu	Val	His	Gly	Lys	His	Glu	Glu	Arg	Gln		
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Asp	Glu	His	Gly	Phe	Ile	Ser	Arg	Glu	Phe	His	Arg	Lys	Tyr	Arg	Ile		
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Pro	Ala	Asp	Val	Asp	Pro	Leu	Thr	Ile	Thr	Ser	Ser	Leu	Ser	Ser	Asp		
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Gly	Val	Leu	Thr	Val	Asn	Gly	Pro	Arg	Lys	Gln	Val	Ser	Gly	Pro	Glu		
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cgc	acc	att	ccc	atc	acc	cgt	gaa	gag	aag	cct	gct	gtc	acc	gca	gcc	830	
Arg	Thr	Ile	Pro	Ile	Thr	Arg	Glu	Glu	Lys	Pro	Ala	Val	Thr	Ala	Ala		
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Pro	Lys	Lys															
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	1				5					10					15		
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Xaa	Gly	Arg	Leu	Leu	Val	Pro	Asp	Arg	Ile	Asn	Gly	Thr	Ala	Asn	Lys		
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Ile His His Pro Trp Ile Arg Arg Pro Phe Phe Pro Phe His Ser Pro			
80	85	90	95
agc cgc ctc ttt gac cag ttc ttc gga gag cac ctg ttg gag tct gat			336
Ser Arg Leu Phe Asp Gln Phe Phe Gly Glu His Leu Leu Glu Ser Asp			
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ctt ttc ccg acg tct act tcc ctg agt ccc ttc tac ctt cgg cca ccc			384
Leu Phe Pro Thr Ser Thr Ser Leu Ser Pro Phe Tyr Leu Arg Pro Pro			
115	120	125	
tcc ttc ctg cgg gca ccc agc tgg ttt gac act gga ctc tca gag atg			432
Ser Phe Leu Arg Ala Pro Ser Trp Phe Asp Thr Gly Leu Ser Glu Met			
130	135	140	
cgc ctg gag aag gac agg ttc tct gtc aac ctg gat gtg aag cac ttc			480
Arg Leu Glu Lys Asp Arg Phe Ser Val Asn Leu Asp Val Lys His Phe			
145	150	155	
tcc cca gag gaa ctc aaa gtt aag gtg ttg gga gat gtg att gag gtg			528
Ser Pro Glu Glu Leu Lys Val Lys Val Leu Gly Asp Val Ile Glu Val			
160	165	170	175
cat gga aaa cat gaa gag cgc cag gat gaa cat ggt ttc atc tcc agg			576
His Gly Lys His Glu Glu Arg Gln Asp Glu His Gly Phe Ile Ser Arg			
180	185	190	
gag ttc cac agg aaa tac cgg atc cca gct gat gta gac cct ctc acc			624
Glu Phe His Arg Lys Tyr Arg Ile Pro Ala Asp Val Asp Pro Leu Thr			
195	200	205	
att act tca tcc ctg tca tct gat ggg gtc ctc act gtg aat gga cca			672
Ile Thr Ser Ser Leu Ser Ser Asp Gly Val Leu Thr Val Asn Gly Pro			
210	215	220	
agg aaa cag gtc tct ggc cct gag cgc acc att ccc atc acc cgt gaa			720
Arg Lys Gln Val Ser Gly Pro Glu Arg Thr Ile Pro Ile Thr Arg Glu			
225	230	235	
gag aag cct gct gtc acc gca gcc ccc aag aaa tagatgccct ttcttgaatt			773
Glu Lys Pro Ala Val Thr Ala Ala Pro Lys Lys			
240	245	250	
gcatttttta aaacaagaaa gtttccccac cagtgaatga aagtcttgtg actaggctga			833
agcttattaa tgctaagggc agg			856

<210> 3892

<211> 695

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 269..592

<400> 3892

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gggtctgatc	accatgagcc	ttaggtatca	ctgtgggtggc	cccctgaagc	agacagctat	120
gtttatttaa	aaaggagatt	ttttaagcag	agaagagaag	gatgaattac	ccggacagaa	180


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agcagctctg cagaataaga cagcacctgt gtaatcagta tttttgccct ctttctccca 240
tcccattccc ttaccttgct atttctag atg cgc ctg gag aag gac agg ttc 292
Met Arg Leu Glu Lys Asp Arg Phe
1 5
tct gtc aac ctg gat gtg aag cac ttc tcc cca gag gaa ctc aaa gtt 340
Ser Val Asn Leu Asp Val Lys His Phe Ser Pro Glu Glu Leu Lys Val
10 15 20
aag gtg ttg gga gat gtg att gag gtg cat gga aaa cat gaa gag cgc 388
Lys Val Leu Gly Asp Val Ile Glu Val His Gly Lys His Glu Glu Arg
25 30 35 40
cag gat gaa cat ggt ttc atc tcc agg gag ttc cac agg aaa tac cgg 436
Gln Asp Glu His Gly Phe Ile Ser Arg Glu Phe His Arg Lys Tyr Arg
45 50 55
atc cca gct gat gta gac cct ctc acc att act tca tcc ctg tca tct 484
Ile Pro Ala Asp Val Asp Pro Leu Thr Ile Thr Ser Ser Leu Ser Ser
60 65 70
gat ggg gtc ctc act gtg aat gga cca agg aaa cag gtc tct ggc cct 532
Asp Gly Val Leu Thr Val Asn Gly Pro Arg Lys Gln Val Ser Gly Pro
75 80 85
gag cgc acc att ccc atc acc cgt gaa gag aag cct gct gtc acc gca 580
Glu Arg Thr Ile Pro Ile Thr Arg Glu Glu Lys Pro Ala Val Thr Ala
90 95 100
gcc ccc aag aaa tagatgccct ttcttgaatt gcatttttta aaacaagaaa 632
Ala Pro Lys Lys
105
gtttcccccac cagtgaatga aagtcttggtg actaggctga agcttattaa tgctaagggc 692
agg 695

<210> 3893
<211> 497
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 36..461

<400> 3893
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Met Glu Ala Thr Thr Ala
1 5
ggt gtg ggc cgg cta gag gaa gag gcg ttg cgg cga aag gaa cgg ctg 101
Gly Val Gly Arg Leu Glu Glu Glu Ala Leu Arg Arg Lys Glu Arg Leu
10 15 20
aag gcc cta cgg gag aaa acc ggg cgc aag gac aag gaa gat ggg gag 149
Lys Ala Leu Arg Glu Lys Thr Gly Arg Lys Asp Lys Glu Asp Gly Glu
25 30 35
cca aag acc aag cat ctc aga gaa gag gag gaa gaa ggc gag aag cac 197
Pro Lys Thr Lys His Leu Arg Glu Glu Glu Glu Glu Gly Glu Lys His
40 45 50
agg gaa ctt agg ctg cgg aac tat gtc ccg gag gat gag gac ctg aag 245
Arg Glu Leu Arg Leu Arg Asn Tyr Val Pro Glu Asp Glu Asp Leu Lys
55 60 65 70

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aag agg agg gtg ccc cag gcc aaa ccg gtt gca gtg gag gag aag gtg      293
Lys Arg Arg Val Pro Gln Ala Lys Pro Val Ala Val Glu Glu Lys Val
              75                      80                      85

aag gag cag ctg gag gcc gcc aag ccc gag ccc gtc atc gag gag gtg      341
Lys Glu Gln Leu Glu Ala Ala Lys Pro Glu Pro Val Ile Glu Glu Val
              90                      95                      100

gac ctg gcc aac ctg rtt tct cgg aag cct gac tgg gac ctc aag aga      389
Asp Leu Ala Asn Leu Xaa Ser Arg Lys Pro Asp Trp Asp Leu Lys Arg
              105                      110                      115

gat gtg gcc aag aag ctg gag aaa cta aaa aag cgg act cag agg gcc      437
Asp Val Ala Lys Lys Leu Glu Lys Leu Lys Lys Arg Thr Gln Arg Ala
              120                      125                      130

att gcc gag ctg atc cgt gaa ggc tgaaargcca ggaagacagc ctagcctctg      491
Ile Ala Glu Leu Ile Arg Glu Gly
135                      140

cagtgg      497

<210> 3894
<211> 482
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 29..352

<400> 3894
gtcggacgac agaccgtgtg tttccaaa atg gcg gca gcg atg gat gtg gat      52
Met Ala Ala Ala Met Asp Val Asp
              1                      5

acc ccg agc ggc acc aac agc ggc gcg ggc aag aag cgc ttt gaa gtg      100
Thr Pro Ser Gly Thr Asn Ser Gly Ala Gly Lys Lys Arg Phe Glu Val
              10                      15                      20

aaa aag tgg aat gca gta gcc ctc tgg gcc tgg gat att gtg gtt gat      148
Lys Lys Trp Asn Ala Val Ala Leu Trp Ala Trp Asp Ile Val Val Asp
25                      30                      35                      40

aac tgt gcc atc tgc agg aac cac att atg gat ctt tgc ata gaa tgt      196
Asn Cys Ala Ile Cys Arg Asn His Ile Met Asp Leu Cys Ile Glu Cys
              45                      50                      55

caa gct aac cag gcg tcc gct act tca gaa gag tgt act gtc gca tgg      244
Gln Ala Asn Gln Ala Ser Ala Thr Ser Glu Glu Cys Thr Val Ala Trp
              60                      65                      70

gga gtc tgt aac cat gct ttt cac ttc cac tgc atc tct cgc tgg ctc      292
Gly Val Cys Asn His Ala Phe His Phe His Cys Ile Ser Arg Trp Leu
              75                      80                      85

aaa aca cga cag gtg tgt cca ttg gac aac aga gag tgg gaa ttc caa      340
Lys Thr Arg Gln Val Cys Pro Leu Asp Asn Arg Glu Trp Glu Phe Gln
              90                      95                      100

aag tat ggg cac taggaaaaga cttcttccat caagcttaat tgttttgtta      392
Lys Tyr Gly His
105

ttcatttart gmctttccct gctgttacct aattacaaat tggatggaac tgtgtttttt      452
tctgctttgt tttttcagtt tgctgtttct      482

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<210> 3895
 <211> 633
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 259..624

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 gataaataaa cactaggaac gcatttccac cctagatttc agcagaaatg ctgaatgtaa 120
 aggaatatatt gagtaaagtg agttgccgtt cttgaagccc gtctcctaag gattctcccg 180
 gtgtccgcgt agggatctca tgctatatag gagggccctg ccaggcacccg tctcctctct 240
 ccgggtccgtg cctccaag atg aca aag aaa aga agg aac aat ggt cgt gcc 291
 Met Thr Lys Lys Arg Arg Asn Asn Gly Arg Ala
 1 5 10
 aaa aag ggc cgc ggc cac gtg cag cct att cgc tgc act aac tgt gcc 339
 Lys Lys Gly Arg Gly His Val Gln Pro Ile Arg Cys Thr Asn Cys Ala
 15 20 25
 cga tgc gtg ccc aag gac aag gcc att aag aaa ttc gtc att cga aac 387
 Arg Cys Val Pro Lys Asp Lys Ala Ile Lys Lys Phe Val Ile Arg Asn
 30 35 40
 ata gtg gag gcc gca gca gtc agg gac att tct gaa gcg agc gtc ttc 435
 Ile Val Glu Ala Ala Ala Val Arg Asp Ile Ser Glu Ala Ser Val Phe
 45 50 55
 gat gcc tat gtg ctt ccc aag ctg tat gtg aag cta cat tac tgt gtg 483
 Asp Ala Tyr Val Leu Pro Lys Leu Tyr Val Lys Leu His Tyr Cys Val
 60 65 70 75
 agt tgt gca att cac agc aaa gta gtc agg aat cga tct cgt gaa gcc 531
 Ser Cys Ala Ile His Ser Lys Val Val Arg Asn Arg Ser Arg Glu Ala
 80 85 90
 cgc aag gac cga aca ccc cca ccc cga ttt aga cct gcg ggt gct gcc 579
 Arg Lys Asp Arg Thr Pro Pro Pro Arg Phe Arg Pro Ala Gly Ala Ala
 95 100 105
 cca cgt ccc can caa agc cca tgt aag gag ctg agt ytt aaa gac 624
 Pro Arg Pro Xaa Gln Ser Pro Cys Lys Glu Leu Ser Xaa Lys Asp
 110 115 120
 tgaagacag 633

<210> 3896
 <211> 463
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 31..459

<400> 3896
 catgaaaata ttcaacaaca actgcaaact atg gag gag aaa aag ggt ata tct 54

	Met	Glu	Glu	Lys	Lys	Gly	Ile	Ser	
	1			5					
gga tat agt tac acc caa gaa gag cta gaa aga gta tct gca ctg aag									102
Gly Tyr Ser Tyr Thr Gln Glu Glu Leu Glu Arg Val Ser Ala Leu Lys									
10 15 20									
agt gaa gtt gat gaa atg aaa gga cga aca ttg gat gat atg tct gaa									150
Ser Glu Val Asp Glu Met Lys Gly Arg Thr Leu Asp Asp Met Ser Glu									
25 30 35 40									
atg gtg aaa aaa ctg tat tca ttg gta tct gaa aag aag tca gct ctt									198
Met Val Lys Lys Leu Tyr Ser Leu Val Ser Glu Lys Lys Ser Ala Leu									
45 50 55									
gcc tca gtt ata aaa gag cta cga cag ttg cgt caa aaa tat caa gaa									246
Ala Ser Val Ile Lys Glu Leu Arg Gln Leu Arg Gln Lys Tyr Gln Glu									
60 65 70									
ctg acc cag gag tgt gat gaa aag aaa tcc cag tat gat agc tgt gca									294
Leu Thr Gln Glu Cys Asp Glu Lys Lys Ser Gln Tyr Asp Ser Cys Ala									
75 80 85									
gca ggc ctc gaa agc aat cgg tcc aaa tta gaa cag gaa gtt aga aga									342
Ala Gly Leu Glu Ser Asn Arg Ser Lys Leu Glu Gln Glu Val Arg Arg									
90 95 100									
ctc cgt gaa gaa tgt ctt caa gaa gaa agt aga tac cat tat aca aat									390
Leu Arg Glu Glu Cys Leu Gln Glu Glu Ser Arg Tyr His Tyr Thr Asn									
105 110 115 120									
tgt atg att aag aac cta gaa gtt caa ctt cgt cgt gct act gat gag									438
Cys Met Ile Lys Asn Leu Glu Val Gln Leu Arg Arg Ala Thr Asp Glu									
125 130 135									
aat gaa ggc ata tat ctc ttc tgat									463
Asn Glu Gly Ile Tyr Leu Phe									
140									

<210> 3897

<211> 506

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 76..468

<400> 3897

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tccggctgtt gcacc atg gcg tcc atg ggg acc ctc gcc ttc gat gaa tat	111
Met Ala Ser Met Gly Thr Leu Ala Phe Asp Glu Tyr	
1 5 10	
ggg cgc cct ttc ctc atc atc aag gat cag gac cgc aag tcc cgt ctt	159
Gly Arg Pro Phe Leu Ile Ile Lys Asp Gln Asp Arg Lys Ser Arg Leu	
15 20 25	
atg gga ctt gag gcc ctc aag tct cat ata atg gca gca aag gct gta	207
Met Gly Leu Glu Ala Leu Lys Ser His Ile Met Ala Ala Lys Ala Val	
30 35 40	
gca aat aca atg aga aca tca ctt gga cca aat ggg ctt gat aag atg	255
Ala Asn Thr Met Arg Thr Ser Leu Gly Pro Asn Gly Leu Asp Lys Met	
45 50 55 60	

atg gtg gat aag gat ggg gat gtg act gta act aat gat ggg gcc acc	303
Met Val Asp Lys Asp Gly Asp Val Thr Val Thr Asn Asp Gly Ala Thr	
65 70 75	
atc tta agc atg atg gat gtt gat cat cag att gcc aag ctg atg gtg	351
Ile Leu Ser Met Met Asp Val Asp His Gln Ile Ala Lys Leu Met Val	
80 85 90	
gaa ctg tcc aag tct cag gat gat gaa att gga gat gga acc aca gga	399
Glu Leu Ser Lys Ser Gln Asp Asp Glu Ile Gly Asp Gly Thr Thr Gly	
95 100 105	
gtg gtt gtc ctg gct ggt gcc ttg tta gag aag cgg asa att gct agc	447
Val Val Val Leu Ala Gly Ala Leu Leu Glu Lys Arg Xaa Ile Ala Ser	
110 115 120	
cgg gca ttc acc caa tca gaa tagccgatgg ctatgagcag gctgctcgcg	498
Arg Ala Phe Thr Gln Ser Glu	
125 130	
ttgctatt	506
<210> 3898	
<211> 515	
<212> DNA	
<213> Homo sapiens	
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<222> 43..471	
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Met Gly Lys Cys	
1	
cgt gga ctt cgt act gct agg aag ctc cgt agt cac cga cga gac cag	102
Arg Gly Leu Arg Thr Ala Arg Lys Leu Arg Ser His Arg Arg Asp Gln	
5 10 15 20	
aag tgg cat gat aaa cag tat aag aaa gct cat ttg ggc aca gcc cta	150
Lys Trp His Asp Lys Gln Tyr Lys Lys Ala His Leu Gly Thr Ala Leu	
25 30 35	
aag gcc aac cct ttt gga ggt gct tct cat gca aaa gga atc gtg ctg	198
Lys Ala Asn Pro Phe Gly Gly Ala Ser His Ala Lys Gly Ile Val Leu	
40 45 50	
gaa aaa gta gga gtt gaa gcc aaa cag cca aat tct gcc att agg aag	246
Glu Lys Val Gly Val Glu Ala Lys Gln Pro Asn Ser Ala Ile Arg Lys	
55 60 65	
tgt gta agg gtc cag ctg atc aag aat ggc aag aaa atc aca gcc ttt	294
Cys Val Arg Val Gln Leu Ile Lys Asn Gly Lys Lys Ile Thr Ala Phe	
70 75 80	
gta ccc aat gac ggt tgc ttg aac ttt att gag gaa aat gat gaa gtt	342
Val Pro Asn Asp Gly Cys Leu Asn Phe Ile Glu Glu Asn Asp Glu Val	
85 90 95 100	
ctg gtt gct gga ttt ggt cgc aaa ggt cat gct gtt ggt gat att cct	390
Leu Val Ala Gly Phe Gly Arg Lys Gly His Ala Val Gly Asp Ile Pro	
105 110 115	
gga gtc cgc ttt aag gtt gtc aaa gta gcc aat gtt tct ctt ttg gcc	438
Gly Val Arg Phe Lys Val Val Lys Val Ala Asn Val Ser Leu Leu Ala	

120 125 130
 cta tac aaa ggc aag aag gaa aga cca aga tca taaatattaa tgggtgaaaac 491
 Leu Tyr Lys Gly Lys Lys Glu Arg Pro Arg Ser
 135 140
 actgtagtaa taaactttca tatg 515

<210> 3899
 <211> 596
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 86..412

<400> 3899
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 tgcagcggcg aggccggccg cgaag atg cca gtg gcg gtg atg gcg gaa agc 112
 Met Pro Val Ala Val Met Ala Glu Ser
 1 5
 gcc ttt agt ttc aaa aag ttg ctg gat cag tgc gag aac cag gag ctc 160
 Ala Phe Ser Phe Lys Lys Leu Leu Asp Gln Cys Glu Asn Gln Glu Leu
 10 15 20 25
 gag gcc cct gga gga att gct aca ccc cca gtg tat ggt cag ctt cta 208
 Glu Ala Pro Gly Gly Ile Ala Thr Pro Pro Val Tyr Gly Gln Leu Leu
 30 35 40
 gct tta tat ttg ctc cat aat gac atg aat aat gca aga tat ctt tgg 256
 Ala Leu Tyr Leu Leu His Asn Asp Met Asn Asn Ala Arg Tyr Leu Trp
 45 50 55
 aaa aga ata cca cct gct ata aaa tct gca aat tct gaa ctt ggg gga 304
 Lys Arg Ile Pro Pro Ala Ile Lys Ser Ala Asn Ser Glu Leu Gly Gly
 60 65 70
 att tgg tca gta gga caa aga atc tgg cag aga gat ttc cct ggg atc 352
 Ile Trp Ser Val Gly Gln Arg Ile Trp Gln Arg Asp Phe Pro Gly Ile
 75 80 85
 tat aca acc atc aac gct cac cag tgg tct gag acg gtc cag cca att 400
 Tyr Thr Thr Ile Asn Ala His Gln Trp Ser Glu Thr Val Gln Pro Ile
 90 95 100 105
 atg gaa agc act tagagatgca acaaggagac ggcctttgc cctggtctct 452
 Met Glu Ser Thr
 caagcgtata cttcaatcat cgccgatgat tttgcagcct ttgttggaact tcctgtagaa 512
 gaggcttggt aaaggcatat tagaacaagg awggcaagct gaattccacc acaagaaatg 572
 gttctgcccc gaaagccagt wgca 596

<210> 3900
 <211> 552
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 126..527

004220 6667560

<400> 3900
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gcggctcccc agtcggcgct tgcgcggaga actcagcgct gagattgtct aaagccccag 120
gaaaa atg gtg gaa aat tca ccg tcg cca ttg cca gaa aga gcg att tat 170
Met Val Glu Asn Ser Pro Ser Pro Leu Pro Glu Arg Ala Ile Tyr
1 5 10 15
ggc ttt gtt ctt ttc tta agc tcc caa ttt ggc ttc ata ctt tac ctc 218
Gly Phe Val Leu Phe Leu Ser Ser Gln Phe Gly Phe Ile Leu Tyr Leu
20 25 30
gtg tgg gcc ttt att cct gaa tct tgg cta aac tct tta ggt tta acc 266
Val Trp Ala Phe Ile Pro Glu Ser Trp Leu Asn Ser Leu Gly Leu Thr
35 40 45
tat tgg cct caa aaa tat tgg gca gtt gca tta cct gtc tac ctc ctt 314
Tyr Trp Pro Gln Lys Tyr Trp Ala Val Ala Leu Pro Val Tyr Leu Leu
50 55 60
att gct ata gta att ggc tac gtg ctc ttg ttt ggg att aac atg atg 362
Ile Ala Ile Val Ile Gly Tyr Val Leu Leu Phe Gly Ile Asn Met Met
65 70 75
agt acc tct cca ctc gac tcc atc cat aca atc aca gat aac tat gca 410
Ser Thr Ser Pro Leu Asp Ser Ile His Thr Ile Thr Asp Asn Tyr Ala
80 85 90 95
aaa aat caa cag cag aag aaa tac caa gag gag gcc att cca gcc tta 458
Lys Asn Gln Gln Gln Lys Lys Tyr Gln Glu Glu Ala Ile Pro Ala Leu
100 105 110
aga gat att tct att agt gaa gta aac caa atg ttc ttt ctt gca gcc 506
Arg Asp Ile Ser Ile Ser Glu Val Asn Gln Met Phe Phe Leu Ala Ala
115 120 125
aaa gaa ctt tac acc aaa aac tgaactgtgt gwaccatagt aacac 552
Lys Glu Leu Tyr Thr Lys Asn
130

<210> 3901
<211> 565
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 29..391

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Met Glu Ala Glu Val Asp Lys Leu
1 5
gaa ctg atg ttc cag aaa gct gag tct gat ctg gat tac att caa tac 100
Glu Leu Met Phe Gln Lys Ala Glu Ser Asp Leu Asp Tyr Ile Gln Tyr
10 15 20
agg ctg gaa tat gaa atc aag act aat cat cct gat tca gca agt gag 148
Arg Leu Glu Tyr Glu Ile Lys Thr Asn His Pro Asp Ser Ala Ser Glu
25 30 35 40
aaa aat cca gtt aca ctc tta aag gaa ttg tca gtg ata aag tct cga 196
Lys Asn Pro Val Thr Leu Leu Lys Glu Leu Ser Val Ile Lys Ser Arg

[illegible]

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<210> 3902
<211> 448
<212> DNA
<213> Homo sapiens
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<222> 97..402
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actagagcag agtacgagtc tgaggcggag ggagta atg gca gga caa gcg ttt															
Met Ala Gly Gln Ala Phe															
1 5															
aga aag ttt ctt cca ctc ttt gac cga gta ttg gtt gaa agg agt gct															162
Arg Lys Phe Leu Pro Leu Phe Asp Arg Val Leu Val Glu Arg Ser Ala															
10 15 20															
gct gaa act gta acc aaa gga ggc att atg ctt cca gaa aaa tct caa															210
Ala Glu Thr Val Thr Lys Gly Gly Ile Met Leu Pro Glu Lys Ser Gln															
25 30 35															
gga aaa gta ttg caa gca aca gta gtc gct gtt gga tcg ggt tct aaa															258
Gly Lys Val Leu Gln Ala Thr Val Val Ala Val Gly Ser Gly Ser Lys															
40 45 50															
gga aag ggt gga gag att caa cca gtt agc gtg aaa gtt gga gat aaa															306
Gly Lys Gly Gly Glu Ile Gln Pro Val Ser Val Lys Val Gly Asp Lys															
55 60 65 70															
gtt ctt ctc cca gaa tat gga ggc acc aaa gta gtt cta gat gac aag															354
Val Leu Leu Pro Glu Tyr Gly Gly Thr Lys Val Val Leu Asp Asp Lys															
75 80 85															
gat tat ttc cta ttt aga gat ggt gac att ctt gga aag tac gta gac															402
Asp Tyr Phe Leu Phe Arg Asp Gly Asp Ile Leu Gly Lys Tyr Val Asp															
90 95 100															
tgaataagt cactattgaa atggcatcaa catgatgctg cccatt															448

<210> 3903
 <211> 615
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 158..508

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 gtgacccgcg caacaagtkc tctgtgacgg ggaagac atg ctc gga agg ggc gga 175
 Met Leu Gly Arg Gly Gly
 1 5
 tgc tgt agg ggt gcc ggg gat gca cca ccc caa gac ccc atg gaa atg 223
 Cys Cys Arg Gly Ala Gly Asp Ala Pro Pro Gln Asp Pro Met Glu Met
 10 15 20
 gca gag gtg gag gag aca ctg aag cga ctg cag anc cag aag gga gtn 271
 Ala Glu Val Glu Glu Thr Leu Lys Arg Leu Gln Xaa Gln Lys Gly Val
 25 30 35
 cag gga atc atc gtc gtg aac aca gaa ggc att ccc atc aag agc acc 319
 Gln Gly Ile Ile Val Val Asn Thr Glu Gly Ile Pro Ile Lys Ser Thr
 40 45 50
 atg gac aac cac acc acc acc cag tat gcc agc ctc atg cac agc ttc 367
 Met Asp Asn His Thr Thr Thr Gln Tyr Ala Ser Leu Met His Ser Phe
 55 60 65 70
 atc ctg aag gca cgg agc acc gtg cgt gac atc gac ccc cag aac gat 415
 Ile Leu Lys Ala Arg Ser Thr Val Arg Asp Ile Asp Pro Gln Asn Asp
 75 80 85
 ctc acc ttc ctt cga att cgc tcc aag aaa aat gaa att atg gtt gca 463
 Leu Thr Phe Leu Arg Ile Arg Ser Lys Lys Asn Glu Ile Met Val Ala
 90 95 100
 cca gat aaa gac tat ttc ctg att gtg att cag aat cca acc gaa 508
 Pro Asp Lys Asp Tyr Phe Leu Ile Val Ile Gln Asn Pro Thr Glu
 105 110 115
 taagccactc tcttggtccc ctgtgtcatt ccttaattta atgcccccca agaatgttaa 568
 tgtcaatcat gtcagtggac tagcacatgg cagtngettg gaaccca 615

<210> 3904
 <211> 632
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 186..515

<400> 3904
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 ccgctgctgc accggccatc ctgagccctt actcggcctt cccgtctccg cttccccgcc 120
 ccgcactagg accccctgcr gatgatcagg gcggcaggag gtgatttctt tcctcttttg 180

gcaac atg gcg ggc gga gaa gct gga gtg act cta ggg cag ccg cat ctt 230
 Met Ala Gly Gly Glu Ala Gly Val Thr Leu Gly Gln Pro His Leu
 1 5 10 15

tcg cgt cag gat ctc acc acc ttg gat gtt acc aag ttg acg cca ctt 278
 Ser Arg Gln Asp Leu Thr Thr Leu Asp Val Thr Lys Leu Thr Pro Leu
 20 25 30

tca cat gaa gtt atc agc aga caa gcc aca att aac ata ggt aca att 326
 Ser His Glu Val Ile Ser Arg Gln Ala Thr Ile Asn Ile Gly Thr Ile
 35 40 45

ggg cat gta gct cat ggg aaa tcc aca gtc gtc aaa gct att tct gga 374
 Gly His Val Ala His Gly Lys Ser Thr Val Val Lys Ala Ile Ser Gly
 50 55 60

ggt cat act gtc agg ttc aaa aat gaa cta gaa aga aat att aca atc 422
 Val His Thr Val Arg Phe Lys Asn Glu Leu Glu Arg Asn Ile Thr Ile
 65 70 75

aag ctt gga tat gct aat gct aag att tat aag ctt gat gac cca agt 470
 Lys Leu Gly Tyr Ala Asn Ala Lys Ile Tyr Lys Leu Asp Asp Pro Ser
 80 85 90 95

tgc cct cgg cca gaa tgt tat aga tnn ttg tgg gag cag tac acc 515
 Cys Pro Arg Pro Glu Cys Tyr Arg Xaa Leu Trp Glu Gln Tyr Thr
 100 105 110

tgacgagttt cctacggaca ttccagggac caaagggact tcaaattagt cagacatggt 575
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 cggtcaccag caacc atg acg gac cag cag gct gag gcc agg tcc tac ctc 171
 Met Thr Asp Gln Gln Ala Glu Ala Arg Ser Tyr Leu
 1 5 10

agc gaa gag atg atc gct gag ttc aag gct gcc ttt gac atg ttt gat 219
 Ser Glu Glu Met Ile Ala Glu Phe Lys Ala Ala Phe Asp Met Phe Asp
 15 20 25

gct gat ggt ggt ggg gac atc agc gtc aag gag ttg ggc acg gtg atg 267
 Ala Asp Gly Gly Gly Asp Ile Ser Val Lys Glu Leu Gly Thr Val Met
 30 35 40

agg atg ctg ggc cag aca ccc acc aag gag gag ctg gac gcc atc atc 315
 Arg Met Leu Gly Gln Thr Pro Thr Lys Glu Glu Leu Asp Ala Ile Ile
 45 50 55 60

gag gag gtg gat gag gac ggc agc ggc acc atc gac ttc gag gag ttc 363
 Glu Glu Val Asp Glu Asp Gly Ser Gly Thr Ile Asp Phe Glu Glu Phe
 65 70 75

ttg gtc atg atg gtg cgc cag atg aaa gag gac gcg aaa ggg aag agc 411
 Leu Val Met Met Val Arg Gln Met Lys Glu Asp Ala Lys Gly Lys Ser

	80	85	90	
gag gag gag ctg gcc gag tgc ttc cgc atc ttc gac agg aat gca gac				459
Glu Glu Glu Leu Ala Glu Cys Phe Arg Ile Phe Asp Arg Asn Ala Asp				
	95	100	105	
ggc tac atc gac ccg gag agc tgg ctg aga ttt tca ggg cct ccg ggg				507
Gly Tyr Ile Asp Pro Glu Ser Trp Leu Arg Phe Ser Gly Pro Pro Gly				
	110	115	120	
agc acg tgactgacga ggagatcgaa tctctgatga aagg				547
Ser Thr				
125				
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			Met Ser Gln	
			1	
acc agg gat tta cag gga gga aaa gct ttc gga ctg ctg aag gcc cag				165
Thr Arg Asp Leu Gln Gly Gly Lys Ala Phe Gly Leu Leu Lys Ala Gln				
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cag gaa gag agg ctg gat gag atc aac aag caa ttc cta gac gat ccc				213
Gln Glu Glu Arg Leu Asp Glu Ile Asn Lys Gln Phe Leu Asp Asp Pro				
	20	25	30	35
aaa tat agc agt gat gag gat ctg ccc tcc aaa ctg gaa ggc ttc aaa				261
Lys Tyr Ser Ser Asp Glu Asp Leu Pro Ser Lys Leu Glu Gly Phe Lys				
	40	45	50	
gag aaa tac atg gag ttt gac ctt aat gga aat ggc gat att gat atc				309
Glu Lys Tyr Met Glu Phe Asp Leu Asn Gly Asn Gly Asp Ile Asp Ile				
	55	60	65	
atg tcc ctg aaa cga atg ctg gag aaa ctt gga gtc ccc aag act cac				357
Met Ser Leu Lys Arg Met Leu Glu Lys Leu Gly Val Pro Lys Thr His				
	70	75	80	
cta gag cta aag aaa tta att gga gag gtg tcc agt ggc tcc ggg gag				405
Leu Glu Leu Lys Lys Leu Ile Gly Glu Val Ser Ser Gly Ser Gly Glu				
	85	90	95	
acg ttc agc tac cct gac ttt ctc agg atg atg ctg ggc aag aga tct				453
Thr Phe Ser Tyr Pro Asp Phe Leu Arg Met Met Leu Gly Lys Arg Ser				
	100	105	110	115
gcc atc cta aaa atg atc ctg atg tat gag gaa aaa gcg aga gaa aag				501
Ala Ile Leu Lys Met Ile Leu Met Tyr Glu Glu Lys Ala Arg Glu Lys				
	120	125	130	
gaa aag cca aca ggc ccc cca gcn aga aag cta tct ctg agt tgc cct				549
Glu Lys Pro Thr Gly Pro Pro Ala Arg Lys Leu Ser Leu Ser Cys Pro				
	135	140	145	
gat ttg aag gga aaa ggg atg atg gga ttg aag ggg ctt cta att acc				597

Asp Leu Lys Gly Lys Gly Met Met Gly Leu Lys Gly Leu Leu Ile Thr
 150 155 160
 cag ata tgg aaa cag aag aca aaa ttg taagccagag tcaacaaatt 644
 Gln Ile Trp Lys Gln Lys Thr Lys Leu
 165 170
 aaataaatta cccc 658

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 Met Lys
 1
 aac ttt gtg acc aag gtt tcg gtt ggg gag ttt gtg ggg gaa ggt gaa 164
 Asn Phe Val Thr Lys Val Ser Val Gly Glu Phe Val Gly Glu Gly Glu
 5 10 15
 ggg aaa agc aag aag att tca aag aaa aat gcc gcc ata gct gtt ctt 212
 Gly Lys Ser Lys Lys Ile Ser Lys Lys Asn Ala Ala Ile Ala Val Leu
 20 25 30
 gag gag ctg aag aag tta ccg ccc ctg cct gca gtt gaa cga gta aag 260
 Glu Glu Leu Lys Lys Leu Pro Pro Leu Pro Ala Val Glu Arg Val Lys
 35 40 45 50
 cct aga atc aaa aag aaa aca aaa ccc ata gtc aag cca cag aca agc 308
 Pro Arg Ile Lys Lys Lys Thr Lys Pro Ile Val Lys Pro Gln Thr Ser
 55 60 65
 cca gaa tat ggc cag ggg atc aat ccg att agc cga ctg gcc cag atc 356
 Pro Glu Tyr Gly Gln Gly Ile Asn Pro Ile Ser Arg Leu Ala Gln Ile
 70 75 80
 cag cag gca aaa aag gag aag gag cag agt aca cgc tcc tca cag agc 404
 Gln Gln Ala Lys Lys Glu Lys Glu Gln Ser Thr Arg Ser Ser Gln Ser
 85 90 95
 gag gcc tcc cgc gcc gca ggg agt ttg tgatgcaggt g 442
 Glu Ala Ser Arg Ala Ala Gly Ser Leu
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 Met Ala Leu
 1
 tca aag agg gag ctg gat gag ctg aaa cca tgg ata gag aag aca gtg 165
 Ser Lys Arg Glu Leu Asp Glu Leu Lys Pro Trp Ile Glu Lys Thr Val
 5 10 15
 aag agg gtc ctg ggt ttc tca gag cct acg gtg gtc aca gca gca ttg 213
 Lys Arg Val Leu Gly Phe Ser Glu Pro Thr Val Val Thr Ala Ala Leu
 20 25 30 35
 aac tgt gtg ggg aag ggc atg gac aag aag aag gca gcc gat cat ctg 261
 Asn Cys Val Gly Lys Gly Met Asp Lys Lys Lys Ala Ala Asp His Leu
 40 45 50
 aaa cct ttt ctt gat gat tct act ctc cga ttt gtg gac aaa ctg ttt 309
 Lys Pro Phe Leu Asp Asp Ser Thr Leu Arg Phe Val Asp Lys Leu Phe
 55 60 65
 gag gct gtg gag gaa ggc cga agc tct agg cat tcc aag tct agc agt 357
 Glu Ala Val Glu Glu Gly Arg Ser Ser Arg His Ser Lys Ser Ser Ser
 70 75 80
 gac agg agc aga aaa cga gag cta aag gag gtg ttt ggt gat gac tct 405
 Asp Arg Ser Arg Lys Arg Glu Leu Lys Glu Val Phe Gly Asp Asp Ser
 85 90 95
 gag atc tct aaa gaa tca tca gga gta aag aag cga cga ata ccc cgt 453
 Glu Ile Ser Lys Glu Ser Ser Gly Val Lys Lys Arg Arg Ile Pro Arg
 100 105 110 115
 ttt gag gag tkg aag aag agc cag agg tgatccctgg gcctccatca 500
 Phe Glu Glu Xaa Lys Lys Ser Gln Arg
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 gagagcctgg cat 513
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 agtgaactcc ggctggctg aggaaggagg aggcacccac aggctgctgg gaggagagca 120
 taaggctcaa a atg gaa aat cat aaa tcc aat aat aag gaa aac ata aca 170
 Met Glu Asn His Lys Ser Asn Asn Lys Glu Asn Ile Thr
 1 5 10
 att gtt gat ata tcc aga aaa att aac cag ctt cca gaa gca gaa agg 218
 Ile Val Asp Ile Ser Arg Lys Ile Asn Gln Leu Pro Glu Ala Glu Arg
 15 20 25
 aat cta ctt gaa aat gga tgc gtt tat gtt gga tta aat gct gct ctt 266
 Asn Leu Leu Glu Asn Gly Ser Val Tyr Val Gly Leu Asn Ala Ala Leu
 30 35 40 45
 tgt ggc ctc ata gca aac agt ctt ttt cga cgc atc ttg aat gtg aca 314

Cys Gly Leu Ile Ala Asn Ser Leu Phe Arg Arg Ile Leu Asn Val Thr	
	50 55 60
aag gct cgc ata gct gct ggc tta cca atg gca ggg ata cct ttt ctt	362
Lys Ala Arg Ile Ala Ala Gly Leu Pro Met Ala Gly Ile Pro Phe Leu	
	65 70 75
aca aca gac tta act tac aga tgt ttt gta agt ttt cct ttg aat aca	410
Thr Thr Asp Leu Thr Tyr Arg Cys Phe Val Ser Phe Pro Leu Asn Thr	
	80 85 90
ggg gat ttg gat tgt gaa acc tgt acc ata aca cgg agt gac	452
Gly Asp Leu Asp Cys Glu Thr Cys Thr Ile Thr Arg Ser Asp	
	95 100 105
tgactgggtct tggtattggt ggtctatacc	482

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<211> 438

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 75..428

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cgcttctctg cact atg tgc ggt ggc ctc ctg aag gcg ctg cgc asc gac	110
	Met Ser Gly Gly Leu Leu Lys Ala Leu Arg Xaa Asp
	1 5 10
tcc tac gtg gag ctg agc cag tac cgg gac cag cac ttc cgg ggt gac	158
Ser Tyr Val Glu Leu Ser Gln Tyr Arg Asp Gln His Phe Arg Gly Asp	
	15 20 25
aat gaa gaa caa gaa aaa tta ctg aag aaa agc tgt acg tta tat gtt	206
Asn Glu Glu Gln Glu Lys Leu Leu Lys Lys Ser Cys Thr Leu Tyr Val	
	30 35 40
gga aat ctt tct ttt tac aca act gaa gaa caa atc tat gaa ctc ttc	254
Gly Asn Leu Ser Phe Tyr Thr Thr Glu Glu Gln Ile Tyr Glu Leu Phe	
	45 50 55 60
agc aaa agt ggt gac ata aag aaa atc att atg ggt ctg gat aaa atg	302
Ser Lys Ser Gly Asp Ile Lys Lys Ile Ile Met Gly Leu Asp Lys Met	
	65 70 75
aag aaa aca gca tgt gga ttc tgt ttg tgg aat att act cac gcg cag	350
Lys Lys Thr Ala Cys Gly Phe Cys Leu Trp Asn Ile Thr His Ala Gln	
	80 85 90
atg cgg aaa acg cca tgc ggt aca tnw atg gga cgc gtc tgg atg acc	398
Met Arg Lys Thr Pro Cys Gly Thr Xaa Met Gly Arg Val Trp Met Thr	
	95 100 105
gaa tca ttc gca cag act ggg acg cag ctt taaggagagc	438
Glu Ser Phe Ala Gln Thr Gly Thr Gln Leu	
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<210> 3911

<211> 663

<212> DNA

<213> Homo sapiens

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 tgacaagaaa acaaagatct tattcaaaag aggtcttaca gcaacccaac gtctcatctt 180
 cccatagtaa agatgacggc gccttgagggt aagctacagg caacaccact tccgcgtttc 240
 tcttgcgccc tgggtccaag atg gcg gat gaa gcc acg cga cgt gtt gtg tct 292
 Met Ala Asp Glu Ala Thr Arg Arg Val Val Ser
 1 5 10
 gag atc ccg gtg ctg aag act aac gcc gga ccc cga gat cgt gag ttg 340
 Glu Ile Pro Val Leu Lys Thr Asn Ala Gly Pro Arg Asp Arg Glu Leu
 15 20 25
 tgg gtg cag cga ctg aag gag gaa tat cag tcc ctt atc cgg tat gtg 388
 Trp Val Gln Arg Leu Lys Glu Glu Tyr Gln Ser Leu Ile Arg Tyr Val
 30 35 40
 gag aac aac aag aat gct gac aac gat tgg ttc cga ctg gag tcc aac 436
 Glu Asn Asn Lys Asn Ala Asp Asn Asp Trp Phe Arg Leu Glu Ser Asn
 45 50 55
 aag gaa gga act cgg tgg ttt gga aaa tgc tgg tat atc cat gac ctc 484
 Lys Glu Gly Thr Arg Trp Phe Gly Lys Cys Trp Tyr Ile His Asp Leu
 60 65 70 75
 ctg aaa tat gag ttt gac atc gag ttt gac att cct atc aca tat cct 532
 Leu Lys Tyr Glu Phe Asp Ile Glu Phe Asp Ile Pro Ile Thr Tyr Pro
 80 85 90
 act act gcc cca gaa att gca gtt cct gag ctg gat gga aag aca gca 580
 Thr Thr Ala Pro Glu Ile Ala Val Pro Glu Leu Asp Gly Lys Thr Ala
 95 100 105
 aag atg tac agc tgg gtc cat ggc tgg cag tgg aaa tcc ctg atc 625
 Lys Met Tyr Ser Trp Val His Gly Trp Gln Trp Lys Ser Leu Ile
 110 115 120
 tgattcagaa gggcgctcatc caacacaaag agaaatgc 663

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<220>
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 <222> 211..576

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 aatcgctcgt ttttaggaata aagatgacgg cgccttgagg taagctacag gcaacaccac 180
 ttccgcgttt ctcttgcgcc ctgggtccaag atg gcg gat gaa gcc acg cga cgt 234
 Met Ala Asp Glu Ala Thr Arg Arg
 1 5

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gtt gtg tct gag atc ccg gtg ctg aag act aac gcc gga ccc cga gat      282
Val Val Ser Glu Ile Pro Val Leu Lys Thr Asn Ala Gly Pro Arg Asp
      10                      15                      20
cgt gag ttg tgg gtg cag cga ctg aag gag gaa tat cag tcc ctt atc      330
Arg Glu Leu Trp Val Gln Arg Leu Lys Glu Glu Tyr Gln Ser Leu Ile
      25                      30                      35                      40
cgg tat gtg gag aac aac aag aat gct gac aac gat tgg ttc cga ctg      378
Arg Tyr Val Glu Asn Asn Lys Asn Ala Asp Asn Asp Trp Phe Arg Leu
      45                      50                      55
gag tcc aac aag gaa gga act cgg tgg ttt gga aaa tgc tgg tat atc      426
Glu Ser Asn Lys Glu Gly Thr Arg Trp Phe Gly Lys Cys Trp Tyr Ile
      60                      65                      70
cat gac ctc ctg aaa tat gag ttt gac atc gag ttt gac att cct atc      474
His Asp Leu Leu Lys Tyr Glu Phe Asp Ile Glu Phe Asp Ile Pro Ile
      75                      80                      85
aca tat cct act act gcc cca gaa att gca gtt cct gag ctg gat gga      522
Thr Tyr Pro Thr Thr Ala Pro Glu Ile Ala Val Pro Glu Leu Asp Gly
      90                      95                      100
aag aca gca aag atg tac agc tgg gtc cat ggc tgg cag tgg aaa tcc      570
Lys Thr Ala Lys Met Tyr Ser Trp Val His Gly Trp Gln Trp Lys Ser
      105                      110                      115                      120
ctg atc tgattcagaa gggcgctcatc caacacaaag agaaatgc      614
Leu Ile

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<211> 392
<212> DNA
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<220>
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<222> 48..383

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Met Pro Lys
      1
ttt tat tgt gac tac tgc gat aca tac ctc acc cat gac tct cca tct      104
Phe Tyr Cys Asp Tyr Cys Asp Thr Tyr Leu Thr His Asp Ser Pro Ser
      5                      10                      15
gtg aga aag aca cac tgc agt gga agg aaa cac aaa gag aat gtg aaa      152
Val Arg Lys Thr His Cys Ser Gly Arg Lys His Lys Glu Asn Val Lys
      20                      25                      30                      35
gac tat tat cag aaa tgg atg gaa gag cag gct cag agc ctg att gac      200
Asp Tyr Tyr Gln Lys Trp Met Glu Glu Gln Ala Gln Ser Leu Ile Asp
      40                      45                      50
aaa aca acg gct gca ttt caa caa gga aag ata cct cct act cca ttc      248
Lys Thr Thr Ala Ala Phe Gln Gln Gly Lys Ile Pro Pro Thr Pro Phe
      55                      60                      65
tct gct cct cct cct gca ggg gcg atg ata cca cct ccc ccc agc ctt      296
Ser Ala Pro Pro Pro Ala Gly Ala Met Ile Pro Pro Pro Ser Leu
      70                      75                      80
ccg ggt cct cct cgc cct ggt atg atg cca gca ccc cat atg ggg ggc      344

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Pro Gly Pro Pro Arg Pro Gly Met Met Pro Ala Pro His Met Gly Gly
 85 90 95
 cct ccc atg atg cca atg atg ggc ctc ctc ctc ctg gga tgatgcagt 392
 Pro Pro Met Met Pro Met Met Gly Leu Leu Leu Leu Gly
 100 105 110

<210> 3914
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 <212> DNA
 <213> Homo sapiens

<220>
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 <222> 25..405

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 Met Glu Glu Val Pro His Asp Cys Pro
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 Gly Ala Asp Ser Ala Gln Ala Gly Arg Gly Ala Ser Cys Gln Gly Cys
 10 15 20 25
 ccc aac cag cgg ctg tgc gct tct gga gcg ggg gcc act ccg gac acg 147
 Pro Asn Gln Arg Leu Cys Ala Ser Gly Ala Gly Ala Thr Pro Asp Thr
 30 35 40
 gct ata gag gaa atc aaa gag aaa atg aag act gta aaa cac aaa atc 195
 Ala Ile Glu Glu Ile Lys Glu Lys Met Lys Thr Val Lys His Lys Ile
 45 50 55
 ttg gta ttg tct ggg aaa ggc ggt gtt ggg aaa agc aca ttc agc gcc 243
 Leu Val Leu Ser Gly Lys Gly Val Gly Lys Ser Thr Phe Ser Ala
 60 65 70
 cac ctt gcc cat ggc cta gca gag gat gaa aac aca cag att gct ctt 291
 His Leu Ala His Gly Leu Ala Glu Asp Glu Asn Thr Gln Ile Ala Leu
 75 80 85
 cta gac atc gat ata tgt ggg cca tcg att ccc aag ata atg gga ttg 339
 Leu Asp Ile Asp Ile Cys Gly Pro Ser Ile Pro Lys Ile Met Gly Leu
 90 95 100 105
 gaa gga gag cag gtt cac cag agt ggc tca ggc tgg tct cca gtg tac 387
 Glu Gly Glu Gln Val His Gln Ser Gly Ser Gly Trp Ser Pro Val Tyr
 110 115 120
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 Val Glu Asp Asn Trp Gly
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<210> 3915
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 <212> DNA
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<220>
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Gly Ala Asp Ser Ala Gln Ala Gly Arg Gly Ala Ser Cys Gln Gly Cys
10 15 20 25
ccc aac cag cgg ctg tgc gct tct gga gcg ggg gcc act gcg gac acg 147
Pro Asn Gln Arg Leu Cys Ala Ser Gly Ala Thr Ala Asp Thr
30 35 40
gct ata gag gaa atc aaa gag aaa atg aag act gtn aaa cac aaa atc 195
Ala Ile Glu Glu Ile Lys Glu Lys Met Lys Thr Val Lys His Lys Ile
45 50 55
ttg gta ttg tct ggg aaa ggc ggt gtt ggg aaa agc aca ttc agc gcc 243
Leu Val Leu Ser Gly Lys Gly Gly Val Gly Lys Ser Thr Phe Ser Ala
60 65 70
cac ctt gcc cat ggc cta gca gag gat ttt gga caa ggc tgc cag aaa 291
His Leu Ala His Gly Leu Ala Glu Asp Phe Gly Gln Gly Cys Gln Lys
75 80 85
gtg ttg cta ctg gaa gaa aag tat atk att tca ctt tgg ttt ttt ttg 339
Val Leu Leu Leu Glu Glu Lys Tyr Xaa Ile Ser Leu Trp Phe Phe Leu
90 95 100 105
tgt att gtt ttt tcc aga gam agg gtc tca ctc tgt tgc cca ggc tgg 387
Cys Ile Val Phe Ser Arg Xaa Arg Val Ser Leu Cys Cys Pro Gly Trp
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Ser Xaa Val Ala Arg Ser
125

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<211> 1007
<212> DNA
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<220>
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caatcaccag tctcctgtca tggcttctct gggcagattg ggggtctgga ccaacaggaa 180
aaggccccgg cccatcccca tggtgaccga gttgtatata gggagccgca tccgcctatg 240
tgccgcaggt tctcttacat cgaccgccta agagtcgcgc tgtaagaagc aacaacctct 300
cctcttcgtc tccgccatca gctcggcagt cgcgaasagc aacc atg cgt gag tgc 356
Met Arg Glu Cys
1
atc tcc atc cac gtt ggc cag gct ggt gtc cag att ggc aat gcc tgc 404
Ile Ser Ile His Val Gly Gln Ala Gly Val Gln Ile Gly Asn Ala Cys
5 10 15 20
tgg gag ctc tac tgc ctg gaa cac ggc atc cag ccc gat ggc cag atg 452
Trp Glu Leu Tyr Cys Leu Glu His Gly Ile Gln Pro Asp Gly Gln Met

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cca agt gac aag acc att ggg gga gga gat gat tcc ttc aac acc ttc				500
Pro Ser Asp Lys Thr Ile Gly Gly Gly Asp Asp Ser Phe Asn Thr Phe				
	40	45	50	
ttc agt gag acg ggg gct ggc aag cat gtg ccc cgg gca gtg ttt gta				548
Phe Ser Glu Thr Gly Ala Gly Lys His Val Pro Arg Ala Val Phe Val				
	55	60	65	
gac ttg gaa ccc aca gtc att gat gaa gtt cgc act ggc acc tac cgc				596
Asp Leu Glu Pro Thr Val Ile Asp Glu Val Arg Thr Gly Thr Tyr Arg				
	70	75	80	
cag ctc ttc cac cct gag car cty atc aca ggc aar gaa gat gct gcc				644
Gln Leu Phe His Pro Glu Gln Leu Ile Thr Gly Lys Glu Asp Ala Ala				
	85	90	95	100
aat aac tat gcc cga ggg cac tac acc att ggc aag gag atc att gac				692
Asn Asn Tyr Ala Arg Gly His Tyr Thr Ile Gly Lys Glu Ile Ile Asp				
	105	110	115	
cty gtg ttg gac cga att cgc aag ctg gcy gac cag tgc acs ggt cty				740
Leu Val Leu Asp Arg Ile Arg Lys Leu Ala Asp Gln Cys Thr Gly Leu				
	120	125	130	
cag ggc ttc ttg gtt ttc cac agc ytt ggt ggg gga act ggt tct ggg				788
Gln Gly Phe Leu Val Phe His Ser Xaa Gly Gly Gly Thr Gly Ser Gly				
	135	140	145	
ttc acc tcs ctg ctc atg gaa cgt ctc tca gtt gat tat ggc aag aag				836
Phe Thr Ser Leu Leu Met Glu Arg Leu Ser Val Asp Tyr Gly Lys Lys				
	150	155	160	
tcc aag ctg gag ttc tcy att tac ccr gcr ccc cag gtt tcc aca gct				884
Ser Lys Leu Glu Phe Ser Ile Tyr Pro Ala Pro Gln Val Ser Thr Ala				
	165	170	175	180
gta gtt gag ccc tac aac tcc atc ctc acc acc cac acc acc ctg gag				932
Val Val Glu Pro Tyr Asn Ser Ile Leu Thr Thr His Thr Thr Leu Glu				
	185	190	195	
cac tct gat tgt gcc ttn cat ggt aga caa tgaggccatc tatgacatct				982
His Ser Asp Cys Ala Xaa His Gly Arg Gln				
	200	205		
gtcgtagaaa cctcgataty gagcg				1007

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<212> DNA

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<221> CDS

<222> 103..720

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cttcgcctcc ttcaccgccg cagaccctt caagttctag tc atg cgt gag tgc	114
	Met Arg Glu Cys
	1

atc tcc atc cac gtt ggc cag gct ggt gtc cag att ggc aat gcc tgc	162
Ile Ser Ile His Val Gly Gln Ala Gly Val Gln Ile Gly Asn Ala Cys	
	5 10 15 20

tgg gag ctc tac tgc ctg gaa cac ggc atc cag ccc gat ggc cag atg	210
Trp Glu Leu Tyr Cys Leu Glu His Gly Ile Gln Pro Asp Gly Gln Met	
25 30 35	
cca agt gac aag acc att ggg gga gga gat gat tcc ttc aac acc ttc	258
Pro Ser Asp Lys Thr Ile Gly Gly Gly Asp Asp Ser Phe Asn Thr Phe	
40 45 50	
ttc agt gaa acg ggt gct ggc aag cat gtg ccc cgg gca gtg ttt gta	306
Phe Ser Glu Thr Gly Ala Gly Lys His Val Pro Arg Ala Val Phe Val	
55 60 65	
gac ttg gaa ccc aca gtc att gat gaa gtt cgc act ggc acy tac cgc	354
Asp Leu Glu Pro Thr Val Ile Asp Glu Val Arg Thr Gly Thr Tyr Arg	
70 75 80	
cag ctc ttc cac cct gag cag ctc atc aca ggc aag gaa gat gct gcc	402
Gln Leu Phe His Pro Glu Gln Leu Ile Thr Gly Lys Glu Asp Ala Ala	
85 90 95 100	
aat aac tat gcc cga ggg cac tac acc att ggc aag gag atc att gac	450
Asn Asn Tyr Ala Arg Gly His Tyr Thr Ile Gly Lys Glu Ile Ile Asp	
105 110 115	
ctt gtg ttg gac cga att cgc aag ctg gcy gac cag tgc acs ggt cty	498
Leu Val Leu Asp Arg Ile Arg Lys Leu Ala Asp Gln Cys Thr Gly Leu	
120 125 130	
cag ggc ttc ttg gtt ttc cac agc yyt kgt ggg gga act ggt tct ggg	546
Gln Gly Phe Leu Val Phe His Ser Xaa Xaa Gly Gly Thr Gly Ser Gly	
135 140 145	
ttc acc tcs ctg ctc atg gaa cgt ctc tca gtt gat tat ggc aag aag	594
Phe Thr Ser Leu Leu Met Glu Arg Leu Ser Val Asp Tyr Gly Lys Lys	
150 155 160	
tcc aag ctg gag ttc tcy att tac ccr gcr ccc cag gtt tcc aca gct	642
Ser Lys Leu Glu Phe Ser Ile Tyr Pro Ala Pro Gln Val Ser Thr Ala	
165 170 175 180	
gta gtt gag ccc tac aac tcc atc ctc acc cac acc acc ctg gag	690
Val Val Glu Pro Tyr Asn Ser Ile Leu Thr Thr His Thr Thr Leu Glu	
185 190 195	
cac tct gat tgt gcc ttn cat ggt aga caa tgaggccatc tatgacatct	740
His Ser Asp Cys Ala Xaa His Gly Arg Gln	
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gtcgtagaaa cctcgataty gagcg	765

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 <212> DNA
 <213> Homo sapiens

<220>
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 <222> 28..351

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Met Glu Ala Val Leu Thr Glu Glu Leu	
1 5	
gat gag gaa gag cag ctg ctg aga agg cat cgc aaa gag aag aag gag	102
Asp Glu Glu Glu Gln Leu Leu Arg Arg His Arg Lys Glu Lys Lys Glu	

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10          15          20          25
ttg caa gcc aaa att cag ggc atg aag aat gct gtt ccc aag aat gac      150
Leu Gln Ala Lys Ile Gln Gly Met Lys Asn Ala Val Pro Lys Asn Asp
          30          35          40
aag aag agg agg aag car ctc acc gaa gat gtg gcc aag ttg gaa aaa      198
Lys Lys Arg Arg Lys Gln Leu Thr Glu Asp Val Ala Lys Leu Glu Lys
          45          50          55
gaa atg gaa cag aaa cat aga gag gaa ctg gag caa ttg aag ctg act      246
Glu Met Glu Gln Lys His Arg Glu Glu Leu Glu Gln Leu Lys Leu Thr
          60          65          70
act aag gag aat aag ata gat tct gtt gct gtt aac att tca aac ttg      294
Thr Lys Glu Asn Lys Ile Asp Ser Val Ala Val Asn Ile Ser Asn Leu
          75          80          85
gtg ctt gag aat cag cca cct cgg ata tca aaa gca caa aag aga cgg      342
Val Leu Glu Asn Gln Pro Pro Arg Ile Ser Lys Ala Gln Lys Arg Arg
          90          95          100          105
gtg cct gga tagaaggagc tctctgtgtt gtccttggtc cctgctctgc      391
Val Pro Gly
tcttaccagc tgtaggcctt tggnaatctc tctgcgtgct gtttcctcag aagaggaaaa      451
tgag      455

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gggaaggtca gcgccgta atg gcg ttc ttg gcg tgc gga ccc tac ctg acc      111
Met Ala Phe Leu Ala Ser Gly Pro Tyr Leu Thr
          1          5          10
cat cag caa aag gtg ttg cgg ctt tat aag cgg gcg cta cgc cac ctc      159
His Gln Gln Lys Val Leu Arg Leu Tyr Lys Arg Ala Leu Arg His Leu
          15          20          25
gag tgc tgg tgc gtc cag aga gac aaa tac cga tac ttt gct tgt ttg      207
Glu Ser Trp Cys Val Gln Arg Asp Lys Tyr Arg Tyr Phe Ala Cys Leu
          30          35          40
atg aga gcc cgg ttt gaa gaa cat aag aat gaa aag grt atg gcg aag      255
Met Arg Ala Arg Phe Glu Glu His Lys Asn Glu Lys Xaa Met Ala Lys
          45          50          55
gcc acc cag ctg aag gag gcc gag gaa gaa ttc tgg tac cgt cag cat      303
Ala Thr Gln Leu Lys Glu Ala Glu Glu Glu Phe Trp Tyr Arg Gln His
          60          65          70          75
cca cag cca tac atc ttc cct gac tct cct ggg ggc acc tcc tat gag      351
Pro Gln Pro Tyr Ile Phe Pro Asp Ser Pro Gly Gly Thr Ser Tyr Glu
          80          85          90
aga tac gat tgc tac aag gtc cca gaa tgg tgc tta gat gac tgg cat      399
Arg Tyr Asp Cys Tyr Lys Val Pro Glu Trp Cys Leu Asp Asp Trp His
          95          100          105

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cct tct gag aag gca atg tat cct gat tac ttt gcc aag aga gaa cag 447
 Pro Ser Glu Lys Ala Met Tyr Pro Asp Tyr Phe Ala Lys Arg Glu Gln
 110 115 120
 tgg aag aaa ctg cgg gga aag ctg gga acg aga ggt taagcagctg 493
 Trp Lys Lys Leu Arg Gly Lys Leu Gly Thr Arg Gly
 125 130 135

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 <212> DNA
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<220>
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 cgcttttgat cgtcttctc tkgccagcca tcaggtaagc caag atg ggt gca tac 116
 Met Gly Ala Tyr
 1
 aag tac atc cag gag cta tgg aga aag aag cag tct gat gtc atg cgc 164
 Lys Tyr Ile Gln Glu Leu Trp Arg Lys Lys Gln Ser Asp Val Met Arg
 5 10 15 20
 ttt ctt ctg agg gtc cgc tgc tgg cag tac cgc cag ctc tct gct ctc 212
 Phe Leu Leu Arg Val Arg Cys Trp Gln Tyr Arg Gln Leu Ser Ala Leu
 25 30 35
 cac agg gct ccc cgc ccc acc cgg cct gat aaa gcg cgc cga ctg ggc 260
 His Arg Ala Pro Arg Pro Thr Arg Pro Asp Lys Ala Arg Arg Leu Gly
 40 45 50
 tac aag gcc aag caa ggt tac gtt ata tat agg att cgt gtt cgc cgt 308
 Tyr Lys Ala Lys Gln Gly Tyr Val Ile Tyr Arg Ile Arg Val Arg Arg
 55 60 65
 ggt ggc cga aaa cgc cca gtt cct aag ggt gca act tac ggc aag cct 356
 Gly Gly Arg Lys Arg Pro Val Pro Lys Gly Ala Thr Tyr Gly Lys Pro
 70 75 80
 gtc cat cat ggt gtt aac cag cta aag ttt gct cga agc ctt cag tcc 404
 Val His His Gly Val Asn Gln Leu Lys Phe Ala Arg Ser Leu Gln Ser
 85 90 95 100
 gtt gca gag gag cga gct gga cgc cac tgt ggg gct ctg aga gtc ctg 452
 Val Ala Glu Glu Arg Ala Gly Arg His Cys Gly Ala Leu Arg Val Leu
 105 110 115
 aat tct tac tgg gtt ggt gaa gat tcc aca tac aaa ttt ttt gag gtt 500
 Asn Ser Tyr Trp Val Gly Glu Asp Ser Thr Tyr Lys Phe Phe Glu Val
 120 125 130
 atc ctc att gat cca ttc cat aaa gct atc aga aga aat cct gac acc 548
 Ile Leu Ile Asp Pro Phe His Lys Ala Ile Arg Arg Asn Pro Asp Thr
 135 140 145
 cag tgg atc acc aaa cca gtc cac aag cac agg gag atg cgt ggg ctg 596
 Gln Trp Ile Thr Lys Pro Val His Lys His Arg Glu Met Arg Gly Leu
 150 155 160
 aca tct gca ggc cga aag agc cgt ggc ctt gga aag ggc cac aag ttc 644
 Thr Ser Ala Gly Arg Lys Ser Arg Gly Leu Gly Lys Gly His Lys Phe

165 170 175 180
 cac cac act att ggt ggc tct cgc cgg gca gct tgg aga agg cgc aat 692
 His His Thr Ile Gly Gly Ser Arg Arg Ala Ala Trp Arg Arg Arg Asn
 185 190 195
 act ctc cag ctc cac cgt tac cgc taatataagt aaagtttgta aaattcatatc 746
 Thr Leu Gln Leu His Arg Tyr Arg
 200
 ttaataaaca atttaggaca gtcattgtctg cttacagggtg ttatttgtct gttaaaacta 806
 gtctgcagat gtttcttgaa tgctttgtca aattaagaaa gttaaagtgc aataatgttt 866
 gaagacaata agtgggtgggtg tatcttgttt ctaataagat aaactttttt gtctttgtct 926
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 ataaattctt taaaaggaga gaactgaaac tagcc 1021

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 <222> 124..735

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 cgtcttattg tacttaaagc ggatgatatt taatacacag ttgatttca caggtaagcc 120
 aag atg ggt gca tac aag tac atc cag gag cta tgg aga aag aag cag 168
 Met Gly Ala Tyr Lys Tyr Ile Gln Glu Leu Trp Arg Lys Lys Gln
 1 5 10 15
 tct gat gtc atg cgc ttt ctt ctg agg gtc cgc tgc tgg cag tac cgc 216
 Ser Asp Val Met Arg Phe Leu Leu Arg Val Arg Cys Trp Gln Tyr Arg
 20 25 30
 cag ctc tct gct ctc cac agg gct ccc cgc ccc acc cgg cct gat aaa 264
 Gln Leu Ser Ala Leu His Arg Ala Pro Arg Pro Thr Arg Pro Asp Lys
 35 40 45
 gcg cgc cga ctg ggc tac aag gcc aag caa ggt tac gtt ata tat agg 312
 Ala Arg Arg Leu Gly Tyr Lys Ala Lys Gln Gly Tyr Val Ile Tyr Arg
 50 55 60
 att cgt gtt cgc cgt ggt ggc cga aaa cgc cca gtt cct aag ggt gca 360
 Ile Arg Val Arg Arg Gly Gly Arg Lys Arg Pro Val Pro Lys Gly Ala
 65 70 75
 act tac ggc aag cct gtc cat cat ggt gtt aac cag cta aag ttt gct 408
 Thr Tyr Gly Lys Pro Val His His Gly Val Asn Gln Leu Lys Phe Ala
 80 85 90 95
 cga agc ctt cag tcc gtt gca gag gag cga gct gga cgc cac tgt ggg 456
 Arg Ser Leu Gln Ser Val Ala Glu Glu Arg Ala Gly Arg His Cys Gly
 100 105 110
 gct ctg aga gtc ctg aat tct tac tgg gtt ggt gaa gat tcc aca tac 504
 Ala Leu Arg Val Leu Asn Ser Tyr Trp Val Gly Glu Asp Ser Thr Tyr
 115 120 125
 aaa ttt ttt gag gtt atc ctc att gat cca ttc cat aaa gct atc aga 552
 Lys Phe Phe Glu Val Ile Leu Ile Asp Pro Phe His Lys Ala Ile Arg
 130 135 140
 aga aat cct gac acc cag tgg atc acc aaa cca gtc cac aag cac agg 600

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Arg Asn Pro Asp Thr Gln Trp Ile Thr Lys Pro Val His Lys His Arg
145                               150           155
gag atg cgt ggg ctg aca tct gca ggc cga aag agc cgt ggc ctt gga      648
Glu Met Arg Gly Leu Thr Ser Ala Gly Arg Lys Ser Arg Gly Leu Gly
160                               165           170           175
aag ggc cac aag ttc cac cac act att ggt ggc tct cgc cgg gca gct      696
Lys Gly His Lys Phe His His Thr Ile Gly Gly Ser Arg Arg Ala Ala
180                               185           190
tgg aga agg cgc aat act ctc cag ctc cac cgt tac cgc taatataagt      745
Trp Arg Arg Arg Asn Thr Leu Gln Leu His Arg Tyr Arg
195                               200
aaagtttgta aaattcatac ttaataaaca atttaggaca gtcattgtctg cttacaggtg      805
ttatttgtct gttaaaacta gtctgcagat gtttcttgaa tgctttgtca aattaagaaa      865
gttaaagtgc aataatgttt gaagacaata agtgggtggtg tatcttgttt ctaataagat      925
aaactttttt gtctttgctt tatcttatta gggagttgta tgtcagtgtg taaaacatac      985
tgtgtggtat aacaggctta ataaattctt taaaaggaga gaactgaaac tagcc      1040

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<211> 472
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 54..359

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Met
1
gcg gac gac gta gac cag caa caa act acc aac act gta gag gag ccc      104
Ala Asp Asp Val Asp Gln Gln Gln Thr Thr Asn Thr Val Glu Glu Pro
5                               10           15
ctg gat ctt atc agg ctc agc cta gat gag cga att tat gtg aaa atg      152
Leu Asp Leu Ile Arg Leu Ser Leu Asp Glu Arg Ile Tyr Val Lys Met
20                               25           30
aga aat gac cga gag ctt cga ggc aga tta cat gct tat gat caa cat      200
Arg Asn Asp Arg Glu Leu Arg Gly Arg Leu His Ala Tyr Asp Gln His
35                               40           45
tta aat atg atc ttg gga gat gtg gaa gaa act gtg act act ata gaa      248
Leu Asn Met Ile Leu Gly Asp Val Glu Glu Thr Val Thr Thr Ile Glu
50                               55           60           65
att gat gaa gaa aca tat gaa gag ata tat aaa tca acg aaa cgg aat      296
Ile Asp Glu Glu Thr Tyr Glu Glu Ile Tyr Lys Ser Thr Lys Arg Asn
70                               75           80
att cca atg ctc ttt gtc cgg gga gat ggc gtt gtc ctg gtt gcc cct      344
Ile Pro Met Leu Phe Val Arg Gly Asp Gly Val Val Leu Val Ala Pro
85                               90           95
cca ctg aga gtt ggc tgaacaaaag aattgtcct gtatggaaaa cgggagactt      399
Pro Leu Arg Val Gly
100
tgtacagtgg cctctctaaa agtacaaaac attcataagw gaaacctgca tacattttga      459
tattaagaaa taa      472

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<220>
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 tgaggtcatc atcagatttg aaatatttaa agtggataca aaactatttc agca atg 117
 Met
 1
 cag aca att aag tgt gtt gtt gtg ggc gat ggt gct gtt ggt aaa aca 165
 Gln Thr Ile Lys Cys Val Val Val Gly Asp Gly Ala Val Gly Lys Thr
 5 10 15
 tgt ctc ctg ata tcc tac aca aca aac aaa ttt cca tcg gaa tat gta 213
 Cys Leu Leu Ile Ser Tyr Thr Thr Asn Lys Phe Pro Ser Glu Tyr Val
 20 25 30
 ccg act gtt ttt gac aac tat gca gtc aca gtt atg att ggt gga gaa 261
 Pro Thr Val Phe Asp Asn Tyr Ala Val Thr Val Met Ile Gly Gly Glu
 35 40 45
 cca tat act ctt gga ctt ttt gat act gca ggg caa gag gat tat gac 309
 Pro Tyr Thr Leu Gly Leu Phe Asp Thr Ala Gly Gln Glu Asp Tyr Asp
 50 55 60 65
 aga tta cga ccg ctg agt tat cca caa aca gat gta ttt cta gtc tgt 357
 Arg Leu Arg Pro Leu Ser Tyr Pro Gln Thr Asp Val Phe Leu Val Cys
 70 75 80
 ttt tca gtg gtc tct cca tct tca ttt gaa aac gtg aaa gaa aag tgg 405
 Phe Ser Val Val Ser Pro Ser Ser Phe Glu Asn Val Lys Glu Lys Trp
 85 90 95
 gtg cct gag ata act cac cac tgt cca aag act cct ttc ttg ctt gtt 453
 Val Pro Glu Ile Thr His His Cys Pro Lys Thr Pro Phe Leu Leu Val
 100 105 110
 ggg act caa att gat ctc aga gat gac ccc tct act att gag aaa ctt 501
 Gly Thr Gln Ile Asp Leu Arg Asp Asp Pro Ser Thr Ile Glu Lys Leu
 115 120 125
 gcc aag aac aaa cag aag cct atc act cca gag act gct gaa aag ctg 549
 Ala Lys Asn Lys Gln Lys Pro Ile Thr Pro Glu Thr Ala Glu Lys Leu
 130 135 140 145
 gcc cgt gac ctg aag gct gtc aag tat gtg gag tgt tct gca ctt aca 597
 Ala Arg Asp Leu Lys Ala Val Lys Tyr Val Glu Cys Ser Ala Leu Thr
 150 155 160
 cag aaa ggc cta aag aat gta ttt gac gaa gca ata ttg gct gcc ctg 645
 Gln Lys Gly Leu Lys Asn Val Phe Asp Glu Ala Ile Leu Ala Ala Leu
 165 170 175
 gag cct cca gaa ccg aag aag agc cgc agg tgt gtg ctg cta 687
 Glu Pro Pro Glu Pro Lys Lys Ser Arg Arg Cys Val Leu Leu
 180 185 190
 tgaacatctc tccagagccc tttctgcaca gctggtgtcg gcatcatact aaaagcaatg 747
 tttaaatcaa actaaagatt aaaaattaaa attcgttttt gcaataatga caaatgccct 807

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867
873

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<213> Homo sapiens

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<222> 241..813

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gcagtgcgcc tctgcccccc gagttcaagc gattctcctg cctcaggctc ctgagtagct 180
gggactacag gtcacatca gatttgaaat atttaaagtg gatacaaaac tatttcagca 240
atg cag aca att aag tgt gtt gtt gtg ggc grk ggt gct gtt ggt aaa 288
Met Gln Thr Ile Lys Cys Val Val Val Gly Xaa Gly Ala Val Gly Lys
1 5 10 15
aca tgt ctc ctg ata tcc tac aca aca rrc aaa ttt cca tcg gaa tat 336
Thr Cys Leu Leu Ile Ser Tyr Thr Thr Xaa Lys Phe Pro Ser Glu Tyr
20 25 30
gta ccg gct gtt ttt gac aac tat gca gtc aca gtt atg att ggt gga 384
Val Pro Ala Val Phe Asp Asn Tyr Ala Val Thr Val Met Ile Gly Gly
35 40 45
gaa cca tat act ctt gga ctt ttt gat act gca ggg caa gag gat tat 432
Glu Pro Tyr Thr Leu Gly Leu Phe Asp Thr Ala Gly Gln Glu Asp Tyr
50 55 60
gac aga tta cga ccg ctg agt tat cca caa aca gat gta ttt cta gtc 480
Asp Arg Leu Arg Pro Leu Ser Tyr Pro Gln Thr Asp Val Phe Leu Val
65 70 75 80
tgt ttt tca gtg gtc tct cca tct tca ttt gaa aac gtg aaa gaa aag 528
Cys Phe Ser Val Val Ser Pro Ser Ser Phe Glu Asn Val Lys Glu Lys
85 90 95
tgg gtg cct gag ata act cac cac tgt cca aag act cct ttc ttg ctt 576
Trp Val Pro Glu Ile Thr His His Cys Pro Lys Thr Pro Phe Leu Leu
100 105 110
gtt ggg act caa att gat ctc aga gat gac ccc tct act att gag aaa 624
Val Gly Thr Gln Ile Asp Leu Arg Asp Asp Pro Ser Thr Ile Glu Lys
115 120 125
ctt gcc aag aac aaa cag aag cct atc act cca gag act gct gaa aag 672
Leu Ala Lys Asn Lys Gln Lys Pro Ile Thr Pro Glu Thr Ala Glu Lys
130 135 140
ctg gcc cgt gac ctg aag gct gtc aag tat gtg gag tgt tct gca ctt 720
Leu Ala Arg Asp Leu Lys Ala Val Lys Tyr Val Glu Cys Ser Ala Leu
145 150 155 160
aca cag aaa ggc cta aag aat gta ttt gac gaa gca ata ttg gct gcc 768
Thr Gln Lys Gly Leu Lys Asn Val Phe Asp Glu Ala Ile Leu Ala Ala
165 170 175
ctg gag cct cca gaa ccg aag aag agc cgc agg tgt gtg ctg cta 813
Leu Glu Pro Pro Glu Pro Lys Lys Ser Arg Arg Cys Val Leu Leu
180 185 190

004220"666T360

tgaacatctc tccagagccc tttctgcaca gctggtgtcg gcatcatact aaaagcaatg 873
 tttaaatcaa actaaagatt aaaaattaaa attcgttttt gcaataatga caaatgccct 933
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<220>
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 <222> 138..446

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 gtagtgcttc taccaac atg tcc cgt ggt tcc agc gcc ggt ttt gac cgc 170
 Met Ser Arg Gly Ser Ser Ala Gly Phe Asp Arg
 1 5 10
 cac att acc att ttt tca ncc gag ggt cgg ctc kas caa gta gaa tat 218
 His Ile Thr Ile Phe Ser Xaa Glu Gly Arg Leu Xaa Gln Val Glu Tyr
 15 20 25
 gct ttt aag gct att aac cag ggt ggc ctt aca tca gta gct gtc aga 266
 Ala Phe Lys Ala Ile Asn Gln Gly Gly Leu Thr Ser Val Ala Val Arg
 30 35 40
 ggg aaa gac tgt gca gka att gtc aca cag aag aaa gta cct gac aaa 314
 Gly Lys Asp Cys Ala Xaa Ile Val Thr Gln Lys Lys Val Pro Asp Lys
 45 50 55
 tta ttg gat tcc agc aca gtg act cac tta ttc aag ata act gaa aac 362
 Leu Leu Asp Ser Ser Thr Val Thr His Leu Phe Lys Ile Thr Glu Asn
 60 65 70 75
 att ggt tgt gtg atg acc gga atg aca gct gac agc aga tcc cag gta 410
 Ile Gly Cys Val Met Thr Gly Met Thr Ala Asp Ser Arg Ser Gln Val
 80 85 90
 ata tct gtt ttg atg aat ttg aag gca att gat ttg taaccaaacc 456
 Ile Ser Val Leu Met Asn Leu Lys Ala Ile Asp Leu
 95 100
 atagaagcca tatccaatcc cattcactgg 486

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 <211> 443
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> 53..388

<400> 3926
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 Met Ala

gca ccc gag gaa cac gat tct ccg acc gaa gcg tcc cag ccg att gtg	1	106
Ala Pro Glu Glu His Asp Ser Pro Thr Glu Ala Ser Gln Pro Ile Val		
5 10 15		
gaa gag gag gaa act aaa aca ttt aaa gac ctg ggt gtg aca gat gtg		154
Glu Glu Glu Glu Thr Lys Thr Phe Lys Asp Leu Gly Val Thr Asp Val		
20 25 30		
ttg tgt gaa gct tgt gac cag ttg gga tgg aca aaa ccc acc aag atc		202
Leu Cys Glu Ala Cys Asp Gln Leu Gly Trp Thr Lys Pro Thr Lys Ile		
35 40 45 50		
cag att gaa gct att cct ttg gcc tta caa ggt cgt gat atc att ggg		250
Gln Ile Glu Ala Ile Pro Leu Ala Leu Gln Gly Arg Asp Ile Ile Gly		
55 60 65		
ctt gca gaa act ggc tct gga aag aca ggc gcc ttt gct ttg ccc att		298
Leu Ala Glu Thr Gly Ser Gly Lys Thr Gly Ala Phe Ala Leu Pro Ile		
70 75 80		
cta aac gca ctg ctg gag acc ccg cag cgt ttg ttt gcc cta gtt ctt		346
Leu Asn Ala Leu Leu Glu Thr Pro Gln Arg Leu Phe Ala Leu Val Leu		
85 90 95		
acc ccg act cgg gag ctg gcc ttt cag atc tca gag cca gtt		388
Thr Pro Thr Arg Glu Leu Ala Phe Gln Ile Ser Glu Pro Val		
100 105 110		
tgaagccctg gggtcctcta ttggagtgcga gaggctgtg attgtagggtg gaatt		443
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<213> Homo sapiens		
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Met Ala Met Glu Met Arg Leu Pro Val Ala		
1 5 10		
cgc aag cct ctt agc gag aga ctg ggc cgc gac act aag aaa cat cta		100
Arg Lys Pro Leu Ser Glu Arg Leu Gly Arg Asp Thr Lys Lys His Leu		
15 20 25		
gtg gtg ccg ggg gat aca atc act acg gac aca gga ttc atg cgg ggc		148
Val Val Pro Gly Asp Thr Ile Thr Thr Asp Thr Gly Phe Met Arg Gly		
30 35 40		
cat gga acg tat atg gga gaa gag aag ctc att gca tct gtt gct ggc		196
His Gly Thr Tyr Met Gly Glu Glu Lys Leu Ile Ala Ser Val Ala Gly		
45 50 55		
tct gtg gag aga gta aac aag ttn atc tgt gtg aaa gct ttg aaa acc		244
Ser Val Glu Arg Val Asn Lys Xaa Ile Cys Val Lys Ala Leu Lys Thr		
60 65 70		
aga tac att ggt gaa gta rga gac atc gta gtg gga cga atc aca gag		292
Arg Tyr Ile Gly Glu Val Xaa Asp Ile Val Val Gly Arg Ile Thr Glu		
75 80 85 90		
gtt caa cag aag agg tgg aag gtg gag acc aac tcc agg ctg gat tcg		340

Val	Gln	Gln	Lys	Arg	Trp	Lys	Val	Glu	Thr	Asn	Ser	Arg	Leu	Asp	Ser		
				95					100					105			
gtc	ttg	ctg	ctc	tgc	tcc	atg	aac	ctt	cct	gga	gga	gag	ctg	agg	aga		388
Val	Leu	Leu	Leu	Ser	Ser	Met	Asn	Leu	Pro	Gly	Gly	Glu	Leu	Arg	Arg		
			110					115					120				
gat	ctg	cag	aag	atg	agc	ttg	caa	tgagaggttt	cttacaggaa	ggggmcttat							442
Asp	Leu	Gln	Lys	Met	Ser	Leu	Gln										
		125					130										470
cagtgc	ctgag	gtcagg	cagt	gttct	ctg												

<210> 3928
 <211> 488
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 74..478

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cagccccaag	gct	atg	gcg	gga	cac	ccg	aaa	gag	agg	gtg	gtc	aca	gat					109
		Met	Ala	Gly	His	Pro	Lys	Glu	Arg	Val	Val	Thr	Asp					
	1					5						10						
gag	gtc	cat	cag	aac	cag	atc	ttg	cg	gag	ctg	tac	ctc	aaa	gag	tta			157
Glu	Val	His	Gln	Asn	Gln	Ile	Leu	Arg	Glu	Leu	Tyr	Leu	Lys	Glu	Leu			
	15					20						25						
cga	acc	cag	aaa	ctc	cac	acg	cag	tac	cat	gtg	aat	ccc	ctg	cg	cag	aag		205
Arg	Thr	Gln	Lys	Leu	His	Thr	Gln	Tyr	His	Val	Asn	Pro	Leu	Arg	Lys			
	30					35					40							
gtt	cac	agg	att	acg	agg	aag	cct	atg	tct	tgg	cat	gat	aac	ctg	gag			253
Val	His	Arg	Ile	Thr	Arg	Lys	Pro	Met	Ser	Trp	His	Asp	Asn	Leu	Glu			
	45					50				55				60				
gaa	ccc	gca	gac	gcc	agg	ttt	ctg	aat	ctc	att	cac	cat	gct	gcc	cag			301
Glu	Pro	Ala	Asp	Ala	Arg	Phe	Leu	Asn	Leu	Ile	His	His	Ala	Ala	Gln			
			65					70					75					
ggg	cca	acg	aag	aag	tac	ccg	gag	gca	cag	act	gaa	aac	cag	gaa	att			349
Gly	Pro	Thr	Lys	Lys	Tyr	Pro	Glu	Ala	Gln	Thr	Glu	Asn	Gln	Glu	Ile			
			80					85					90					
ggg	tgg	gac	tca	gaa	scc	ttg	gtc	gac	cca	gra	cg	cgt	gac	cac	agg			397
Gly	Trp	Asp	Ser	Glu	Xaa	Leu	Val	Asp	Pro	Xaa	Arg	Arg	Asp	His	Arg			
		95					100					105						
atg	aac	cac	ttc	agg	gtc	tac	agt	gac	atc	act	ctg	tac	aaa	gct	aaa			445
Met	Asn	His	Phe	Arg	Val	Tyr	Ser	Asp	Ile	Thr	Leu	Tyr	Lys	Ala	Lys			
		110				115					120							
atg	tng	gac	ttg	gga	gaa	gat	gat	cg	cac	aag	tagcatctca							488
Met	Xaa	Asp	Leu	Gly	Glu	Asp	Asp	Arg	His	Lys								
		125				130				135								

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 <211> 745
 <212> DNA
 <213> Homo sapiens

<220>
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 aggttgtggt gctagtttct ctaagccatc cagtgccatc ctcgtcgctg cagcgacaca 120
 cgctctcgcc gccgcc atg act gag cag atg acc ctt cgt ggc acc ctc aag 172
 Met Thr Glu Gln Met Thr Leu Arg Gly Thr Leu Lys
 1 5 10
 ggc cac aac ggc tgg gta acc cag atc gct act acc ccg cag ttc ccg 220
 Gly His Asn Gly Trp Val Thr Gln Ile Ala Thr Thr Pro Gln Phe Pro
 15 20 25
 gac atg atc ctc tcc gcc tct cga gat aag acc atc atc atg tgg aaa 268
 Asp Met Ile Leu Ser Ala Ser Arg Asp Lys Thr Ile Ile Met Trp Lys
 30 35 40
 ctg acc agg gat gag acc aac tat gga att cca cag cgt gct ctg cgg 316
 Leu Thr Arg Asp Glu Thr Asn Tyr Gly Ile Pro Gln Arg Ala Leu Arg
 45 50 55 60
 ggt cac tcc cac ttt gtt agt gat gtg gtt atc tcc tca gat ggc cag 364
 Gly His Ser His Phe Val Ser Asp Val Val Ile Ser Ser Asp Gly Gln
 65 70 75
 ttt gcc ctc tca ggc tcc tgg gat gga acc ctg cgc ctc tgg gat ctc 412
 Phe Ala Leu Ser Gly Ser Trp Asp Gly Thr Leu Arg Leu Trp Asp Leu
 80 85 90
 aca acg ggc acc acc acg agg cga ttt gtg ggc cat acc aag gat gtg 460
 Thr Thr Gly Thr Thr Thr Arg Arg Phe Val Gly His Thr Lys Asp Val
 95 100 105
 ctg agt gtg gcc ttc tcc tct gac aac cgg cag att gtc tct gga tct 508
 Leu Ser Val Ala Phe Ser Ser Asp Asn Arg Gln Ile Val Ser Gly Ser
 110 115 120
 cga gat aaa acc atc aag cta tgg aat acc ctg ggt gtg tgc aaa tac 556
 Arg Asp Lys Thr Ile Lys Leu Trp Asn Thr Leu Gly Val Cys Lys Tyr
 125 130 135 140
 act gtc cag gat gag agc cac tca gag tgg gtg tct tgt gtc cgc ttc 604
 Thr Val Gln Asp Glu Ser His Ser Glu Trp Val Ser Cys Val Arg Phe
 145 150 155
 tcg ccc aac agc agc aac cct atc atc gtc tcc tgt ggc tgg gac aag 652
 Ser Pro Asn Ser Ser Asn Pro Ile Ile Val Ser Cys Gly Trp Asp Lys
 160 165 170
 ctg srn twa ggt atg gaa cct ggc taactgcaag ctgaagacca accacattgg 706
 Leu Xaa Xaa Gly Met Glu Pro Gly
 175 180
 ccacacaggc tatctgaaca cggtgactgt ctctccarw 745

<210> 3930
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 <212> DNA
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<220>
 <221> CDS

<222> 100..426

<400> 3930

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gcactaggaa cagccccggg cggcgagacg gtccccgcc atg tct gcg gcc atg 114
Met Ser Ala Ala Met
1 5
agg gag agg ttc gac cgg ttc ctg cac gag aag aac tgc atg act gac 162
Arg Glu Arg Phe Asp Arg Phe Leu His Glu Lys Asn Cys Met Thr Asp
10 15 20
ctt ctg gcc aag ctc gag gcc aaa acc ggc gtg aac agg agc ttc atc 210
Leu Leu Ala Lys Leu Glu Ala Lys Thr Gly Val Asn Arg Ser Phe Ile
25 30 35
gct ctt ggt gtc atc gga ctg gtg gcc ttg tac ctg gtg ttc ggt tat 258
Ala Leu Gly Val Ile Gly Leu Val Ala Leu Tyr Leu Val Phe Gly Tyr
40 45 50
gga gcc tct ctc ctc tgc aac ctg ata gga ttt ggc tac cca gcc tac 306
Gly Ala Ser Leu Leu Cys Asn Leu Ile Gly Phe Gly Tyr Pro Ala Tyr
55 60 65
atc tca att aaa gct ata gag agc ccc gat caa gaa cat cct gtg cca 354
Ile Ser Ile Lys Ala Ile Glu Ser Pro Asp Gln Glu His Pro Val Pro
70 75 80 85
gaa ggt aag aaa ata tta aag ggt gat gga aac atg tta aaa aga cac 402
Glu Gly Lys Lys Ile Leu Lys Gly Asp Gly Asn Met Leu Lys Arg His
90 95 100
aga agc cag cat gaa aat gcc tgg tgattaagga taatttgagc attgaagtaa 456
Arg Ser Gln His Glu Asn Ala Trp
105
atgatagaaa tggatgccat tccatagatt aaataagaat cta 499

<210> 3931

<211> 452

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 51..419

<400> 3931

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Met Ala
1
aag atc aag gct cga gat ctt cgc ggg aag aag aag gag gag ctg ctg 104
Lys Ile Lys Ala Arg Asp Leu Arg Gly Lys Lys Lys Glu Glu Leu Leu
5 10 15
aaa cag ctg gac gac ctg aag gtg gag ctg tcc cag ctg cgc gtc gcc 152
Lys Gln Leu Asp Asp Leu Lys Val Glu Leu Ser Gln Leu Arg Val Ala
20 25 30
aaa gtg aca ggc ggt gcg gcc tcc aag ctc tct aag atc cga gtc gtc 200
Lys Val Thr Gly Gly Ala Ala Ser Lys Leu Ser Lys Ile Arg Val Val
35 40 45 50

cgg aaa tcc att gcc cgt gtt ctc aca gtt att aac cag act cag aaa 248
 Arg Lys Ser Ile Ala Arg Val Leu Thr Val Ile Asn Gln Thr Gln Lys
 55 60 65
 gaa aac ctc agg aaa ttc tac aag ggc aag aag tac aag ccc ctg gac 296
 Glu Asn Leu Arg Lys Phe Tyr Lys Gly Lys Lys Tyr Lys Pro Leu Asp
 70 75 80
 ctg cgg cct aag aag aca cgt gcc atg cgc cgc cgg ctc aac aag cac 344
 Leu Arg Pro Lys Lys Thr Arg Ala Met Arg Arg Arg Leu Asn Lys His
 85 90 95
 gag gag aac ctg aag acc aag aag cag cag cgg aag gar mgg ctg tac 392
 Glu Glu Asn Leu Lys Thr Lys Lys Gln Gln Arg Lys Glu Arg Leu Tyr
 100 105 110
 ccg ctg cgg aag tac gcg gtc aag gcc tgargggcgc attgtcaata 439
 Pro Leu Arg Lys Tyr Ala Val Lys Ala
 115 120
 aagcacagct ggc 452

 <210> 3932
 <211> 627
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> CDS
 <222> 74..433

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 aggggaagtg gag atg tgg gcc tcg gag ctg cgt ggc ccg ggc tgt gcg 109
 Met Trp Ala Ser Glu Leu Arg Gly Pro Gly Cys Ala
 1 5 10
 gat tcc cta aac gcc gca ctt gcg cac agc ccc tta cgt aac cgt cag 157
 Asp Ser Leu Asn Ala Ala Leu Ala His Ser Pro Leu Arg Asn Arg Gln
 15 20 25
 tgc cgg gga ttc cct gga ggg ggt cat tct att caa cca tta tac aca 205
 Cys Arg Gly Phe Pro Gly Gly His Ser Ile Gln Pro Leu Tyr Thr
 30 35 40
 ccc cgg gct cct gcc gcc gcg ccg ccg ccg cct cac aaa atg gcg gcg 253
 Pro Arg Ala Pro Ala Ala Ala Pro Pro Pro Pro His Lys Met Ala Ala
 45 50 55 60
 ccc ata gag gag acc gcg gcc gcc tcc ccg gcc cca ttt tgt ggg agg 301
 Pro Ile Glu Glu Thr Ala Ala Ala Ser Pro Ala Pro Phe Cys Gly Arg
 65 70 75
 cga gag atc tgt caa cat gga aaa cct ctg ctg agg atg cat ccg agt 349
 Arg Glu Ile Cys Gln His Gly Lys Pro Leu Leu Arg Met His Pro Ser
 80 85 90
 ttg gaa acc cca ctt aag gga tgg agc ctg ggg gat cac att aaa cgg 397
 Leu Glu Thr Pro Leu Lys Gly Trp Ser Leu Gly Asp His Ile Lys Arg
 95 100 105
 aaa atg cca acg act tct acc acc tct acg cgt ttt tagtttttca 443
 Lys Met Pro Thr Thr Ser Thr Thr Ser Thr Arg Phe
 110 115 120
 ttttctcgaa ggaagcgcca gaagcctgtg gagtaattgt aactagaggg agaacggaaa 503

gctgaggtga ctgctccggg gacttgggcg ggcgccttgg tggctttggt tgctcttcca 563
 cgctcccggc agctgaccag aatctcttgg agggctctct gggcnactcg gccgcgccag 623
 tcgt 627

<210> 3933
 <211> 511
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 36..404

<400> 3933
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 Met Gly Ala Pro Gly Gly
 1 5
 aag atc aac cgg ccc cga acg gag ctg aag aag aag ctg ttc aaa cgc 101
 Lys Ile Asn Arg Pro Arg Thr Glu Leu Lys Lys Lys Leu Phe Lys Arg
 10 15 20
 cgg cgg gtg ttg aat cgg gag cgg cgt ctg agg cac cgg gtg gtc ggg 149
 Arg Arg Val Leu Asn Arg Glu Arg Arg Leu Arg His Arg Val Val Gly
 25 30 35
 gct gtg ata gac caa ggg ctg atc acg cgg cac cac ctc aag aag cgg 197
 Ala Val Ile Asp Gln Gly Leu Ile Thr Arg His His Leu Lys Lys Arg
 40 45 50
 gcg tcc agt gca cgt gcc aac att aca ctg tca ggg aag aag cgc aga 245
 Ala Ser Ser Ala Arg Ala Asn Ile Thr Leu Ser Gly Lys Lys Arg Arg
 55 60 65 70
 aaa ctc ctc cag cag atc cgg ctt gcc cag aaa gag aag aca gcc atg 293
 Lys Leu Leu Gln Gln Ile Arg Leu Ala Gln Lys Glu Lys Thr Ala Met
 75 80 85
 gaa gtg gaa gcc cct tca aag cca gcc agg act agt gaa cca cag ctc 341
 Glu Val Glu Ala Pro Ser Lys Pro Ala Arg Thr Ser Glu Pro Gln Leu
 90 95 100
 aaa agg caa aag aag aca aaa gcc ccc cag gat gta gaa atg aag gac 389
 Lys Arg Gln Lys Lys Thr Lys Ala Pro Gln Asp Val Glu Met Lys Asp
 105 110 115
 ctt gaa gat gag agc taaacctctt ccactagaag rttctcaact ggagccagcc 444
 Leu Glu Asp Glu Ser
 120
 ttcagactca gtggttggtt cagaggactt tgacaaaagc aaggcccttt tcaacttcca 504
 gatttcc 511

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 <211> 449
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 58..396

<400> 3934
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 atg acg gtg aaa act gag gct gct aag ggc acc ctc act tac tcc agg 105
 Met Thr Val Lys Thr Glu Ala Ala Lys Gly Thr Leu Thr Tyr Ser Arg
 1 5 10 15
 atg agg ggc atg gtg gca att ctc atc gct ttc atg aag cag agg agg 153
 Met Arg Gly Met Val Ala Ile Leu Ile Ala Phe Met Lys Gln Arg Arg
 20 25 30
 atg ggt ctg aac gac ttt att cag aag att gcc aat aac tcc tat gca 201
 Met Gly Leu Asn Asp Phe Ile Gln Lys Ile Ala Asn Asn Ser Tyr Ala
 35 40 45
 tgc aaa cac cct gaa gtt cag tcc atc ttg aag atc tcc caa cct cag 249
 Cys Lys His Pro Glu Val Gln Ser Ile Leu Lys Ile Ser Gln Pro Gln
 50 55 60
 gag cct gag ctt atg aat gcc aac cct tct cct cca cca agt cct tct 297
 Glu Pro Glu Leu Met Asn Ala Asn Pro Ser Pro Pro Pro Ser Pro Ser
 65 70 75 80
 cag caa atc aac ctt ggc ccg tcg tcc aat cct cat gct aaa cca tct 345
 Gln Gln Ile Asn Leu Gly Pro Ser Ser Asn Pro His Ala Lys Pro Ser
 85 90 95
 gac ttt cac ttc ttg aaa gtg atc gga aag ggc agt ttg gaa agg ttc 393
 Asp Phe His Phe Leu Lys Val Ile Gly Lys Gly Ser Leu Glu Arg Phe
 100 105 110
 ttc tagcaagaca caaggcagaa gaagtgttct atgcagtcaa agttttacag aag 449
 Phe

<210> 3935
 <211> 420
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 37..393

<400> 3935
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 Met Ala Ser Gly Leu Val
 1 5
 aga ttg ctg cag cag gga cat cgc tgc ctc ctg gct cca gtc gcc ccc 102
 Arg Leu Leu Gln Gln Gly His Arg Cys Leu Leu Ala Pro Val Ala Pro
 10 15 20
 aag ctg gtc cct ccg gtt cgg gga gtg aag aag gga ttc cgc gcc gcc 150
 Lys Leu Val Pro Pro Val Arg Gly Val Lys Lys Gly Phe Arg Ala Ala
 25 30 35
 ttc cgc ttc cag aag gag tta gag cgg cag cgc ctt ctg cgg tgc ccg 198
 Phe Arg Phe Gln Lys Glu Leu Glu Arg Gln Arg Leu Leu Arg Cys Pro
 40 45 50
 ccg ccg ccc gtg cgc cgt tca gag aag ccg aac tgg gat tac cat gca 246
 Pro Pro Pro Val Arg Arg Ser Glu Lys Pro Asn Trp Asp Tyr His Ala
 55 60 65 70
 gaa ata caa gct ttt gga cat cgg tta cag gaa aac ttt tcc tta gat 294

Glu Ile Gln Ala Phe Gly His Arg Leu Gln Glu Asn Phe Ser Leu Asp	
75 80 85	
ctt ctc aaa act gca ttt gtt aat agc tgc tat att aaa agt gag gag	342
Leu Leu Lys Thr Ala Phe Val Asn Ser Cys Tyr Ile Lys Ser Glu Glu	
90 95 100	
gcc aaa cgc caa caa ctt ggg ata gga gaa aga agc tgt tct tct gaa	390
Ala Lys Arg Gln Gln Leu Gly Ile Gly Glu Arg Ser Cys Ser Ser Glu	
105 110 115	
tct taaaagtaat caagaactat ccgaaca	420
Ser	

<210> 3936
 <211> 419
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 70..411

<400> 3936	
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gctgctaaa atg ccg gat tac ctc ggt gcc gat cag cgg aag acc aaa gag	111
Met Pro Asp Tyr Leu Gly Ala Asp Gln Arg Lys Thr Lys Glu	
1 5 10	
gat gag aag gac gac aag ccc atc cga gct ctg gat gag ggg gat att	159
Asp Glu Lys Asp Asp Lys Pro Ile Arg Ala Leu Asp Glu Gly Asp Ile	
15 20 25 30	
gcc ttg ttg aaa act tat ggt cag agc act tac tct agg cag atc aag	207
Ala Leu Leu Lys Thr Tyr Gly Gln Ser Thr Tyr Ser Arg Gln Ile Lys	
35 40 45	
caa gtt gaa gat gac att cag caa ctt ctc aag aaa att aat gag ctc	255
Gln Val Glu Asp Asp Ile Gln Gln Leu Leu Lys Lys Ile Asn Glu Leu	
50 55 60	
act ggt att aaa gaa tct gac act ggc ctg gcc cca cca gca ctc tgg	303
Thr Gly Ile Lys Glu Ser Asp Thr Gly Leu Ala Pro Pro Ala Leu Trp	
65 70 75	
gat ttg gct gca gat aag cag aca ctc cag agt gaa cag cct tta cag	351
Asp Leu Ala Ala Asp Lys Gln Thr Leu Gln Ser Glu Gln Pro Leu Gln	
80 85 90	
gtt gcc agg tgt aca aag ata atc aat gct gat tcg gag gac caa aat	399
Val Ala Arg Cys Thr Lys Ile Ile Asn Ala Asp Ser Glu Asp Gln Asn	
95 100 105 110	
aca tta tca acg taaagcag	419
Thr Leu Ser Thr	

<210> 3937
 <211> 357
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS

<222> 20..346

<400> 3937

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Met Ala Ala Ser Ala Ala Arg Gly Ala Ala Ala
1 5 10
ctg cgt aga agt atc aat cag ccg gtt gct ttt gtg aga aga att cct 100
Leu Arg Arg Ser Ile Asn Gln Pro Val Ala Phe Val Arg Arg Ile Pro
15 20 25
tgg act gcg gcg tcg agt cag ctg aaa gaa cac ttt gca cag ttc ggc 148
Trp Thr Ala Ala Ser Ser Gln Leu Lys Glu His Phe Ala Gln Phe Gly
30 35 40
cat gtc aga agg tgc att tta cct ttt gac aag gag act ggc ttt cac 196
His Val Arg Arg Cys Ile Leu Pro Phe Asp Lys Glu Thr Gly Phe His
45 50 55
aga ggt ttg ggt tgg gtt cag ttt tct tca gaa gaa gga ctt cgg aat 244
Arg Gly Leu Gly Trp Val Gln Phe Ser Ser Glu Glu Gly Leu Arg Asn
60 65 70 75
gca cta caa cag gaa aat cat att ata gat gga gta aag gtc cag gtt 292
Ala Leu Gln Gln Glu Asn His Ile Ile Asp Gly Val Lys Val Gln Val
80 85 90
cac act aga agg cca aaa ctt ccg caa aca tct gat gat gaa aag aaa 340
His Thr Arg Arg Pro Lys Leu Pro Gln Thr Ser Asp Asp Glu Lys Lys
95 100 105
gat ttt tgagactgca g 357
Asp Phe

<210> 3938

<211> 518

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 75..467

<400> 3938

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cctgcagctc cgcc atg gct cct aaa ggc agc tcc aaa cag cag tct gag 110
Met Ala Pro Lys Gly Ser Ser Lys Gln Gln Ser Glu
1 5 10
gag gac ctg ctc ctg cag gat ttc agc cgc aat ctc tcg gcc aag tcc 158
Glu Asp Leu Leu Leu Gln Asp Phe Ser Arg Asn Leu Ser Ala Lys Ser
15 20 25
tcc gcg ctc ttc ttc gga aac gcg ttc atc gtg tct gcc atc ccc atc 206
Ser Ala Leu Phe Phe Gly Asn Ala Phe Ile Val Ser Ala Ile Pro Ile
30 35 40
tgg tta tac tgg cga ata tgg cat atg gat ctt att cag tct gct gtt 254
Trp Leu Tyr Trp Arg Ile Trp His Met Asp Leu Ile Gln Ser Ala Val
45 50 55 60
ttg tat agt gtg atg acc cta gta agc aca tat ttg gta gcc ttt gca 302
Leu Tyr Ser Val Met Thr Leu Val Ser Thr Tyr Leu Val Ala Phe Ala

	65	70	75	
tac aag aat gtg aaa ttt gtt ctc aag cac aaa gta gca cag aag agg				350
Tyr Lys Asn Val Lys Phe Val Leu Lys His Lys Val Ala Gln Lys Arg				
	80	85	90	
gag gat gct gtt tcc aaa gaa gtg act cga aaa ctt tct gaa gct gat				398
Glu Asp Ala Val Ser Lys Glu Val Thr Arg Lys Leu Ser Glu Ala Asp				
	95	100	105	
aat aga aag atg tct cgg aag gag aaa gat gaa aga atc ttg tgg aag				446
Asn Arg Lys Met Ser Arg Lys Glu Lys Asp Glu Arg Ile Leu Trp Lys				
	110	115	120	
aag aat gaa gtt gct gca tta tgaagctaca acattttccw tcttctataa				497
Lys Asn Glu Val Ala Ala Leu				
	125	130		
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	Met Ala Leu Arg Tyr Pro Met
	1 5
gcc gtg ggc ctc aac aag ggc cac aaa gtg acc aag aac gtg agc aag	160
Ala Val Gly Leu Asn Lys Gly His Lys Val Thr Lys Asn Val Ser Lys	
	10 15 20
ccc agg cac agc cga cgc cgc ggg cgt ctg acc aaa cac acc aag ttc	208
Pro Arg His Ser Arg Arg Arg Gly Arg Leu Thr Lys His Thr Lys Phe	
	25 30 35
gtg cgg gac atg att cgg gag gtg tgt ggc ttt gcc ccg tac gag cgg	256
Val Arg Asp Met Ile Arg Glu Val Cys Gly Phe Ala Pro Tyr Glu Arg	
	40 45 50 55
cgc gcc atg gag tta ctg aag gtc tcc aag gac aaa cgg gcc ctc aaa	304
Arg Ala Met Glu Leu Leu Lys Val Ser Lys Asp Lys Arg Ala Leu Lys	
	60 65 70
ttt atc aag aaa agg gtg ggg acg cac atc cgc gcc aag agg aag cgg	352
Phe Ile Lys Lys Arg Val Gly Thr His Ile Arg Ala Lys Arg Lys Arg	
	75 80 85
gag gag ctg agc aac gta ctg gcc gcc atg agg aaa gct gct gcc aag	400
Glu Glu Leu Ser Asn Val Leu Ala Ala Met Arg Lys Ala Ala Lys	
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aaa gac tgagccccctc ccctgccctc tccctgaaat aaagaacagc ttgac	451
Lys Asp	
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Met Ala Asp Glu Glu Glu Asp Pro Thr Phe Glu Glu Glu
1 5 10
aat gaa gaa att gga gga ggt gca gaa ggt gga cag ggt aaa aga aag 157
Asn Glu Glu Ile Gly Gly Gly Ala Glu Gly Gly Gln Gly Lys Arg Lys
15 20 25
aga ctt ttt tct aaa gaa ttg cga tgt atg atg tat ggc ttt ggg gat 205
Arg Leu Phe Ser Lys Glu Leu Arg Cys Met Met Tyr Gly Phe Gly Asp
30 35 40 45
gac cag aat cct tat act gag tca gtg gat att ctt gaa gat ctt gtc 253
Asp Gln Asn Pro Tyr Thr Glu Ser Val Asp Ile Leu Glu Asp Leu Val
50 55 60
ata gag ttt atc act gaa atg act cac aag gca atg tca att gga aga 301
Ile Glu Phe Ile Thr Glu Met Thr His Lys Ala Met Ser Ile Gly Arg
65 70 75
caa ggt cga gta caa gtt gaa gat atc gtc ttc ttg att cga aag grc 349
Gln Gly Arg Val Gln Val Glu Asp Ile Val Phe Leu Ile Arg Lys Xaa
80 85 90
cca agg aag ttt gcc agg tta aag act tgc tta cta tgaatgaaga 395
Pro Arg Lys Phe Ala Arg Leu Lys Thr Cys Leu Leu
95 100 105
atnggaaacg agctagaaaa gcatttgatg aagcaaatta tggatcttga cactttttgt 455
agtttccgaa aattaccat 474

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agactacgga cctgtctggg tctcagccgc caaagacccc gtccggtagg aagtactagc 180
cggacatc atg agt ggc tgt cgg gta ttc atc ggg aga cta aat cca gcg 230
Met Ser Gly Cys Arg Val Phe Ile Gly Arg Leu Asn Pro Ala
1 5 10
gcc agg gag aag gac gtg gaa aga ttc ttc aag gga tat gga cgg ata 278
Ala Arg Glu Lys Asp Val Glu Arg Phe Phe Lys Gly Tyr Gly Arg Ile
15 20 25 30

aga gat att gat ctg aaa aga ggc ttt ggt ttt gtg gaa ttt gag gat	326
Arg Asp Ile Asp Leu Lys Arg Gly Phe Gly Phe Val Glu Phe Glu Asp	
35 40 45	
cca agg gat gca gat gat gct gtg tat gag ctt gat gga aaa gaa ctc	374
Pro Arg Asp Ala Asp Asp Ala Val Tyr Glu Leu Asp Gly Lys Glu Leu	
50 55 60	
tgt agt gaa agg gtt act att gaa cat gct agg gct cgg tca cga ggt	422
Cys Ser Glu Arg Val Thr Ile Glu His Ala Arg Ala Arg Ser Arg Gly	
65 70 75	
gga aga ggt aga gga cga tac tct gac cgt ttt agt agt cgc aga cct	470
Gly Arg Gly Arg Gly Arg Tyr Ser Asp Arg Phe Ser Ser Arg Arg Pro	
80 85 90	
cga aat gat aga cga aat gsy scn acc tgt aag aac aga aaa tcg tct	518
Arg Asn Asp Arg Arg Asn Xaa Xaa Thr Cys Lys Asn Arg Lys Ser Ser	
95 100 105 110	
tat agt tgagaattta tcctcaagag tcagctggca ggtttggtga aatacagttt	574
Tyr Ser	
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aag atg gat gca cag tgt tca gcc aag gtc aat gca agg aag agg aga	168
Met Asp Ala Gln Cys Ser Ala Lys Val Asn Ala Arg Lys Arg Arg	
1 5 10 15	
aaa gag gcg ccc gga ccc aac ggg gca aca gaa gaa gat ggg gtt cct	216
Lys Glu Ala Pro Gly Pro Asn Gly Ala Thr Glu Glu Asp Gly Val Pro	
20 25 30	
tcc aaa gtg cag cgc tgt gca gtg ggc tta cgg caa cca gct cct ttt	264
Ser Lys Val Gln Arg Cys Ala Val Gly Leu Arg Gln Pro Ala Pro Phe	
35 40 45	
tct gat gaa att gaa gtt gac ttt agt aag ccc tat gtc agg gta act	312
Ser Asp Glu Ile Glu Val Asp Phe Ser Lys Pro Tyr Val Arg Val Thr	
50 55 60	
atg gaa gaa gcc agc aga gga act cct tgt gag cga cct gtg aga gtt	360
Met Glu Glu Ala Ser Arg Gly Thr Pro Cys Glu Arg Pro Val Arg Val	
65 70 75	
tat gcc gat gga ata ttt gac tta ttt cac tct ggt cac gcc cga gct	408
Tyr Ala Asp Gly Ile Phe Asp Leu Phe His Ser Gly His Ala Arg Ala	
80 85 90 95	
ctg atg caa gcg aga acc ttt tcc taatacgtac ctcattgtgg gagtttgcag	462
Leu Met Gln Ala Arg Thr Phe Ser	
100	
tgatgagctc a	473

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 <212> DNA
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 gaattacca gaaggcaacg cttctctttc tgggtcaaa atg gct ggt aag cag gcc 116
 Met Ala Gly Lys Gln Ala
 1 5
 gtt tca gca tca ggc aag tgg ctg gat ggt att cga aaa tgg tat tac 164
 Val Ser Ala Ser Gly Lys Trp Leu Asp Gly Ile Arg Lys Trp Tyr Tyr
 10 15 20
 aat gct gca gga ttc aat aaa ctg ggg tta atg cga gat gat aca ata 212
 Asn Ala Ala Gly Phe Asn Lys Leu Gly Leu Met Arg Asp Asp Thr Ile
 25 30 35
 tac gag gat gaa gat gta aaa gaa gcc ata aga aga ctt cct gag aac 260
 Tyr Glu Asp Glu Asp Val Lys Glu Ala Ile Arg Arg Leu Pro Glu Asn
 40 45 50
 ctt tat aat gac agg atg ttt cgc att aag agg gca ctg gac ctg aac 308
 Leu Tyr Asn Asp Arg Met Phe Arg Ile Lys Arg Ala Leu Asp Leu Asn
 55 60 65 70
 ttg aag cat cag atc ttg cct aaa gag cag tgg acc aaa tat gaa gag 356
 Leu Lys His Gln Ile Leu Pro Lys Glu Gln Trp Thr Lys Tyr Glu Glu
 75 80 85
 gaa aat ttc tac ctt gaa ccg tat ctg aaa gag gtt att cgg gaa aga 404
 Glu Asn Phe Tyr Leu Glu Pro Tyr Leu Lys Glu Val Ile Arg Glu Arg
 90 95 100
 aaa gaa aga gaa gaa tgg gca aag aag taatcatgta gttgaagtct 451
 Lys Glu Arg Glu Glu Trp Ala Lys Lys
 105 110
 gtggatgcag ctgttatgaa gatgggttaaa cttgaaacaa acaattttta gaattatttg 511
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<210> 3944
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 <212> DNA
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<220>
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 <222> 40..492

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 Met Ala Pro Arg Lys
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ggg aag gaa aag aag gaa gaa cag gtc atc agc ctc gga cct cag gtg      102
Gly Lys Glu Lys Lys Glu Glu Gln Val Ile Ser Leu Gly Pro Gln Val
                                10                                15                                20

gct gaa gga gag aat gta ttt ggt gtc tgc cat atc ttt gca tcc ttc      150
Ala Glu Gly Glu Asn Val Phe Gly Val Cys His Ile Phe Ala Ser Phe
                                25                                30                                35

aat gac act ttt gtc cat gtc act gat ctt tct ggc aag gaa acc atc      198
Asn Asp Thr Phe Val His Val Thr Asp Leu Ser Gly Lys Glu Thr Ile
                                40                                45                                50

tgc cgt gtg act ggt ggg atg aag gta aag gca gac cga gat gaa tcc      246
Cys Arg Val Thr Gly Gly Met Lys Val Lys Ala Asp Arg Asp Glu Ser
                                55                                60                                65

tca cca tat gct gct atg ttg gct gcc cag gat gtg gcc cag agg tgc      294
Ser Pro Tyr Ala Ala Met Leu Ala Ala Gln Asp Val Ala Gln Arg Cys
                                70                                75                                80                                85

aag gag ctg ggt atc acc gcc cta cac atc aaa ctc cgg gcc aca gga      342
Lys Glu Leu Gly Ile Thr Ala Leu His Ile Lys Leu Arg Ala Thr Gly
                                90                                95                                100

gga aat agg acc aag acc cct gga cct ggg gcc cag tcg gcc ctc aga      390
Gly Asn Arg Thr Lys Thr Pro Gly Pro Gly Ala Gln Ser Ala Leu Arg
                                105                                110                                115

gcc ctt gcc cgc tcg ggt atg aag atc ggg cgg att gag gat gtc acc      438
Ala Leu Ala Arg Ser Gly Met Lys Ile Gly Arg Ile Glu Asp Val Thr
                                120                                125                                130

ccc atc ccc tct gac agc act cgc agg aag ggg ggt cgc cgt ggt cgc      486
Pro Ile Pro Ser Asp Ser Thr Arg Arg Lys Gly Gly Arg Arg Gly Arg
                                135                                140                                145

cgt ctg tgaa
Arg Leu
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<211> 687
<212> DNA
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<222> 115..654

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acggcgtggt ggtcccagcg gttcagctga ggtagggacg tgctgtaggc cgga atg      117
                                Met
                                1

tta ccg gct gtt gga tct gyg gat gag gar gag gat cct gcg gag gag      165
Leu Pro Ala Val Gly Ser Xaa Asp Glu Glu Glu Asp Pro Ala Glu Glu
                                5                                10                                15

gat tgt cct gaa ttg gtt ccc att gag acg acg caa agc gag gag gag      213
Asp Cys Pro Glu Leu Val Pro Ile Glu Thr Thr Gln Ser Glu Glu Glu
                                20                                25                                30

gaa aag tct ggc ctc ggc gcc aag atc cca gtc aca att atc acc ggg      261
Glu Lys Ser Gly Leu Gly Ala Lys Ile Pro Val Thr Ile Ile Thr Gly

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Thr Met Lys Arg Leu Val Cys Val Leu Leu Val Cys Ser Ser Ala Val	
55 60 65	
gca cag ttg cat aaa gat cct acc ctg gat cac cac tgg cat ctc tgg	357
Ala Gln Leu His Lys Asp Pro Thr Leu Asp His His Trp His Leu Trp	
70 75 80	
aag aaa acc tat ggc aaa caa tac aag gaa aag aat gaa gaa gca gta	405
Lys Lys Thr Tyr Gly Lys Gln Tyr Lys Glu Lys Asn Glu Glu Ala Val	
85 90 95 100	
cga cgt ctc atc tgg gaa aag aat cta aag ttt gtg atg ctt cac aac	453
Arg Arg Leu Ile Trp Glu Lys Asn Leu Lys Phe Val Met Leu His Asn	
105 110 115	
ctg gag cat tca atg gga atk cac tca tac gat ctg ggc atg aac cac	501
Leu Glu His Ser Met Gly Xaa His Ser Tyr Asp Leu Gly Met Asn His	
120 125 130	
ctg gga gac atg acc agt gaa gaa gtg atg tct ttg atg agt tcc ctg	549
Leu Gly Asp Met Thr Ser Glu Glu Val Met Ser Leu Met Ser Ser Leu	
135 140 145	
aga gtt ccc agc cag tgg cag aga aaa tat cac ata taagtcaaac	595
Arg Val Pro Ser Gln Trp Gln Arg Lys Tyr His Ile	
150 155 160	
cctaatcgga tattgacctga ttctgtggac tggagagaga a	636
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Met Ser His Thr Ile Leu	
1 5	
ctg gta cag cct acc aag agg cca gaa ggc aga act tat gct gac tac	164
Leu Val Gln Pro Thr Lys Arg Pro Glu Gly Arg Thr Tyr Ala Asp Tyr	
10 15 20	
gaa tct gtg aat gaa tgc atg gaa ggt gtt tgt aaa atg tat gaa gaa	212
Glu Ser Val Asn Glu Cys Met Glu Gly Val Cys Lys Met Tyr Glu Glu	
25 30 35	
cat ctg aaa aga atg aat ccc aac agt ccc tct atc aca tat gac atc	260
His Leu Lys Arg Met Asn Pro Asn Ser Pro Ser Ile Thr Tyr Asp Ile	
40 45 50	
agt cag ttg ttt gat ttc atc gat gat ctg gca gac ctc agc tgc ctg	308
Ser Gln Leu Phe Asp Phe Ile Asp Asp Leu Ala Asp Leu Ser Cys Leu	
55 60 65 70	
gtt tac cga gct gat acc cag aca tac cag cct tat aac aaa gac tgg	356
Val Tyr Arg Ala Asp Thr Gln Thr Tyr Gln Pro Tyr Asn Lys Asp Trp	
75 80 85	
att aaa gag aag atc tac gtg ctc ctt cgt cgg cag gcc caa cag gct	404
Ile Lys Glu Lys Ile Tyr Val Leu Leu Arg Arg Gln Ala Gln Gln Ala	

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90	95	100	
ggg aaa taattgtgtt ggaagcactg ggggggttgg ggtgggcttg gaacacaggt			460
Gly Lys			482
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Gly Ala Ser Pro Glu Asp Pro Trp Val Lys Val Glu Tyr Ala Tyr Ser			
5 10 15 20			
gac aac agc ctg gac ccc gat gat gag gac agt gat tac cac cag gag			152
Asp Asn Ser Leu Asp Pro Asp Asp Glu Asp Ser Asp Tyr His Gln Glu			
25 30 35			
gcc tac aag gag tcc tac aaa gac cgg cgg cgg cgc gca cac act cag			200
Ala Tyr Lys Glu Ser Tyr Lys Asp Arg Arg Arg Arg Ala His Thr Gln			
40 45 50			
gct gag cag aag agg agg gac gcc atc aag aga ggc tat gat gac ctt			248
Ala Glu Gln Lys Arg Arg Asp Ala Ile Lys Arg Gly Tyr Asp Asp Leu			
55 60 65			
cag acc atc gtc ccc act tgc cag cag cag gac ttc tcc att ggc tcc			296
Gln Thr Ile Val Pro Thr Cys Gln Gln Gln Asp Phe Ser Ile Gly Ser			
70 75 80			
caa aag ctc agc aaa gcc atc gtt cta caa aag acc att gac tac att			344
Gln Lys Leu Ser Lys Ala Ile Val Leu Gln Lys Thr Ile Asp Tyr Ile			
85 90 95 100			
cag ttt ttg cac aag gag aag aaa aag cag gag gag gag gtg tcc acg			392
Gln Phe Leu His Lys Glu Lys Lys Lys Gln Glu Glu Glu Val Ser Thr			
105 110 115			
tta cgc aag gat gtc acc gcc cta aag atc atg aaa gtg aac tat gag			440
Leu Arg Lys Asp Val Thr Ala Leu Lys Ile Met Lys Val Asn Tyr Glu			
120 125 130			
cag att gtg aag gca cac cag gac aac ccc atg aag ggg agg aca ggt			488
Gln Ile Val Lys Ala His Gln Asp Asn Pro Met Lys Gly Arg Thr Gly			
135 140 145			
ctc tgaccaggtc aagttc			507
Leu			

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<220>
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 Met Val
 1
 cga tac cgc gtg agg agc ctg agc gaa cgc tcg cac gag gtg tac agg 165
 Arg Tyr Arg Val Arg Ser Leu Ser Glu Arg Ser His Glu Val Tyr Arg
 5 10 15
 cag cag ttg cat ggg caa gag caa gga cac cac ggc caa gag gag caa 213
 Gln Gln Leu His Gly Gln Glu Gln Gly His His Gly Gln Glu Glu Gln
 20 25 30
 ggg ctg agc ccg gag cac gtc gag gtc tac gag agg acc cat ggc cag 261
 Gly Leu Ser Pro Glu His Val Glu Val Tyr Glu Arg Thr His Gly Gln
 35 40 45 50
 tct cac tat agg cgc aga cac tgc tct cga agg agg ctg cac cgg atc 309
 Ser His Tyr Arg Arg Arg His Cys Ser Arg Arg Arg Leu His Arg Ile
 55 60 65
 cac agg cgg cag atc gct cct gca gaa ggc gca aaa gac gct cct gca 357
 His Arg Arg Gln Ile Ala Pro Ala Glu Gly Ala Lys Asp Ala Pro Ala
 70 75 80
 ggc acc gga gna ggc atc gca gag gct gca gaa cca gga aga gaa cat 405
 Gly Thr Gly Xaa Gly Ile Ala Glu Ala Ala Glu Pro Gly Arg Glu His
 85 90 95
 gca gaa ggc cac taagcttct gggccctca cccccrgctg gaaaattaag 457
 Ala Glu Gly His
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 aaaaagtcgc cccgaaacac caagtgaggc cata 491

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 Met Ala Arg Gly Pro Lys Lys His Leu Lys Arg Val Ala Ala Pro Lys
 1 5 10 15
 cat tgg atg ctg gat aaa ttg acc ggt gtg ttt gct cct cgt cca tcc 153
 His Trp Met Leu Asp Lys Leu Thr Gly Val Phe Ala Pro Arg Pro Ser
 20 25 30
 acc ggt ccc cac aag ttg aga gag tgt ctc ccc ctc atc att ttc ctg 201
 Thr Gly Pro His Lys Leu Arg Glu Cys Leu Pro Leu Ile Ile Phe Leu
 35 40 45

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50                      55                      60
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Cys Met Gln Arg Phe Ile Lys Ile Asp Gly Lys Val Arg Thr Asp Ile
65                      70                      75                      80
acc tac cct gct gga ttc atg gat gtc atc agc att gac aag acg gga      345
Thr Tyr Pro Ala Gly Phe Met Asp Val Ile Ser Ile Asp Lys Thr Gly
85                      90                      95
gag aat ttc cgt ctg atc tat gac acc aag ggt cgc ttt gct gta cat      393
Glu Asn Phe Arg Leu Ile Tyr Asp Thr Lys Gly Arg Phe Ala Val His
100                      105                      110
cgt att aca cct gag gag gcc aag tac aag ttg tgc aaa gtg aga aag      441
Arg Ile Thr Pro Glu Glu Ala Lys Tyr Lys Leu Cys Lys Val Arg Lys
115                      120                      125
atc ttt gtg ggc aca aaa gga atc cct cat ctg gtg act cat gat gcc      489
Ile Phe Val Gly Thr Lys Gly Ile Pro His Leu Val Thr His Asp Ala
130                      135                      140
cgc acc atc cgc tac ccc gat ccc ctc atc aag gtg aat gat acc att      537
Arg Thr Ile Arg Tyr Pro Asp Pro Leu Ile Lys Val Asn Asp Thr Ile
145                      150                      155                      160
cag att gat ttr gag act ggc aag att act gat ttc atc aag ttc gac      585
Gln Ile Asp Leu Glu Thr Gly Lys Ile Thr Asp Phe Ile Lys Phe Asp
165                      170                      175
act ggt aac ctg tgt atg gtg act gga ggt gct aac cta gga aga att      633
Thr Gly Asn Leu Cys Met Val Thr Gly Gly Ala Asn Leu Gly Arg Ile
180                      185                      190
ggt gtg atc acc aac aga gag agg cac cct gga tct ttt gac gtg gtt      681
Gly Val Ile Thr Asn Arg Glu Arg His Pro Gly Ser Phe Asp Val Val
195                      200                      205
cac gtg aaa gat gcc aat ggc aac agc ttt gcc act cga ctt tcc aac      729
His Val Lys Asp Ala Asn Gly Asn Ser Phe Ala Thr Arg Leu Ser Asn
210                      215                      220
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Ile Phe Val Ile Gly Lys Gly Asn Lys Pro Trp Ile Ser Leu Pro Arg
225                      230                      235                      240
gga aag ggt atc cgc ctc acc att gct gaa gag aga gac aaa aga ctg      825
Gly Lys Gly Ile Arg Leu Thr Ile Ala Glu Glu Arg Asp Lys Arg Leu
245                      250                      255
gcg gcc aaa cag agc agt ggg tgaaatgggt ccctgggtga catgtcagat      876
Ala Ala Lys Gln Ser Ser Gly
260
ctttgtacgt aattaaat attgtg      902

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<221> CDS

<222> 23..652

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Pro Trp Xaa Pro Val Val His Leu Pro Gly Gln Pro Gln Arg Met Met
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ggt cct ctc tca caa gca tca agg tat ata ggc ccg cag aat ttt tac      153
Gly Pro Leu Ser Gln Ala Ser Arg Tyr Ile Gly Pro Gln Asn Phe Tyr
      20                                25                                30
cag gtt aaa gac att cgg agg cca gaa agg cgc cat agt gac cct tgg      201
Gln Val Lys Asp Ile Arg Arg Pro Glu Arg Arg His Ser Asp Pro Trp
      35                                40                                45                                50
ggt agg caa gac caa cag caa ctg gat agg cca ttt aat agg ggt aaa      249
Gly Arg Gln Asp Gln Gln Gln Leu Asp Arg Pro Phe Asn Arg Gly Lys
      55                                60                                65
ggg gac cgc cag aga ttt tat agt gat tca cac cat ttg aaa aga gag      297
Gly Asp Arg Gln Arg Phe Tyr Ser Asp Ser His His Leu Lys Arg Glu
      70                                75                                80
cga cat gaa aag gaa tgg gag caa gaa tct gaa agg cat aga cgc aga      345
Arg His Glu Lys Glu Trp Glu Gln Glu Ser Glu Arg His Arg Arg Arg
      85                                90                                95
gac aga agc maa gac agg aca gag aca gaa aaa gca ggg agg aag ggc      393
Asp Arg Ser Xaa Asp Arg Thr Glu Thr Glu Lys Ala Gly Arg Lys Gly
      100                                105                                110
aca aag ata aag aga ggg cac ggt tat cac atg gtg atc gag gaa cag      441
Thr Lys Ile Lys Arg Gly His Gly Tyr His Met Val Ile Glu Glu Gln
      115                                120                                125                                130
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Met Glu Lys Gln Ala Glu Ile Val Gly Met
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<210> 3953

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<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 59..391

<400> 3953

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gcatttccgg agcgccaggg aagaggggaag tcgtggtggt cgcgagggag ccggaaag      58
atg gtg gtt acc aga tct gca cgg gct aag gcc agc atc caa gcc gcg      106
Met Val Val Thr Arg Ser Ala Arg Ala Lys Ala Ser Ile Gln Ala Ala
      1                                5                                10                                15
tcg gct gaa agt tcc ggg caa aag agt ttt gct gct aat ggg att caa      154
Ser Ala Glu Ser Ser Gly Gln Lys Ser Phe Ala Ala Asn Gly Ile Gln
      20                                25                                30
gcg cat cca gaa agt agt act gga tct gat gcc cga act act gct gaa      202
Ala His Pro Glu Ser Ser Thr Gly Ser Asp Ala Arg Thr Thr Ala Glu
      35                                40                                45

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004220" 666E550

tca cag acc act ggg aag caa agt tta atc cct aga act cct aaa gct	250
Ser Gln Thr Thr Gly Lys Gln Ser Leu Ile Pro Arg Thr Pro Lys Ala	
50 55 60	
aga aag agg aag agc aga act aca ggc tca cta cca aag ggg act gaa	298
Arg Lys Arg Lys Ser Arg Thr Thr Gly Ser Leu Pro Lys Gly Thr Glu	
65 70 75 80	
cca tct acg gat gga gar acc tct gag gca gag tca aat tat tct gtg	346
Pro Ser Thr Asp Gly Glu Thr Ser Glu Ala Glu Ser Asn Tyr Ser Val	
85 90 95	
tct gag cac atg ata cat ttt aag ggt act agg aga ggc aga tct	391
Ser Glu His Met Ile His Phe Lys Gly Thr Arg Arg Gly Arg Ser	
100 105 110	
taattgcatg ctcccagtgt ccagtgttag gaaaaagccg aaagtactcc aacaaaggag	451
tcttacactg aagaaatag	470

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 <212> DNA
 <213> Homo sapiens

<220>
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 <222> 94..429

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tgatactaca gacagtacaa cagatcaaga agt atg gca gtg aca act cgt ttg	114
Met Ala Val Thr Thr Arg Leu	
1 5	
aca tgg ttg cac gaa aag atc ctg caa aat cat ttt gga ggg aag cgg	162
Thr Trp Leu His Glu Lys Ile Leu Gln Asn His Phe Gly Gly Lys Arg	
10 15 20	
ctt agc ctt ctc tat aag ggt agt gtc cat gga ttc cgt aat gga gtt	210
Leu Ser Leu Leu Tyr Lys Gly Ser Val His Gly Phe Arg Asn Gly Val	
25 30 35	
ttg ctt gac aga tgt tgt aat caa ggg cct act cta aca gtg att tat	258
Leu Leu Asp Arg Cys Cys Asn Gln Gly Pro Thr Leu Thr Val Ile Tyr	
40 45 50 55	
agt gaa gat cat att att gga gca tat gca gaa gag agt tac cag gaa	306
Ser Glu Asp His Ile Ile Gly Ala Tyr Ala Glu Glu Ser Tyr Gln Glu	
60 65 70	
gga aag tat gct tcc atc atc ctt ttt gca ctt caa gat act aaa att	354
Gly Lys Tyr Ala Ser Ile Ile Leu Phe Ala Leu Gln Asp Thr Lys Ile	
75 80 85	
tca gaa tgg aaa cta gga cta tgt aca cca gaa aca ctg ttt tgt tgt	402
Ser Glu Trp Lys Leu Gly Leu Cys Thr Pro Glu Thr Leu Phe Cys Cys	
90 95 100	
gat gtt aca aaa tat aac tcc cca aca tgacctcttt cgcatttgtg	449
Asp Val Thr Lys Tyr Asn Ser Pro Thr	
105 110	
ctttctcakr tataagaaca cagtatacat aataagcaga ata	492

<210> 3955

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 <212> DNA
 <213> Homo sapiens

<220>
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 <222> 165..548

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 cttgggctta tttggtgtgc tgttgaaggg gggagactag agaa atg gca ggg aac 176
 Met Ala Gly Asn
 1
 ctc tta tcc ggg gca ggt agg cgc ctg tgg gac tgg gtg cct ctg gcg 224
 Leu Leu Ser Gly Ala Gly Arg Arg Leu Trp Asp Trp Val Pro Leu Ala
 5 10 15 20
 tgc aga agc ttc tct ctt ggt gtg cct aga ttg atc ggt ata agg ctc 272
 Cys Arg Ser Phe Ser Leu Gly Val Pro Arg Leu Ile Gly Ile Arg Leu
 25 30 35
 act ctc ccg ccc ccc aaa gtg gtt gat cgt tgg aac gag aaa agg gcc 320
 Thr Leu Pro Pro Pro Lys Val Val Asp Arg Trp Asn Glu Lys Arg Ala
 40 45 50
 atg ttc gga gtg tat gac aac atc ggg atc ctg gga aac ttt gaa aag 368
 Met Phe Gly Val Tyr Asp Asn Ile Gly Ile Leu Gly Asn Phe Glu Lys
 55 60 65
 cac ccc aaa gaa ctg atc agg ggg ccc ata tgg ctt cga ggt tgg aaa 416
 His Pro Lys Glu Leu Ile Arg Gly Pro Ile Trp Leu Arg Gly Trp Lys
 70 75 80
 ggg aat gaa ttg caa cgt tgt atc cga aag agg aaa atg gtt gga agt 464
 Gly Asn Glu Leu Gln Arg Cys Ile Arg Lys Arg Lys Met Val Gly Ser
 85 90 95 100
 aga atg ttc gct gat gac ctg cac aac ctt aat aaa cgc atc cgc tat 512
 Arg Met Phe Ala Asp Asp Leu His Asn Leu Asn Lys Arg Ile Arg Tyr
 105 110 115
 ctc tac aaa cac ttt aac cga cat ggg aag ttt cga tagaagagaa 558
 Leu Tyr Lys His Phe Asn Arg His Gly Lys Phe Arg
 120 125
 agctgagaac ttcggaaaag gctcatctgt caccctggag aagggaaact gtacttttcc 618
 ct 620

<210> 3956
 <211> 512
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 47..502

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[illegible]

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taaaggcgcg cgagtgtagg cgacaggccg ctgacggccg gaagggaaa atg agt gag      117
                                     Met Ser Glu
                                     1
tct ttg gwt gtt tgt gat gtt gcc gaa gat tta gtg gaa aag ctg aga      165
Ser Leu Xaa Val Cys Asp Val Ala Glu Asp Leu Val Glu Lys Leu Arg
5                               10                15
aag ttt cgt ttt cgc aaa gaa acg aac aac gct gct att ata atg aag      213
Lys Phe Arg Phe Arg Lys Glu Thr Asn Asn Ala Ala Ile Ile Met Lys
20                                25                    30                      35
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att gac aag gat aaa cgc ctg gtg gta ctg gat gag gag ctt gag ggc      261
Ile Asp Lys Asp Lys Arg Leu Val Val Leu Asp Glu Glu Leu Glu Gly
      40      45      50
att tca cca gat gaa ctt aaa gat gaa cta cct gaa cga caa cct cga      309
Ile Ser Pro Asp Glu Leu Lys Asp Glu Leu Pro Glu Arg Gln Pro Arg
      55      60      65
acc ttc att gtg tat agt tat aaa tat caa cat gat gat gga aga gtt      357
Thr Phe Ile Val Tyr Ser Tyr Lys Tyr Gln His Asp Asp Gly Arg Val
      70      75      80
tca tat cct ctg tgc ttt att ttc tcc agt cct gtt gga tgt aag ynt      405
Ser Tyr Pro Leu Cys Phe Ile Phe Ser Ser Pro Val Gly Cys Lys Xaa
      85      90      95
gaa caa cag atg atg tat gct gga agt aag aat aaa gct agt cca gac      453
Glu Gln Gln Met Met Tyr Ala Gly Ser Lys Asn Lys Ala Ser Pro Asp
100      105      110      115
agc tga
Ser

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<210> 3958
 <211> 531
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> CDS
 <222> 123..509

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gaaccagac acaagtcttc actccttcct gcgagccctg aggaagcctt ctttccccag      120
ac atg gcc aac aag ggt cct tcc tat ggc atg agc cgc gaa gtg cag      167
Met Ala Asn Lys Gly Pro Ser Tyr Gly Met Ser Arg Glu Val Gln
1      5      10      15
tcc aaa atc gag aag aag tat gac gag gag ctg gag gag cgg ctg gtg      215
Ser Lys Ile Glu Lys Lys Tyr Asp Glu Glu Leu Glu Glu Arg Leu Val
      20      25      30
gag tgg atc ata gtg cag tgt ggc cct gat gtg ggc cgc cca gac cgt      263
Glu Trp Ile Ile Val Gln Cys Gly Pro Asp Val Gly Arg Pro Asp Arg
      35      40      45
ggg cgc ttg ggc ttc cag gtc tgg ctg aag aat ggc gtg att ctg agc      311
Gly Arg Leu Gly Phe Gln Val Trp Leu Lys Asn Gly Val Ile Leu Ser
      50      55      60
aag ctg gtg aac agc ctg tac cct gat ggc tcc aag ccg gtg aag gtg      359
Lys Leu Val Asn Ser Leu Tyr Pro Asp Gly Ser Lys Pro Val Lys Val
      65      70      75
ccc gag aac cca ccc tcc atg gtc ttc aag cag atg gag cag gtg gct      407
Pro Glu Asn Pro Pro Ser Met Val Phe Lys Gln Met Glu Gln Val Ala
      80      85      90      95
cag ttc ctg aag gcg gct gag gac tat ggg gtc atc aag act gac atg      455
Gln Phe Leu Lys Ala Ala Glu Asp Tyr Gly Val Ile Lys Thr Asp Met
      100      105      110
ttc cag act gtt gac ctc ttt gaa ngc aag aca tgg cag cag tgc aga      503
Phe Gln Thr Val Asp Leu Phe Glu Xaa Lys Thr Trp Gln Gln Cys Arg

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004223-004350

115 120 125 531
gga ccc tgatggcttt gggcagcttg gc
Gly Pro

<210> 3959
<211> 503
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 164..490

<400> 3959
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ccagctcttc ccctactccc tctcggtccc ttgtggccca aaggcctaac cgggggtccgg 120
cggctctggcc tagggatctt ccccgttgcc cctttggggc ggg atg gct gcg gaa 175
Met Ala Ala Glu
1
gaa gaa gac gag gtg gag tgg gta gtg gag agc atc gcg ggg ttc ctg 223
Glu Glu Asp Glu Val Glu Trp Val Val Glu Ser Ile Ala Gly Phe Leu
5 10 15 20
cga ggc cca gac tgg tcc atc ccc atc ttg gac ttt gtg gaa cag aaa 271
Arg Gly Pro Asp Trp Ser Ile Pro Ile Leu Asp Phe Val Glu Gln Lys
25 30 35
tgt gaa gtt ttt gat gat gaa gaa gaa agc aaa ttg acc tat aca gag 319
Cys Glu Val Phe Asp Asp Glu Glu Glu Ser Lys Leu Thr Tyr Thr Glu
40 45 50
att cat cag gaa tac aaa gaa cta gtt gaa aag ctg tta gaa ggt tac 367
Ile His Gln Glu Tyr Lys Glu Leu Val Glu Lys Leu Leu Glu Gly Tyr
55 60 65
ctc aaa gaa att gga att aat gaa gat caa ttt caa gaa gca tgc act 415
Leu Lys Glu Ile Gly Ile Asn Glu Asp Gln Phe Gln Glu Ala Cys Thr
70 75 80
tct cct yct tgc aaa gac cca tac atc aca ggc cat ttt gca acc tgt 463
Ser Pro Xaa Cys Lys Asp Pro Tyr Ile Thr Gly His Phe Ala Thr Cys
85 90 95 100
gtt ggc agc aga aga ttt tac tat ctt taaagcaatg acg 503
Val Gly Ser Arg Arg Phe Tyr Tyr Leu
105

<210> 3960
<211> 516
<212> DNA
<213> Homo sapiens

<220>
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<222> 126..440

<400> 3960
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tgtttggtgc tttggatcca ttccatcgg tccttacagc cgctcgtcag actccagcag	120
ccaag atg gtg aag cag atc gag agc aag act gct ttt cag gaa gcc ttg	170
Met Val Lys Gln Ile Glu Ser Lys Thr Ala Phe Gln Glu Ala Leu	
1 5 10 15	
gac gct gca ggt gat aaa ctt gta gta gtt gac ttc tca gcc acg tgg	218
Asp Ala Ala Gly Asp Lys Leu Val Val Val Asp Phe Ser Ala Thr Trp	
20 25 30	
tgt ggg cct tgc aaa atg atc aag cct ttc ttt cat tcc ctc tct gaa	266
Cys Gly Pro Cys Lys Met Ile Lys Pro Phe Phe His Ser Leu Ser Glu	
35 40 45	
aag tat tcc aac gtg ata ttc ctt gaa gta gat gtg gat gac tgt cag	314
Lys Tyr Ser Asn Val Ile Phe Leu Glu Val Asp Val Asp Asp Cys Gln	
50 55 60	
gat gtt gct tca gag tgt gaa gtc aaa tgc atg cca aca ttc cag ttt	362
Asp Val Ala Ser Glu Cys Glu Val Lys Cys Met Pro Thr Phe Gln Phe	
65 70 75	
ttt aag aag gga caa aag gtg ggt gaa ttt tct gga gcc aat aag gaa	410
Phe Lys Lys Gly Gln Lys Val Gly Glu Phe Ser Gly Ala Asn Lys Glu	
80 85 90 95	
aag ctt gaa gcc acc att aat gaa tta gtc taannatggt ttctgnaaaa	460
Lys Leu Glu Ala Thr Ile Asn Glu Leu Val	
100 105	
cataaccagc cattggctat ttaaaacttg taattttttt taatttacaa aaatat	516
<210> 3961	
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<213> Homo sapiens	
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<222> 206..601	
<400> 3961	
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tttaaatacac tggatttttg cccaccctct ttccaaataa gaaggcagga gctgcttgct	120
gaggtgtaaa aggggtcttct gagctgcagt ggcaattaga ccagaagatc cccgctcctg	180
tctctaaaga ggggaaaggg caagg atg gtg gag gct ttc tgt gct acc tgg	232
Met Val Glu Ala Phe Cys Ala Thr Trp	
1 5	
aag ctg acc aac agt cag aac ttt gat gag tac atg aag gct cta ggc	280
Lys Leu Thr Asn Ser Gln Asn Phe Asp Glu Tyr Met Lys Ala Leu Gly	
10 15 20 25	
gtg ggc ttt gcc act agg cag gtg gga aat gtg acc aaa cca acg gta	328
Val Gly Phe Ala Thr Arg Gln Val Gly Asn Val Thr Lys Pro Thr Val	
30 35 40	
att atc agt caa gaa gga gac aaa gtg gtc atc agg act ctc agc aca	376
Ile Ile Ser Gln Glu Gly Asp Lys Val Val Ile Arg Thr Leu Ser Thr	
45 50 55	
ttc aag aac acg gag att agt ttc cag ctg gga gaa gag ttt gat gaa	424
Phe Lys Asn Thr Glu Ile Ser Phe Gln Leu Gly Glu Glu Phe Asp Glu	
60 65 70	
acc act gca gnn tat aga aac tgt aag tct gtt gtt agc ctg gat gga	472

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 <221> CDS
 <222> 134..547

<400> 3963
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 gatgtagccg cttgcggaga ctgcaagcag ccgcggcgcg cccggccctc cctcttcgcg 120
 tgccgccgtg gga atg gaa aca tct gcc cca cgt gcc gga agc caa gtg 169
 Met Glu Thr Ser Ala Pro Arg Ala Gly Ser Gln Val
 1 5 10
 gtg gcg aca act gcg cgc cac tcc gcg gcc tac cgc gca gat cct cta 217
 Val Ala Thr Thr Ala Arg His Ser Ala Ala Tyr Arg Ala Asp Pro Leu
 15 20 25
 cgt gtg tcc tcg cga gac aag ctc acc gaa atg gcc gcg tcc agt caa 265
 Arg Val Ser Ser Arg Asp Lys Leu Thr Glu Met Ala Ala Ser Ser Gln
 30 35 40
 gga aac ttt gag gga aat ttt gag tca ctg gac ctt gcg gaa ttt gct 313
 Gly Asn Phe Glu Gly Asn Phe Glu Ser Leu Asp Leu Ala Glu Phe Ala
 45 50 55 60
 aag aag cag cca tgg tgg cgt aas tgt tcg ggc agg aat ctg gac ctt 361
 Lys Lys Gln Pro Trp Trp Arg Xaa Cys Ser Gly Arg Asn Leu Asp Leu
 65 70 75
 cag cag aaa agt ata gcg tgg caa ccc agc tgt tca ttg gag gtg tca 409
 Gln Gln Lys Ser Ile Ala Trp Gln Pro Ser Cys Ser Leu Glu Val Ser
 80 85 90
 ctg gat ggt gca cag gtt tca tat tcc aga agg ttg gaa agt tgg ctg 457
 Leu Asp Gly Ala Gln Val Ser Tyr Ser Arg Arg Leu Glu Ser Trp Leu
 95 100 105
 caa cag ctg tgg gag gtg gat ttt ttc tcc ttc agc ttg caa acc ata 505
 Gln Gln Leu Trp Glu Val Asp Phe Phe Ser Phe Ser Leu Gln Thr Ile
 110 115 120
 ctg ggt aca tca aag ttg act ggc aac gag tgg aga agg aca 547
 Leu Gly Thr Ser Lys Leu Thr Gly Asn Glu Trp Arg Arg Thr
 125 130 135
 tgaagaaagc caaagagcag ctgaagatcc gtaagagcaa tcagatacct actgaggtca 607
 ggagcaaagc tgaggaggtg gtgtcatatt 636

<210> 3964
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 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 36..422

<400> 3964
 agtcagttgc cggaagtcgg cgtgaggtgg ggctt atg cgg cgg cgt ggt gaa 53
 Met Arg Arg Arg Gly Glu
 1 5
 ata gat atg gcg acc gag ggg gat gtg gag ctg gag ttg gag act gag 101

Ile Asp Met Ala Thr Glu Gly Asp Val Glu Leu Glu Leu Glu Thr Glu	
10 15 20	
acc agt gga cca gag cgg cct ccg gag aag cca cgg aaa cat gac agc	149
Thr Ser Gly Pro Glu Arg Pro Pro Glu Lys Pro Arg Lys His Asp Ser	
25 30 35	
ggt gcg gcg gac ttg gag cgg gtc acc gac tat gca gag gag aag gag	197
Gly Ala Ala Asp Leu Glu Arg Val Thr Asp Tyr Ala Glu Glu Lys Glu	
40 45 50	
atc cag agt tcc aat ctg gag acg gcc atg tct gtg att gga gac aga	245
Ile Gln Ser Ser Asn Leu Glu Thr Ala Met Ser Val Ile Gly Asp Arg	
55 60 65 70	
agg tcc cgg gag cag aaa gcc aaa cag gag cgg gag aaa gaa ctg gca	293
Arg Ser Arg Glu Gln Lys Ala Lys Gln Glu Arg Glu Lys Glu Leu Ala	
75 80 85	
aaa gtc act atc aag aag gaa gat ctg gag cta ata atg act gag atg	341
Lys Val Thr Ile Lys Lys Glu Asp Leu Glu Leu Ile Met Thr Glu Met	
90 95 100	
gag ata tct cga gca gca gca gaa cgc agt ttg cgg gaa cac atg ggc	389
Glu Ile Ser Arg Ala Ala Ala Glu Arg Ser Leu Arg Glu His Met Gly	
105 110 115	
aac gtg gta gag gcg ctt att gcc cta acc aac tgatgcgtgc tttctcaa	442
Asn Val Val Glu Ala Leu Ile Ala Leu Thr Asn	
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atacc	447
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Met	
1	
gag ccc gac ggg act tac gag ccg ggc ttc gtg ggt att cgc ttc tgc	107
Glu Pro Asp Gly Thr Tyr Glu Pro Gly Phe Val Gly Ile Arg Phe Cys	
5 10 15	
cag gaa tgt aac aac atg ctg tac ccc aag gaa gac aag gag aac cgc	155
Gln Glu Cys Asn Asn Met Leu Tyr Pro Lys Glu Asp Lys Glu Asn Arg	
20 25 30	
att ctg ctc tac gcg tgc cgg aac tgt gat tac cag cag gag gcc gac	203
Ile Leu Leu Tyr Ala Cys Arg Asn Cys Asp Tyr Gln Gln Glu Ala Asp	
35 40 45	
aac agc tgc atc tat gtc aac aag atc acg cac gaa gtg gac gaa ctg	251
Asn Ser Cys Ile Tyr Val Asn Lys Ile Thr His Glu Val Asp Glu Leu	
50 55 60 65	
acc cag att atc gcc gac gtg tcc cag gac ccc acg ttg ccg cgg acc	299
Thr Gln Ile Ile Ala Asp Val Ser Gln Asp Pro Thr Leu Pro Arg Thr	
70 75 80	

gag gac cac ccg tgc caa aag tgc ggc cac aag gag gct gtg ttc ttc	347
Glu Asp His Pro Cys Gln Lys Cys Gly His Lys Glu Ala Val Phe Phe	
85 90 95	
cag tca cac agt gcg cgg gcc gag gac gcc atg cgc ctt tac tac gtg	395
Gln Ser His Ser Ala Arg Ala Glu Asp Ala Met Arg Leu Tyr Tyr Val	
100 105 110	
tgc aca gcc cca cac tgc ggc cam cgc tgg acc gag tractcctct ctcc	445
Cys Thr Ala Pro His Cys Gly Xaa Arg Trp Thr Glu	
115 120 125	

<210> 3966
 <211> 506
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 91..408

<400> 3966	
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ccgattttct cctgctgctg tggcccggac atg gcg act ccc gcc cct gtg att	114
Met Ala Thr Pro Gly Pro Val Ile	
1 5	
ccg gag gtc ccc ttt gaa cca tgc aag cct cca gtc att gag ggg ctg	162
Pro Glu Val Pro Phe Glu Pro Ser Lys Pro Pro Val Ile Glu Gly Leu	
10 15 20	
agc ccc act gtt tac agg aat cca gag agt ttc aag gaa aag ttc gtt	210
Ser Pro Thr Val Tyr Arg Asn Pro Glu Ser Phe Lys Glu Lys Phe Val	
25 30 35 40	
cgc aag acc cgc gag aac ccg gtg gta ccc ata ggt tgc ctg gcc acg	258
Arg Lys Thr Arg Glu Asn Pro Val Val Ile Gly Cys Leu Ala Thr	
45 50 55	
gcg gcc gcc ctc acc tac ggc ctc tac tcc ttc cac cgg ggc aac agc	306
Ala Ala Ala Leu Thr Tyr Gly Leu Tyr Ser Phe His Arg Gly Asn Ser	
60 65 70	
cag cgc tct cag ctc atg atg cgc acc cgg atc gcc gcc cag ggt ttc	354
Gln Arg Ser Gln Leu Met Met Arg Thr Arg Ile Ala Ala Gln Gly Phe	
75 80 85	
acg gtc gca gcc atc ttg ctg ggt ctg gct gtc act gct atg aag tct	402
Thr Val Ala Ala Ile Leu Leu Gly Leu Ala Val Thr Ala Met Lys Ser	
90 95 100	
cga ccc taagcccagg gtctggcctt gaaagcyskg cagaaatgat tccaaaaccc	458
Arg Pro	
105	
aggagcaac cactggccct accgtgggac ttactcctc ctctcctt	506

<210> 3967
 <211> 425
 <212> DNA
 <213> Homo sapiens

<220>

<221> CDS
<222> 39..341

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Met Ala Ala Trp Ser Pro
1 5
gcc gcg gca gsc ctc tcc tcc gcg gga tcc gcg ggc ttc cac ttc acc 104
Ala Ala Ala Xaa Leu Ser Ser Ala Gly Ser Ala Gly Phe His Phe Thr
10 15 20
atc gga tgt ttg cca ctc agc act gag ggg gag ctc aga gtg acc can 152
Ile Gly Cys Leu Pro Leu Ser Thr Glu Gly Glu Leu Arg Val Thr Xaa
25 30 35
att ctc aaa gaa aag ttt cca cga gct aca gct ata aaa gtc act gac 200
Ile Leu Lys Glu Lys Phe Pro Arg Ala Thr Ala Ile Lys Val Thr Asp
40 45 50
att tca ggc act aaa aga aga aat caa aga gat gca tgg att gcg gat 248
Ile Ser Gly Thr Lys Arg Arg Asn Gln Arg Asp Ala Trp Ile Ala Asp
55 60 65 70
att tac ctc trt ccc caa acg ctg acc acg ccc tgg ctg cat aga tgc 296
Ile Tyr Leu Xaa Pro Gln Thr Leu Thr Thr Pro Trp Leu His Arg Cys
75 80 85
tgc tgc tta aga cct tgg atg aac ttc act gac atc att ctt ccc 341
Cys Cys Leu Arg Pro Trp Met Asn Phe Thr Asp Ile Ile Leu Pro
90 95 100
taagcagtca ccaaaaaatt tatatatattt gctcatatac atttccatat tatmattata 401
gaagatgtat aatctattta gatg 425

<210> 3968
<211> 381
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 27..341

<400> 3968
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Met Gly Glu Arg Leu Ala Lys Ala Ser
1 5
cat gaa agc aaa gca tct gag att gaa tac aag ctg gga aag gtc aac 101
His Glu Ser Lys Ala Ser Glu Ile Glu Tyr Lys Leu Gly Lys Val Asn
10 15 20 25
gac cgg tgg cag cat ctc ctg gac ctc att gca gcc agg gtg aag aag 149
Asp Arg Trp Gln His Leu Leu Asp Leu Ile Ala Ala Arg Val Lys Lys
30 35 40
ctg aag gag acc ctg gta gcc gtg cag cag ctt gat aag aac atg agc 197
Leu Lys Glu Thr Leu Val Ala Val Gln Gln Leu Asp Lys Asn Met Ser
45 50 55
agc ctg agg acc tgg ctc gct cac atc gag tca gag ctg gcc aag cca 245
Ser Leu Arg Thr Trp Leu Ala His Ile Glu Ser Glu Leu Ala Lys Pro

60	65	70	
ata gtc tac gat tcc tgt aac tcg gaa gaa ata cag aga tgg atc tgc			293
Ile Val Tyr Asp Ser Cys Asn Ser Glu Glu Ile Gln Arg Trp Ile Cys			
75	80	85	
agc tca cta ata ttg aac att ttt ctg agt gtg atg ttc aag cta aaa			341
Ser Ser Leu Ile Leu Asn Ile Phe Leu Ser Val Met Phe Lys Leu Lys			
90	95	100	105
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ccttctggat tcaagaagac gaggctcacc tggtactcgg cctcccagaa ag atg gat	118
	Met Asp
	1
agg aga aat gac tac gga tat agg gtg cct cta ttt cag ggc cct ctg	166
Arg Arg Asn Asp Tyr Gly Tyr Arg Val Pro Leu Phe Gln Gly Pro Leu	
5	10
cct ccc ccg ggg agc ctg ggg ctt ccc ttc cct cca gat ata cag act	214
Pro Pro Pro Gly Ser Leu Gly Leu Pro Phe Pro Pro Asp Ile Gln Thr	
20	25
gag acc aca gaa gag gac agt gtc ctg ctg atg cat acc ctg ttg gcg	262
Glu Thr Thr Glu Glu Asp Ser Val Leu Leu Met His Thr Leu Leu Ala	
35	40
gca acc aag gac tcc ctg gcc atg gac cca cca gtt gtc aac cgg cct	310
Ala Thr Lys Asp Ser Leu Ala Met Asp Pro Pro Val Val Asn Arg Pro	
55	60
aag aaa agc aak acc aag aag gcc cct ata aag act att act rnn nct	358
Lys Lys Ser Xaa Thr Lys Lys Ala Pro Ile Lys Thr Ile Thr Xaa Xaa	
70	75
gca cct gct gcc cct cca gts cag ctg cca atg aga ttg cca cca aca	406
Ala Pro Ala Ala Pro Pro Val Gln Leu Pro Met Arg Leu Pro Pro Thr	
85	90
agc cca aaa taacttggca ggctttaaac ctgccagtca ttaccagat	455
Ser Pro Lys	
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tcattgtcaa gatcaagttc aatatcatcg cctctctcta cgactacaac cccaacctgg 180
caacctac atg aag cca gag atg tgg ggg aag tgc ctg gac tgc atc aat 230
Met Lys Pro Glu Met Trp Gly Lys Cys Leu Asp Cys Ile Asn
1 5 10
gag ctg atg gat atc ctg ttt gca aat ccc aac att ttt gtt gga gag 278
Glu Leu Met Asp Ile Leu Phe Ala Asn Pro Asn Ile Phe Val Gly Glu
15 20 25 30
aat att ctg gaa gag agt gag aac ctg cac aac gct gac cag cca ctg 326
Asn Ile Leu Glu Ser Glu Asn Leu His Asn Ala Asp Gln Pro Leu
35 40 45
cgt gtc cgt ggc tgc atc cta act ctg gtg gaa cga atg gat gaa gaa 374
Arg Val Arg Gly Cys Ile Leu Thr Leu Val Glu Arg Met Asp Glu Glu
50 55 60
ttt acc aaa ata atg caa aat act gac cct cac tcc caa gag tac gtg 422
Phe Thr Lys Ile Met Gln Asn Thr Asp Pro His Ser Gln Glu Tyr Val
65 70 75
gag cac ttg aag gat gag gcc cag gtg tgt gcc atc atc gag cgt gtg 470
Glu His Leu Lys Asp Glu Ala Gln Val Cys Ala Ile Ile Glu Arg Val
80 85 90
cag cgc tac ctg gas gna gaa ggg cac tac cga ggm ggt ctg ccg cat 518
Gln Arg Tyr Leu Xaa Xaa Glu Gly His Tyr Arg Gly Gly Leu Pro His
95 100 105 110
cta cct gct gcg cat cct gca cac cta cta caa gtt tgattacaag g 565
Leu Pro Ala Ala His Pro Ala His Leu Leu Gln Val
115 120

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caaagtataa ttatttttaga tgctaatttt gaatagtttta ttaaacagtt ataaat atg 119
Met
1
caa agt agc tgg cat gta gtg tca cgg att ttc tgg ata gag gaa gtg 167
Gln Ser Ser Trp His Val Val Ser Arg Ile Phe Trp Ile Glu Glu Val
5 10 15
att gga agt att cca ctt aaa gcc atg gaa tta gca ata gtt tgc ttt 215
Ile Gly Ser Ile Pro Leu Lys Ala Met Glu Leu Ala Ile Val Cys Phe
20 25 30
tta ata gaa ggc cca ttt gta aga atg ttg aaa ata tgt gta ccg ttt 263

Leu Ile Glu Gly Pro Phe Val Arg Met Leu Lys Ile Cys Val Pro Phe
 35 40 45
 aaa gra aaa gcn rgc ttt aaa agt grc ran caa aaa tac cct ttt tct 311
 Lys Xaa Lys Ala Xaa Phe Lys Ser Xaa Xaa Gln Lys Tyr Pro Phe Ser
 50 55 60 65
 ttt agt atg gtt tat ttt tct agg ttt tct gtc cct ccc tca gta gtg 359
 Phe Ser Met Val Tyr Phe Ser Arg Phe Ser Val Pro Pro Ser Val Val
 70 75 80
 aag agt ttt ctt tat tcc tgg cag tgt cag gaa tat tgg ttt gaa aag 407
 Lys Ser Phe Leu Tyr Ser Trp Gln Cys Gln Glu Tyr Trp Phe Glu Lys
 85 90 95
 ctg ttg gcc tat ctg gag ttt ggc ctt gtt aac cta gta ttc 449
 Leu Leu Ala Tyr Leu Glu Phe Gly Leu Val Asn Leu Val Phe
 100 105 110
 taaccagtta accagcctta gtatgcatta aaattgtatt gtccagaaag tttgtttctc 509
 attttctgca aattcttact ttgaaaatga atcaccacat agtatgnnct ttaaagcatt 569
 gacgcacaga caa 582

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 atgtcttcaa agccacagct gtt atg cca gat ggt cag ttt aaa gat atc agc 173
 Met Pro Asp Gly Gln Phe Lys Asp Ile Ser
 1 5 10
 ctg tct gac tac aaa gga aaa tat gtt gtg ttc ttc ttt tac cct ctt 221
 Leu Ser Asp Tyr Lys Gly Lys Tyr Val Val Phe Phe Phe Tyr Pro Leu
 15 20 25
 gac ttc acc ttt gtg tgc ccc acg gag atc att gct ttc agt gat agg 269
 Asp Phe Thr Phe Val Cys Pro Thr Glu Ile Ile Ala Phe Ser Asp Arg
 30 35 40
 gca gaa gaa ttt aag aaa ctc aac tgc caa gtg att ggt gct tct gtg 317
 Ala Glu Glu Phe Lys Lys Leu Asn Cys Gln Val Ile Gly Ala Ser Val
 45 50 55
 gat tct cac ttc tgt cat cta gca tgg gtc aat aca cct aag aaa caa 365
 Asp Ser His Phe Cys His Leu Ala Trp Val Asn Thr Pro Lys Lys Gln
 60 65 70
 gga gga ctg gga ccc atg aac att cct ttg gta tca gac ccg aag cgc 413
 Gly Gly Leu Gly Pro Met Asn Ile Pro Leu Val Ser Asp Pro Lys Arg
 75 80 85 90
 acc att gct cag gat tat ggg gtc tta aag gct gat gag gca tct cgt 461
 Thr Ile Ala Gln Asp Tyr Gly Val Leu Lys Ala Asp Glu Ala Ser Arg
 95 100 105
 tca ggg gcc ttt tta tca ttg atg ata rgg tat tct tcg gca gat cac 509
 Ser Gly Ala Phe Leu Ser Leu Met Ile Xaa Tyr Ser Ser Ala Asp His

110
tgt aaa tgacctc
Cys Lys

115

120

522

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tctgctacgg taacttcatac agcccgccaa g atg gcg atg caa gcg gcc aag 172
Met Ala Met Gln Ala Ala Lys
1 5
agg gcg aac att cga ctt cca cct gaa gta aat cgg ata ttg tat ata 220
Arg Ala Asn Ile Arg Leu Pro Pro Glu Val Asn Arg Ile Leu Tyr Ile
10 15 20
aga aat ttg cca tac aaa atc aca gct gaa gaa atg tat gat ata ttt 268
Arg Asn Leu Pro Tyr Lys Ile Thr Ala Glu Glu Met Tyr Asp Ile Phe
25 30 35
ggg aaa tat gga cct att cgt caa atc aga gtg ggg aac aca cct gaa 316
Gly Lys Tyr Gly Pro Ile Arg Gln Ile Arg Val Gly Asn Thr Pro Glu
40 45 50 55
act aga gga aca gct tat gtg gtc tat gag gac atc ttt gat gcc aag 364
Thr Arg Gly Thr Ala Tyr Val Val Tyr Glu Asp Ile Phe Asp Ala Lys
60 65 70
aat gca tgt gat cac cta tcg gga ttc aat gtt tgt aac aga tac ctt 412
Asn Ala Cys Asp His Leu Ser Gly Phe Asn Val Cys Asn Arg Tyr Leu
75 80 85
gtg gtt ttg tac tat aat gcc aac agg gca ttt cag aag atg gac aca 460
Val Val Leu Tyr Tyr Asn Ala Asn Arg Ala Phe Gln Lys Met Asp Thr
90 95 100
aag aag aag gag gaa cag ttg aag ctt ctc aag gag aaa tat ggc atc 508
Lys Lys Lys Glu Glu Gln Leu Lys Leu Leu Lys Glu Lys Tyr Gly Ile
105 110 115
aac aca gat cca cca aaa taaatgtttt ctacattttc atttggacta 556
Asn Thr Asp Pro Pro Lys
120 125
aatcccacga atgac 571

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<212> DNA
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Met Ala Asp Tyr Leu Ile Ser Gly Gly Thr Ser Tyr Val Pro Asp
1 5 10 15
gac gga ctc aca gca cag cag ctc ttc aac tgc gga gac ggc ctc acc 156
Asp Gly Leu Thr Ala Gln Gln Leu Phe Asn Cys Gly Asp Gly Leu Thr
20 25 30
tac aat gac ttt ctc att ctc cct ggg tac atc gac ttc act gca gac 204
Tyr Asn Asp Phe Leu Ile Leu Pro Gly Tyr Ile Asp Phe Thr Ala Asp
35 40 45
cag gtg gac ctg act tct gct ctg acc aag aaa atc act ctt aag acc 252
Gln Val Asp Leu Thr Ser Ala Leu Thr Lys Lys Ile Thr Leu Lys Thr
50 55 60
cca ctg gtt tcc tct ccc atg gac aca gtc aca gag gct ggg atg gcc 300
Pro Leu Val Ser Ser Pro Met Asp Thr Val Thr Glu Ala Gly Met Ala
65 70 75
ata gca atg gcg ctt aca ggc ggt att ggc ttc atc cac cac aac tgt 348
Ile Ala Met Ala Leu Thr Gly Gly Ile Gly Phe Ile His His Asn Cys
80 85 90 95
aca cct gaa ttc cag gcc aat gaa gtt cgg aaa gtg ang amm tat gaa 396
Thr Pro Glu Phe Gln Ala Asn Glu Val Arg Lys Val Xaa Xaa Tyr Glu
100 105 110
cag gga ttc atc aca gac cct gtg gtc ctc agc ccc aag gat cgc gtg 444
Gln Gly Phe Ile Thr Asp Pro Val Val Leu Ser Pro Lys Asp Arg Val
115 120 125
cgg gat gtt ttt gag gca agg ccg gca tgg ttt ctg cgg tat ccc aat 492
Arg Asp Val Phe Glu Ala Arg Pro Ala Trp Phe Leu Arg Tyr Pro Asn
130 135 140
cac ara cac agg ccg gat ggg gar ccg ctg gtg gca wca tct cct mma 540
His Xaa His Arg Pro Asp Gly Glu Pro Leu Val Ala Xaa Ser Pro Xaa
145 150 155
gga cat tgatttct 554
Gly His
160

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<212> DNA
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<222> 113..490

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cctcccttct tccgagcctc tcctctggcc gccgcgcggg agagaggccg ag atg gca 118
Met Ala
1
gat gag att gcc aag gct cag gtc gct cgg cct ggt ggc gac acg atc 166

004220" 666E T560

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Phe	Gly	Lys	Ile	Ile	Arg	Lys	Glu	Ile	Pro	Ala	Lys	Ile	Ile	Phe	Glu		
	20					25					30						
gat	gac	cgg	tgc	ctt	gct	ttc	cat	gac	att	tcc	cct	caa	gca	cca	aca	262	
Asp	Asp	Arg	Cys	Leu	Ala	Phe	His	Asp	Ile	Ser	Pro	Gln	Ala	Pro	Thr		
	35				40				45						50		
cat	ttt	ctg	gtg	ata	ccc	aag	aaa	cat	ata	tcc	cag	att	tct	gtg	gca	310	
His	Phe	Leu	Val	Ile	Pro	Lys	Lys	His	Ile	Ser	Gln	Ile	Ser	Val	Ala		
			55						60					65			
gaa	gat	gat	gat	gaa	agt	ctt	ctt	gga	cac	tta	atg	att	gtt	ggc	aag	358	
Glu	Asp	Asp	Asp	Glu	Ser	Leu	Leu	Gly	His	Leu	Met	Ile	Val	Gly	Lys		
			70					75				80					
aaa	tgt	gct	gct	gat	ctg	ggc	ctg	aat	aag	ggg	tat	cga	atg	gtg	gtg	406	
Lys	Cys	Ala	Ala	Asp	Leu	Gly	Leu	Asn	Lys	Gly	Tyr	Arg	Met	Val	Val		
		85				90					95						
aat	gaa	ggg	tca	gat	ggg	gga	cag	tct	gtc	tat	cac	gtt	cat	ctc	cat	454	
Asn	Glu	Gly	Ser	Asp	Gly	Gly	Gln	Ser	Val	Tyr	His	Val	His	Leu	His		
	100					105				110							
gtt	ctt	gga	ggg	cgg	caa	atg	cat	tgg	cct	cct	ggg	taagcaggtt				500	
Val	Leu	Gly	Gly	Arg	Gln	Met	His	Trp	Pro	Pro	Gly						
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					Met												
					1												
gct	caa	gag	ttt	gtg	aac	tgc	aaa	atc	cag	cct	ggg	aag	gtg	gtt	gtg	166	
Ala	Gln	Glu	Phe	Val	Asn	Cys	Lys	Ile	Gln	Pro	Gly	Lys	Val	Val	Val		
			5					10					15				
ttc	atc	aag	ccc	acc	tgc	ccg	tac	tgc	agg	agg	gcc	caa	gag	atc	ctc	214	
Phe	Ile	Lys	Pro	Thr	Cys	Pro	Tyr	Cys	Arg	Arg	Ala	Gln	Glu	Ile	Leu		
		20				25					30						
agt	caa	ttg	ccc	atc	aaa	caa	ggg	ctt	ctg	gaa	ttt	gtc	gat	atc	aca	262	
Ser	Gln	Leu	Pro	Ile	Lys	Gln	Gly	Leu	Leu	Glu	Phe	Val	Asp	Ile	Thr		
		35			40					45							
gcc	acc	aac	cac	act	aac	gag	att	caa	gat	tat	ttg	caa	cag	ctc	acg	310	
Ala	Thr	Asn	His	Thr	Asn	Glu	Ile	Gln	Asp	Tyr	Leu	Gln	Gln	Leu	Thr		
	50				55				60					65			
gga	gca	aga	acg	gtg	cct	cga	gtc	ttt	aty	ggg	aaa	gat	tgt	ata	ggc	358	

Gly Ala Arg Thr Val Pro Arg Val Phe Ile Gly Lys Asp Cys Ile Gly
70 75 80
gga tgc agt gat cta gtc tct ttg caa cag agt ggg gaa ctg ctg acg 406
Gly Cys Ser Asp Leu Val Ser Leu Gln Gln Ser Gly Glu Leu Leu Thr
85 90 95
cgg cta aag cag att gga gct ctg cag taaccacaga tctcatagga 453
Arg Leu Lys Gln Ile Gly Ala Leu Gln
100 105
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tagttg 519

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Asn Ile Thr Glu Leu Asn Leu Pro Gln Leu Glu Met Leu Lys Asn Gln
10 15 20
ctg gac cag gaa gtg gag ttc ttg tcc acg tcc att gct cag ctc aaa 152
Leu Asp Gln Glu Val Glu Phe Leu Ser Thr Ser Ile Ala Gln Leu Lys
25 30 35
gtg gta cag acc aag tat gtg gaa gcc aag gac tgt ctg aac gtg ctg 200
Val Val Gln Thr Lys Tyr Val Glu Ala Lys Asp Cys Leu Asn Val Leu
40 45 50
aac aag agc aac gag ggg aaa gaa tta ctc gtc cca ctg acg agt tct 248
Asn Lys Ser Asn Glu Gly Lys Glu Leu Leu Val Pro Leu Thr Ser Ser
55 60 65
atg tat gtc cct ggg aag ctg cat gat gtg gaa cac gtg ctc atc gat 296
Met Tyr Val Pro Gly Lys Leu His Asp Val Glu His Val Leu Ile Asp
70 75 80 85
gtg gga act ggg tac tat gta gag aag aca gct gag gat gcc aag gac 344
Val Gly Thr Gly Tyr Tyr Val Glu Lys Thr Ala Glu Asp Ala Lys Asp
90 95 100
ttc ttc aag agg aag ata gat ttt cta acc aag cag atg gag aaa atc 392
Phe Phe Lys Arg Lys Ile Asp Phe Leu Thr Lys Gln Met Glu Lys Ile
105 110 115
caa cca gct ctt cag gag aag cac gcc atg aaa cag gcc gtc atg gaa 440
Gln Pro Ala Leu Gln Glu Lys His Ala Met Lys Gln Ala Val Met Glu
120 125 130
atg atg agt cag aag att cag cag ctc aca gcc ctg ggg gca gct cag 488
Met Met Ser Gln Lys Ile Gln Gln Leu Thr Ala Leu Gly Ala Ala Gln
135 140 145
gct act gct aag gcc tgagagtttt tgcagaaatg gggcagaggg acaccctttg 543
Ala Thr Ala Lys Ala

150
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598

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ttcttacaac ctccaggc atg cgt ctt tct gcc ctg ctg gcc ttg gca tcc 171
Met Arg Leu Ser Ala Leu Leu Ala Leu Ala Ser
1 5 10
aag gtc act ctg ccc ccc cat tac cgc tat ggg atg agc ccc cca ggc 219
Lys Val Thr Leu Pro Pro His Tyr Arg Tyr Gly Met Ser Pro Pro Gly
15 20 25
tct gtt gca gac aag agg aag aac ccc cca tgg atc agg cgg cgc cca 267
Ser Val Ala Asp Lys Arg Lys Asn Pro Pro Trp Ile Arg Arg Arg Pro
30 35 40
gtg gtt gtg gaa ccc atc tct gat gaa gac tgg tat ctg ttc tgt ggg 315
Val Val Val Glu Pro Ile Ser Asp Glu Asp Trp Tyr Leu Phe Cys Gly
45 50 55
gac acg gtg gag atc cta gaa ggc aag gat gcc ggg aag cag ggc aaa 363
Asp Thr Val Glu Ile Leu Glu Gly Lys Asp Ala Gly Lys Gln Gly Lys
60 65 70 75
gtg gtt caa gtt atc cgg cag cga aac tgg gtg gtc gtg gga ggg ctg 411
Val Val Gln Val Ile Arg Gln Arg Asn Trp Val Val Val Gly Gly Leu
80 85 90
aac aca cat tac cgc tac att ggc aag acc atg gat tac cgg gga aca 459
Asn Thr His Tyr Arg Tyr Ile Gly Lys Thr Met Asp Tyr Arg Gly Thr
95 100 105
tgatcctagt gaagcccct 478

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Met Ala
1

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00513939 "022400

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Glu Lys Pro Lys Leu His Tyr Phe Asn Ala Arg Gly Arg Met Glu Ser	
5 10 15	
acc cgg tgg ctc ctg gct gca gct gga gta gag ttt gaa gag aaa ttt	214
Thr Arg Trp Leu Leu Ala Ala Ala Gly Val Glu Phe Glu Glu Lys Phe	
20 25 30	
ata aaa tct gca gaa gat ttg gac aag tta aga aat gat gga tat ttg	262
Ile Lys Ser Ala Glu Asp Leu Asp Lys Leu Arg Asn Asp Gly Tyr Leu	
35 40 45 50	
atg ttc cag caa gtg cca atg gtt gag att gat ggg atg aag ctg gtg	310
Met Phe Gln Gln Val Pro Met Val Glu Ile Asp Gly Met Lys Leu Val	
55 60 65	
cag acc aga gcc att ctc aac tac att gcc agc aaa tac aac ctc tat	358
Gln Thr Arg Ala Ile Leu Asn Tyr Ile Ala Ser Lys Tyr Asn Leu Tyr	
70 75 80	
ggg aaa gac ata aag gag aga gcc ctg att gat atg tat ata gaa ggt	406
Gly Lys Asp Ile Lys Glu Arg Ala Leu Ile Asp Met Tyr Ile Glu Gly	
85 90 95	
ata gca gat ttg ggt gaa atg atc ctc ctt ctg ccc gta tgt cca cct	454
Ile Ala Asp Leu Gly Glu Met Ile Leu Leu Leu Pro Val Cys Pro Pro	
100 105 110	
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Glu Glu Lys Met Pro Ser Leu Pro	
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ctctctggag accctcggcg gtggttgctg tattttgact tggagtaagg atg act	176
Met Thr	
1	
ttt cgg gcc aca gat agt gaa ttt gac ctg aca aat att gaa gag tat	224
Phe Arg Ala Thr Asp Ser Glu Phe Asp Leu Thr Asn Ile Glu Glu Tyr	
5 10 15	
gcc gaa aat tct gca ctt tca aga ctg aat aat ata aaa gcc awa caa	272
Ala Glu Asn Ser Ala Leu Ser Arg Leu Asn Asn Ile Lys Ala Xaa Gln	
20 25 30	
aga gtg agt nat gtg aca tcc aca gaa aat gaa tct gat aca caa atc	320
Arg Val Ser Xaa Val Thr Ser Thr Glu Asn Glu Ser Asp Thr Gln Ile	
35 40 45 50	
cta acg ttt agg cac att acw aaa gct cag gag aag aca agw waa cga	368
Leu Thr Phe Arg His Ile Thr Lys Ala Gln Glu Lys Thr Xaa Xaa Arg	
55 60 65	
ywg cag cct ata aaa cta gag cct ttg gta agt tca aaa acc att gtk	416

Xaa Gln Pro Ile Lys Leu Glu Pro Leu Val Ser Ser Lys Thr Ile Val
70 75 80
tta gcc tct gta gcc aca gmg gam gyn gta aaa ttg ctt tgg agg ata 464
Leu Ala Ser Val Ala Thr Xaa Xaa Xaa Val Lys Leu Leu Trp Arg Ile
85 90 95
gaa gtc atg tcc aga ctc tgaa 486
Glu Val Met Ser Arg Leu
100

<210> 3981
<211> 382
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 44..367

<400> 3981
aggatccggc gccgaatcac tgactggcac aggtgttggg aaa atg atc cac agt 55
Met Ile His Ser
1
cta ttt ctc ata aac tgt tcc ggt gac ata ttt cta gag aag cac tgg 103
Leu Phe Leu Ile Asn Cys Ser Gly Asp Ile Phe Leu Glu Lys His Trp
5 10 15 20
aag agc gtt gtg agc cag tct gtc tgt gat tat ttc ttt gaa gct caa 151
Lys Ser Val Val Ser Gln Ser Val Cys Asp Tyr Phe Phe Glu Ala Gln
25 30 35
gag aaa gct gct gat gtt gaa aat gta cca cct gtc att tca aca cct 199
Glu Lys Ala Ala Asp Val Glu Asn Val Pro Pro Val Ile Ser Thr Pro
40 45 50
cac cac tac ctc atc agt atc tac cgg gat aag ctc ttc ttt gta tct 247
His His Tyr Leu Ile Ser Ile Tyr Arg Asp Lys Leu Phe Phe Val Ser
55 60 65
gtc ata cag acc gaa gtg cca cct ctc ttt gta att grn gtt cct aca 295
Val Ile Gln Thr Glu Val Pro Pro Leu Phe Val Ile Xaa Val Pro Thr
70 75 80
tcc gag ttg ctg aca ctt ttc agg act act ttg gtg agt gtt cag agg 343
Ser Glu Leu Leu Thr Leu Phe Arg Thr Thr Leu Val Ser Val Gln Arg
85 90 95 100
ctg caa tta agg awa atg tgg tca tagtatatga actct 382
Leu Gln Leu Arg Xaa Met Trp Ser
105

<210> 3982
<211> 509
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 125..505

004220"666EFS60

<400> 3982
 attgtgcggc tcctactaaa cggaaggggc cgggagaggc cgcgttcagt cgggtcccgg 60
 cagcggctgc agcgtctcgc tcttctgcgg ctctcgggtgc cctctccttt tcgtttccgg 120
 aaac atg gcc tcc ggt gtg gct gtc tct gat ggt gtc atc aag gtg ttc 169
 Met Ala Ser Gly Val Ala Val Ser Asp Gly Val Ile Lys Val Phe
 1 5 10 15
 aac gac atg aag gtg cgt aag tct tca acg cca gag gag gtg aag aag 217
 Asn Asp Met Lys Val Arg Lys Ser Ser Thr Pro Glu Glu Val Lys Lys
 20 25 30
 cgc aag aag gcg gtg ctc ttc tgc ctg agt gag gac aag aag aac atc 265
 Arg Lys Lys Ala Val Leu Phe Cys Leu Ser Glu Asp Lys Lys Asn Ile
 35 40 45
 atc ctg gag gag ggc aag gag atc ctg gtg ggc gat gtg ggc cag act 313
 Ile Leu Glu Glu Gly Lys Glu Ile Leu Val Gly Asp Val Gly Gln Thr
 50 55 60
 gtc gac gay ccc tac gcc acc ttt gtc aag atg ctg cca gat aag gac 361
 Val Asp Asp Pro Tyr Ala Thr Phe Val Lys Met Leu Pro Asp Lys Asp
 65 70 75
 tgc cgc tat gcc ctc tat gat gca acc tat gag acc aag gag agc aag 409
 Cys Arg Tyr Ala Leu Tyr Asp Ala Thr Tyr Glu Thr Lys Glu Ser Lys
 80 85 90 95
 aag gag gat ctg gtg ttt atc ttc tgg gcc ccw gag tct gcg ccc ctt 457
 Lys Glu Asp Leu Val Phe Ile Phe Trp Ala Pro Glu Ser Ala Pro Leu
 100 105 110
 aag agc aaa atg att tat gcc agc tcc aag rcg cca tca aga aga agc 505
 Lys Ser Lys Met Ile Tyr Ala Ser Ser Lys Xaa Pro Ser Arg Arg Ser
 115 120 125
 tgac 509

<210> 3983
 <211> 467
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 39..422

<400> 3983
 gcaaaggggt ggggttgtgg agtggatgct ttggcaag atg gcg ggg agc ggc gtc 56
 Met Ala Gly Ser Gly Val
 1 5
 cgc caa gyt act tct acc gcc agc acc ttc gtg aag ccc att ttc agt 104
 Arg Gln Xaa Thr Ser Thr Ala Ser Thr Phe Val Lys Pro Ile Phe Ser
 10 15 20
 cgg gac atg aac gag gcc aag cgg agg gtg cgc gag ctc tac cgc gcc 152
 Arg Asp Met Asn Glu Ala Lys Arg Arg Val Arg Glu Leu Tyr Arg Ala
 25 30 35
 tgg tat cgg gag gtg ccg aac act gtg cac caa ttc cag ctg gac atc 200
 Trp Tyr Arg Glu Val Pro Asn Thr Val His Gln Phe Gln Leu Asp Ile
 40 45 50
 act gtg aaa atg gga cgg gat aaa gtc cga gaa atg ttt atg aag aat 248

Thr Val Lys Met Gly Arg Asp Lys Val Arg Glu Met Phe Met Lys Asn
55 60 65 70
gcc cat gtc aca gac ccc agg gtg gtt gat ctt ctg gtc att aag gga 296
Ala His Val Thr Asp Pro Arg Val Val Asp Leu Leu Val Ile Lys Gly
75 80 85
aag atc gaa ctg gaa gaa aca att aaa gta tgg aag cag cgg aca cat 344
Lys Ile Glu Leu Glu Glu Thr Ile Lys Val Trp Lys Gln Arg Thr His
90 95 100
gtt atg cgg ttc ttc cat gaa aca gaa gcg cca agg cca aag gat ttc 392
Val Met Arg Phe Phe His Glu Thr Glu Ala Pro Arg Pro Lys Asp Phe
105 110 115
cta tcc aag ttc tat gtt ggc cac gat cca tgaagtcatt cagtggaaag 442
Leu Ser Lys Phe Tyr Val Gly His Asp Pro
120 125
atgcacgttg atactatttt agagc 467

<210> 3984
<211> 456
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 31..390

<400> 3984
tcctttccgc ttccggtgtc ccctacagtc atg gct gcc gcc gtc gct gct gcc 54
Met Ala Ala Ala Val Ala Ala Ala
1 5
ggt gca ggg gaa ccc cag tcc ccg gac gaa ttg ctc ccg aaa ggc gac 102
Gly Ala Gly Glu Pro Gln Ser Pro Asp Glu Leu Leu Pro Lys Gly Asp
10 15 20
gcg gag aag cct gag gag gag ctg gag gag gac gac gat gag gag cta 150
Ala Glu Lys Pro Glu Glu Leu Glu Glu Asp Asp Asp Glu Glu Leu
25 30 35 40
gat gag acc ctg tcg gag aga cta tgg ggc ctg acg gag atg ttt ccg 198
Asp Glu Thr Leu Ser Glu Arg Leu Trp Gly Leu Thr Glu Met Phe Pro
45 50 55
gag agg gtc cgg tcc gcg gcc gga gcc act ttt gat ctt tcc ctc ttt 246
Glu Arg Val Arg Ser Ala Ala Gly Ala Thr Phe Asp Leu Ser Leu Phe
60 65 70
gtg gct cag aaa atg tac agg ttt tcc agg gca gcc ttg tgg att ggg 294
Val Ala Gln Lys Met Tyr Arg Phe Ser Arg Ala Ala Leu Trp Ile Gly
75 80 85
acc act tcc ttt atg atc ctg gtt ctt ccc gtt gtc ttt gag acg gag 342
Thr Thr Ser Phe Met Ile Leu Val Leu Pro Val Val Phe Glu Thr Glu
90 95 100
aag ttg caa atg gag caa cag cag caa ctn ngc agc ggc aga tac ttc 390
Lys Leu Gln Met Glu Gln Gln Gln Gln Leu Xaa Ser Gly Arg Tyr Phe
105 110 115 120
taggacctaa cacagggttc tcaggaggaa tgccaggggc tctamcctca cttcctggaa 450
agatct 456

<210> 3985
 <211> 490
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 95..481

<400> 3985
 actaggggac tccgcctctc ccgatttcct ccgggctaca ggcgacagag ctgagccaag 60
 cgtttactgg gcagctgtta cgctcagatt ccaa atg aaa atg ttt gag agc gct 115
 Met Lys Met Phe Glu Ser Ala
 1 5
 gac tct aca gcc aca aga tct ggc cag gat ctc tgg gct gaa att tgt 163
 Asp Ser Thr Ala Thr Arg Ser Gly Gln Asp Leu Trp Ala Glu Ile Cys
 10 15 20
 tcc tgt ctg cca aat cct gaa caa gaa gat ggt gcc aac aat gca ttc 211
 Ser Cys Leu Pro Asn Pro Glu Gln Glu Asp Gly Ala Asn Asn Ala Phe
 25 30 35
 tca gac tcc ttt gtg gat tct tgc cct gaa ggt gaa ggc cag agg gag 259
 Ser Asp Ser Phe Val Asp Ser Cys Pro Glu Gly Glu Gly Gln Arg Glu
 40 45 50 55
 gtg gct gac ttt gct gtc cag cca gct gta aag cct tgg gct ccc ttg 307
 Val Ala Asp Phe Ala Val Gln Pro Ala Val Lys Pro Trp Ala Pro Leu
 60 65 70
 cag gat tca gaa gtg tat tta gca tct cta gag aag aag cta aga aga 355
 Gln Asp Ser Glu Val Tyr Leu Ala Ser Leu Glu Lys Lys Leu Arg Arg
 75 80 85
 atc aaa ggt tta aat cag gaa gtg act tcc aag gac atg ctt cga act 403
 Ile Lys Gly Leu Asn Gln Glu Val Thr Ser Lys Asp Met Leu Arg Thr
 90 95 100
 ctg ggc cca agc caa gaa gga atg ctg gga tgc gtt cct cca gga gaa 451
 Leu Gly Pro Ser Gln Glu Gly Met Leu Gly Ser Val Pro Pro Gly Glu
 105 110 115
 gtt agc ttc aga gtt ctt tgt gga tgg act tgattctga 490
 Val Ser Phe Arg Val Leu Cys Gly Trp Thr
 120 125

<210> 3986
 <211> 483
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 114..431

<400> 3986
 gacttgcttc cagacaaagg ttgtctcaag tttgttgctc aaaccgagtt ctggagaacg 60
 ccatcagctc gctgcttaaa attaaaccac aggttcatt atgggtcgac ttg atg 116
 Met

004220-666T560

ggc aaa gtc atc atc ctg acg gcc gct gct cag ggg att ggc caa gca 164
 Gly Lys Val Ile Ile Leu Thr Ala Ala Gln Gly Ile Gly Gln Ala
 5 10 15
 gct gcc tta gct ttt gca aga gaa ggt gcc aaa gtc ata gcc aca gac 212
 Ala Ala Leu Ala Phe Ala Arg Glu Gly Ala Lys Val Ile Ala Thr Asp
 20 25 30
 att aat gag tcc aaa ctt cag gaa ctg gaa aag tac ccg ggt att caa 260
 Ile Asn Glu Ser Lys Leu Gln Glu Leu Glu Lys Tyr Pro Gly Ile Gln
 35 40 45
 act cgt gtc ctt gat gtc aca aag aag aaa caa att gat cag ttt gcc 308
 Thr Arg Val Leu Asp Val Thr Lys Lys Lys Gln Ile Asp Gln Phe Ala
 50 55 60 65
 aat gaa gtt gag aga ctt gat gtt ctc ttt aat gtt gct ggt ttt gtc 356
 Asn Glu Val Glu Arg Leu Asp Val Leu Phe Asn Val Ala Gly Phe Val
 70 75 80
 cat cat gga act gtc ctg gat tgt gag gag aaa gac tgg gac ttc tcg 404
 His His Gly Thr Val Leu Asp Cys Glu Glu Lys Asp Trp Asp Phe Ser
 85 90 95
 atg aat ctc aat gtg cgc asa tgt acc tgatgatcaa ggcattcctt 451
 Met Asn Leu Asn Val Arg Xaa Cys Thr
 100 105
 cctaaaatgc ttgctcagaa atctggcaat at 483

 <210> 3987
 <211> 400
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> CDS
 <222> 55..393

 <400> 3987
 aatcgacgcc ggaagtagca attactagac aagcattccg ccgccggctt cgct atg 57
 Met
 1
 gcg gca att ccc cca gat tcc tgg cag cca ccc aac gtt tac ttg gag 105
 Ala Ala Ile Pro Pro Asp Ser Trp Gln Pro Pro Asn Val Tyr Leu Glu
 5 10 15
 acc agc atg gga atc att gtg ctg gag ctg tac tgg aag cat gct cca 153
 Thr Ser Met Gly Ile Ile Val Leu Glu Leu Tyr Trp Lys His Ala Pro
 20 25 30
 aag acc tst aag aac ttt gct gag ttg gct cgt cga ggt tac tac aat 201
 Lys Thr Xaa Lys Asn Phe Ala Glu Leu Ala Arg Arg Gly Tyr Tyr Asn
 35 40 45
 ggc mca aaa ttc cac aga att atc aaa gac ttc atg atc caa gga ggt 249
 Gly Xaa Lys Phe His Arg Ile Ile Lys Asp Phe Met Ile Gln Gly Gly
 50 55 60 65
 gac cca aca ggg aca ggt cga ggt ggt gca tct atc tat ggc aaa cag 297
 Asp Pro Thr Gly Thr Gly Arg Gly Gly Ala Ser Ile Tyr Gly Lys Gln
 70 75 80
 ttt gaa gat gaa ctt cat cca gac ttg aaa ttc acg ggg gct gaa ttc 345

004220" 666T550

Phe Glu Asp Glu Leu His Pro Asp Leu Lys Phe Thr Gly Ala Glu Phe
 85 90 95
 tcg caa tgg cca atg cgg ggc cag ata cca ntg gca gcc agt tct ttg 393
 Ser Gln Trp Pro Met Arg Gly Gln Ile Pro Xaa Ala Ala Ser Ser Leu
 100 105 110
 tgacctc 400

<210> 3988
 <211> 341
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 14..328

<400> 3988
 agtacttggg cgc atg cgg caa ccg tat ctc agt tct cgc gag gtt tcg 49
 Met Arg Gln Pro Tyr Leu Ser Ser Arg Glu Val Ser
 1 5 10
 tct tcc cgg aag cgt tgg agg aca ttc cct gtt gac tgc gtc gcg atg 97
 Ser Ser Arg Lys Arg Trp Arg Thr Phe Pro Val Asp Cys Val Ala Met
 15 20 25
 tgt ggc gac tgt gtg gag aag gaa tat ccc aac cgg ggt aat acc tgc 145
 Cys Gly Asp Cys Val Glu Lys Glu Tyr Pro Asn Arg Gly Asn Thr Cys
 30 35 40
 ctg gag aat gga tct ttc tta ctg aac ttt aca ggc tgt gca gtg tgc 193
 Leu Glu Asn Gly Ser Phe Leu Leu Asn Phe Thr Gly Cys Ala Val Cys
 45 50 55 60
 agt aag cgg gat ttt atg ctg atc aca aac aaa tcc ttg awa gaw gaa 241
 Ser Lys Arg Asp Phe Met Leu Ile Thr Asn Lys Ser Leu Xaa Xaa Glu
 65 70 75
 gat gga gaa gaw ata gtt acc tat gat cga gta tac cat gct gtg tct 289
 Asp Gly Glu Xaa Ile Val Thr Tyr Asp Arg Val Tyr His Ala Val Ser
 80 85 90
 gtt atg cgg caa agc cga aga tac tat cag tat tct ccc tgatgacccc 338
 Val Met Arg Gln Ser Arg Arg Tyr Tyr Gln Tyr Ser Pro
 95 100 105
 cga 341

<210> 3989
 <211> 596
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 6..371

<400> 3989
 aaaaa atg cct cat ccc tac tcc aga aac gag aac aac gga ggc aga gga 50
 Met Pro His Pro Tyr Ser Arg Asn Glu Asn Asn Gly Gly Arg Gly